A STUDY OF SOME GENOTYPE x ENVIRONMENT INTERACTIONS IN PIG PRODUCTION

by

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March 1976
DECLARATION

I declare that this thesis has been composed by myself and that the work it contains is my own.

[Signature]

[Name: W. Thorne]
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SUMMARY

The study comprised five genotype x feeding level interaction experiments with 1404 bacon pigs and one genotype x protein level interaction experiment with 806 pork and 752 heavy hog pigs.

The feeding level experiments used crossbred fattening pigs from an experiment evaluating the performance of the Hampshire, Pietrain, Lacombe, Large White, Landrace and Wessex breeds. The feeding regimes were ad libitum and a scale with a maximum of 5 lbs/pig/day. In addition, in the fourth and fifth experiments a pair of pigs were fed to appetite at a MLC test station. There were no statistically significant growth efficiency interactions and only occasional interactions for carcass composition characters. To increase the power of the statistical test for interaction, the third, fourth and fifth experiments were combined in an analysis of 488 crossbred progeny sired by Large White and Hampshire/Pietrain boars. There were no sire genotype x feeding levels interactions and it was concluded that, within the crossbred comparisons, genotype x feeding level interactions were not important.

The protein level experiment compared progeny of Wessex, Essex, Pietrain and Landrace sires out of Large White dams and progeny of the reciprocal Wessex cross with control herd Large White progeny. The progeny were fed ad libitum diets of high and low protein concentrations. Subsamples of each group (447 pork and 423 heavy hog pigs) were dissected. Of the possible 62 genotype x protein level interactions at each
slaughter weight, there were only 2 at pork weight and 3 at heavy hog weight which were statistically significant. The interactions were not consistent at the two slaughter weights and it was concluded that interactions of genotype and protein level were unimportant.

Problems in genotype x nutrition interaction experimentation and the possible influence of appetite, lean tissue growth rate and daily maintenance requirement variation on the incidence of interaction between genotype and nutrition were discussed.
I wish to acknowledge my gratitude to Dr. J.W.B. King for suggesting the topic of this study and for his guidance and constructive criticism throughout its development.

I am also indebted to Dr. King and his predecessor, Professor H.P. Donald, for allowing me to use the facilities of the A.R.C. Animal Breeding Research Organisation and to Professor N.F. Robertson for acting as my University supervisor.

In addition, I am extremely grateful to members of the staff of A.B.R.O. and especially my fellow postgraduates, A.J. Webb, B.J. McGuirk and C.A. Morris, for their encouragement and advice.

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The Ministry of Overseas Development provided the studentship which enabled me to undertake this work.
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CHAPTER 1

INTRODUCTION

The genetic diversity among the world's pig breeds is a resource of great potential value for the genetic improvement of British pig production. Use of this resource is, however, difficult as breeds are generally localised and the objective comparative information necessary for optimum breed utilisation is often lacking. Breed differences have remained largely undefined and the evaluation of indigenous and exotic breeds has only come to the fore in recent years.

The selection of promising breeds should ideally be based on comparisons using criteria consistent with both biological objectives and efficient management systems. In making breed comparisons it is necessary to consider if the ranking of genotypes is dependent upon particular environmental factors. If such dependencies are found, they complicate decision making but do imply that specific combinations of genotype and management systems should lead to yet more efficient production. Experimentally these questions are answered by the estimation of genotype x environment interaction, which is simply the change in relative performance of two or more genotypes measured in two or more environments (Haldane, 1946).

The experiments reported here investigate possible interactions between major environmental sources of variation and genotypes derived from indigenous and exotic pig breeds. The study aims to test the consistency of the genotypes over different environments and the suitability of these genotypes and environments for production purposes. Following examination of the results, particularly in respect of component characters, the implications of the genotype x environment interactions are discussed.
CHAPTER 2

REVIEW

2.1 Theoretical basis

The estimation of genotypes from phenotypic performance is the basis of all genetic improvement. If the effects of genotype and environment on the phenotype are additive, the evaluation of genotypes can be made simply, but complications arise where there are non-additive effects of genotype and environment which are referred to as genotype x environment interactions. The interaction may involve changes in rank order for genotypes between environments and changes in the absolute and relative magnitude of the genetic and environmental variances between environments (Bowman, 1972).

The importance of these interactions in pig production lies in their practical implications for selection between and within breeds. Classification therefore requires a statement of type and of statistical significance. Pani (1971) has formulated a classification, shown in Figure 2.1, to meet these requirements. If we assume that experiments are designed on a sufficient scale so that changes of a magnitude likely to be economically important will also be statistically significant, then the practically important interactions are types 3 and 4.

When many genotypes are compared type 3 interactions, which show changes in scale, are important because (1) reduced genetic variance will decrease ranking accuracy and therefore increase the chances of inferior genotypes being selected, and (2) the change in genetic and environmental variance may reduce
FIG. 2.1 A CLASSIFICATION OF GENOTYPE X ENVIRONMENT INTERACTION

(PANI, 1971)
heritability and therefore decrease the rate of genetic improvement possible by intra-population selection. In addition, small differences in response shown in one generation may accumulate through selection to produce an interaction of important magnitude. Measurement of type 3 interaction therefore requires the estimation of heritability and genetic correlations or a dynamic approach with selection experiments.

Pani's (1971) type 4 interaction corresponds to the type 4 of Haldane's (1946) classification and is the classical genotype x environment interaction in which genotype ranking depends on the environment used for the comparison. For example, genotype A is superior to genotype B in environment X but inferior in environment Y (Figure 2.1). This interaction has particular relevance to comparisons of breeds and crosses because, in these circumstances, only the changes in rank order and of phenotypic variance are important, the former as the criterion of merit and the latter for its effect on experimental sensitivity. In this case factorial experiments (Fisher, 1955) are suitable.

2.2 Experimental results

The dynamic approach to the study of genotype x environment interactions in pig production occurs only once in the literature, a selection experiment by Fowler and Ensminger (1960). King (1972a) has pointed out that the reported differences between the selection lines are subject to large sampling errors and therefore the experiment cannot be taken as definitive. Experimentation with other species may give a possible basis for explaining and predicting genotype x environment interactions in pig production. From his review of the evidence
Kempster (1974) concludes that the studies with mice and rats give little support for a general theory, but Bateman (1974) considers that of two equally selected strains developed in two environments, the better strain will be the one selected under the less favourable conditions.

The majority of pig studies are factorial experiments principally concerned with the relative performances of different genotypes on different nutritional treatments. Level of feeding, dietary energy and protein levels and minor dietary differences are the main environmental contrasts chosen by experimenters and many different genotypes have been exposed to many different nutritional treatments. Unfortunately, the arbitrary choice of the genotype x nutrition combinations means that the range of treatments give little indication of the principles underlying pig genotype x nutrition interaction. In addition, the incidence of significant interactions must be judged against the random level expected at the appropriate significance level. King (1972a) has also noted that some selection of published data is possible which may have created a bias towards positive genotype x nutrition interactions.

The implications of the available factorial evidence must therefore be assessed with these limitations in mind. King (1972a), in his review, attempted such an assessment and concluded that serious errors in genotype comparisons were unlikely through the neglect of possible interactions. However, he suggested that geneticists and nutritionalists should expand the range of genotypes and environments they use to include, for example, the
crossbreds in contemporary use. This would make possible an appreciation of the importance of interactions although the probability of detecting small interactions would be low. A criticism of this assessment and approach is that while the occurrence of interaction is accepted, and therefore differential responses may accumulate in alternative selection environments, no direct proposal to investigate their importance is suggested. Moreover, the possibility of accumulated differential responses emphasises the importance of understanding the biological processes governing genotype x nutrition interactions. Particularly important is the identification of the component characters explaining differential growth responses to dietary energy and protein concentrations.

Unfortunately, studies of possible protein level interactions are often complicated by appetite effects so that responses to different dietary protein levels are confounded with differences in protein intakes. Nevertheless, the experimental evidence suggests that interactions do occur with widely different protein levels, but around the recommended levels these interactions are much less likely.

Experiments with different feeding or energy levels can be assumed to have a common base as reduction in feeding level is likely to influence growth primarily by limiting energy intake. Interactions are frequently reported in these experiments, which have been reviewed by King (1972a) and Kempster (1974), and one can conclude that interactions, which occur predominantly for daily liveweight gain with some consequential effects on food conversion efficiency and carcass fatness, have practical significance.
The complex nature of daily liveweight gain was emphasised by Falconer and Latyszewski (1952) in their study of mice selected for daily liveweight gain on alternative feeding regimes. Differential selection responses could be rationalised by considering the effects in terms of the characters daily feed intake and food conversion efficiency. King (1972a) reiterated the rationalisation and suggested that where there are genetic differences for appetite, a comparison of ad libitum and a restricted feeding regime could give expression and suppression of the appetite variation. Interactions might result for average daily feed intake, a character seldom reported, and consequently for daily liveweight gain, the character most widely measured in interaction experiments.

Fowler's (1968) graphic presentation of the partition of metabolisable energy in the growing pig extends the growth concepts involved (Figure 2.2). Total energy is partitioned into daily maintenance requirement, lean (lean tissue + essential fat) and fat (variable fat). The model assumes that the metabolisable energy is derived from a dynamic pool with priorities rather than strict partitions. With increasing energy intake, energetic sufficiency for lean growth will be met and lean tissue response will rapidly diminish. Consequently lean growth will become a progressively smaller proportion of the total gain and fat deposition an increasing proportion. The greater energetic cost of fat compared to lean deposition (Kielanowski, 1972) will lead to decreased efficiency of feed utilisation.
FIGURE 2.2 PARTITION OF METABOLIZABLE ENERGY IN THE GROWING PIG ON AD LIBITUM FEEDING.

(FOWLER, 1968).
The principal growth components are therefore the pig's potential for lean gain and its appetite. The pig's appetite controls the total energy intake and lean gain the partitioning of the energy. Any genetic variation in daily maintenance requirement will also influence the partition of energy. However, it is only when feed restriction is severe that maintenance requirement will be a large proportion of the total energy balance. Only then will genetic variation for maintenance requirement make a significant contribution to interaction.

Genetic variation in appetite, lean gain and daily maintenance requirement does seem to provide a realistic basis for the interpretation of interactions found in genotype x nutrition experiments. By describing differential responses for growth in these terms, Kempster (1974) has been able to rationalize the interactions reported in certain experiments for the complex characters, daily liveweight gain and food conversion efficiency.

There are few direct estimates of the heritabilities of the main components of the model, lean gain and appetite, and it is assumed that both have moderate heritabilities (see e.g. Smith, King and Gilbert, 1962; Smith and Ross, 1965; Strang, 1969). Further estimates can be calculated from the parameters of their components (Turner and Young, 1969) and while no suitable parameters were found for lean gain, parameter estimates for the appetite components were available. The appetite heritability calculations are presented in Appendix I and gave estimates of 0.3 to 0.4. The assumed moderate heritabilities would seem justified.
That genetic variation exists for appetite and lean gain is therefore beyond question although the proportion of interaction variation attributable to each component character, including daily maintenance requirement, is uncertain. Moreover, estimates of genetic variation for maintenance requirement are limited (Chavossa, 1971; Sharma, Young and Smith, 1972) and estimates are required for the relevant correlation parameters, particularly with ad libitum feeding (Owen and Morton, 1969). Also, there is no evidence for genetic variation for the point at which energy restriction significantly reduces rate of lean gain (Davey, Morgan and Kincaid, 1969; Whittemore and Fawcett, 1976). Nevertheless by measuring, directly or indirectly, these component characters, the principles underlying genotype x nutrition interactions should be more clearly understood.

Among the many environmental factors that may be responsible for interactions, the effects of climate and disease are probably important in some circumstances. However the differential effects of climate are generally so extreme as not to require experimentation (King, 1972a) and, despite some experimental evidence to show breed differences in disease resistance, current veterinary practise with pigs tends to favour minimal disease conditions. Hence climatic factors are unlikely to play an important part in complicating inter- or intra-population selection and disease resistance will have a low priority as a criterion for selection or as a factor affecting the ranking of breeds for intensive conditions.
A programme of breed evaluation, which includes imported breeds, is in progress at the A.R.C. Animal Breeding Research Organisation (ABRO) and the breeds available for comparison include the Large White, British Landrace, British Saddleback, Hampshire, Pietrain, Lacombe, Duroc and American Yorkshire. The last five are exotic breeds imported between 1962 and 1970. There have been only piecemeal comparisons of the listed breeds; but from reports in the literature, breed performances can be characterised in a qualitative way expressing pure breed performance as deviations from the average performance of British Large Whites (Table 2.1). Breed differences for appetite (daily feed intake with ad libitum feeding) are presented, as well as the usual economic characters, e.g. daily liveweight gain, backfat thickness and litter traits.

The listed breeds represent a wide range of component characters, and the qualitative breed differences suggest, for example, that the Duroc and Pietrain breeds are extreme genotypes for appetite and lean gain and, as has been discussed earlier, this combination of characters may explain the incidence of some genotype x nutrition interactions.

The ABRO breed comparisons were made using 2 or more nutritional environments and, because of the range of component characters, the experiments provided information on which to assess the role of appetite and lean gain in genotype x nutrition interaction. In addition the experiments would show whether specific combinations of genotype and feeding regime gave more efficient production of lean pig meat.
Table 2.1.  Deviations of the purebred performance of indigenous and exotic breeds from the average performance of the British Large White breed.

<table>
<thead>
<tr>
<th></th>
<th>DAILY GAIN</th>
<th>FOOD CONVERSION EFFICIENCY</th>
<th>DAILY FEED INTAKE</th>
<th>BACKFAT THICKNESS</th>
<th>CARCASS LENGTH</th>
<th>EYE MUSCLE AREA</th>
<th>CARCASS LEAN %</th>
<th>MEAT QUALITY</th>
<th>LITTER TRAITS</th>
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<tbody>
<tr>
<td>LANDRACE</td>
<td>0/-</td>
<td>0/-</td>
<td>0/-</td>
<td>0</td>
<td>+</td>
<td>0</td>
<td>0</td>
<td>-</td>
<td>0</td>
</tr>
<tr>
<td>BRITISH SADDLEBACK</td>
<td>-</td>
<td>-</td>
<td>0</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>0</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>HAMPSHIRE</td>
<td>-</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>PIETRAIN</td>
<td>0/-</td>
<td>0/-</td>
<td>0</td>
<td>0</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>LAOCOMBE</td>
<td>+</td>
<td>0</td>
<td>+</td>
<td>0</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Duroc</td>
<td>+</td>
<td>-</td>
<td>+</td>
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A + sign means a deviation in the desirable direction; a - sign means an undesirable deviation; 0 means performance approximating to that of British Large White.
The study involved genotypes derived from the breeds presented in Table 2.1 and included genotype x feeding level interaction experiments which are reported in Chapter 3 and, in Chapter 4, a genotype x protein level interaction experiment. The conclusions drawn from the experiments are discussed in Chapter 5.
CHAPTER 3

INTERACTION BETWEEN CROSSBRED GENOTYPE AND FEEDING LEVEL FOR POST WEANING PERFORMANCE

The five genotype x feeding level interaction experiments to be described were a subsection of a series of experiments designed to ascertain the crossing ability of exotic and indigenous breeds. Possible genotype x feeding level interactions were studied by feeding crossbred fattening pigs at two or three levels. The comparisons used split-plot factorial designs with litters of a given genotype constituting the whole plots and feeding levels the subplot treatments.

Descriptions of the experiments, their materials, methods, results and discussion will be preceded by a general material and methods relevant to all experiments. A discussion of the genotype x feeding level experiments concludes the chapter.

3.1 Material and methods

Preweaning management

All pigs studied were farrowed, reared and weaned at ABRO's Pig Research Station, 'Mountmarle', Roslin, Midlothian, hereafter referred to as Mountmarle. Farrowing was usually in outdoor arks and pigs were identified at birth by ear notchings. Birth weights and sex were recorded. Male pigs were castrated, and given an erysipelas injection (Wellcome Swine Erysipelas Vaccine (A.T.)) at 50 days of age. A further erysipelas injection was given at 100 days of age. At 60 days litters were weaned and wormed with an I.C.I. wormer. Litters for the trials were transferred to a Danish-type finishing house at 74 days, or as near to that age as was possible.
Experimental housing

The house had four identical wings, each with twenty pens either side of a 5ft wide central feeding passage. Pen size was 5ft x 14ft, including a 3ft wide dunging passage. A feeding trough spanned the front width of the pen and water was always available from nipple drinkers in the dunging passage. Some straw bedding was used and pens were cleaned three times weekly.

Ventilation was manually controlled by means of side wall windows and electric ridge fans. Electric end-wall heaters helped ventilation to maintain a house temperature of 60-65°F (15.5-18.3°C). Temperature recordings were available for the house and wings generally had equivalent temperatures.

On transfer to the experimental accommodation all pigs were washed with a solution of Boot’s mange dressing (20% gamma BHC) and the experimental diets were immediately made available. Each pen contained a subplot of 3 or 4 pigs depending on litter size. The subplot groups were balanced as far as possible for initial weight and sex.

Nutrition

Acclimatisation to housing and diet lasted from the transfer until the pen mean liveweight reached 60 lbs. The experimental feeding levels were fed from this point and throughout the remainder of the experiment, that is until slaughter at about 200 lbs, live weight. In later experiments an additional subplot was submitted to a Meat and Livestock Commission (MLC) central test station and fed an MLC diet. Diet composition is given in Table 3.1.1 and chemical composition, derived by proximate analysis,
Table 3.1.1. Dietary ingredients (percentages of air dry weight)

<table>
<thead>
<tr>
<th>Ingredient*</th>
<th>Weaners (to 100 lbs. liveweight)</th>
<th>Fatteners (100 lbs. to slaughter)</th>
<th>M.L.C</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barley meal</td>
<td>30.0</td>
<td>65.0</td>
<td>60.0</td>
</tr>
<tr>
<td>Wheat meal</td>
<td>-</td>
<td>-</td>
<td>20.0</td>
</tr>
<tr>
<td>Weatlings (fine white thirds)</td>
<td>60.0</td>
<td>30.0</td>
<td>-</td>
</tr>
<tr>
<td>White fish meal</td>
<td>10.0</td>
<td>5.0</td>
<td>5.0</td>
</tr>
<tr>
<td>Extracted soya bean meal</td>
<td>-</td>
<td>-</td>
<td>12.5</td>
</tr>
<tr>
<td>Molasses</td>
<td>-</td>
<td>-</td>
<td>2.5</td>
</tr>
<tr>
<td>Copper (1¼ lbs. CuSO₄ per ton)*</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Vitamin-mineral supplements**</td>
<td>-</td>
<td>-</td>
<td>++</td>
</tr>
</tbody>
</table>

* Added to diet where shown by +
** Added to diet where shown by ++ and consisting of

- Di-Calcium Phosphate 0.75%
- Ground Limestone 0.5%
- Salt (NaCl) 0.25%
- Riboflavin 2.0g, Vitamin A 4.0 million I.U., Vitamin D 0.8 million I.U., Calcium Pantothenate 5.0g, Vitamin B₁₂ 15.0mg, Copper Sulphate 800g, Zinc Oxide 80g, Ferrous Sulphate 280g.

Table 3.1.2 Diets - Chemical Composition

<table>
<thead>
<tr>
<th>% Crude Protein</th>
<th>Weaners</th>
<th>Fatteners</th>
<th>M.L.C</th>
</tr>
</thead>
<tbody>
<tr>
<td>% Ether Extract</td>
<td>3.3</td>
<td>2.9</td>
<td>2.5</td>
</tr>
<tr>
<td>% Crude Fibre</td>
<td>2.4</td>
<td>4.5</td>
<td>4.5</td>
</tr>
<tr>
<td>% Nitrogen Free Extract</td>
<td>58.6</td>
<td>61.3</td>
<td>*</td>
</tr>
<tr>
<td>% Ash</td>
<td>5.2</td>
<td>5.9</td>
<td>*</td>
</tr>
<tr>
<td>% Moisture</td>
<td>12.7</td>
<td>15.4</td>
<td>13.0</td>
</tr>
<tr>
<td>Metabolisable energy (kcal/kg)</td>
<td>2.75</td>
<td>2.86</td>
<td>2.98</td>
</tr>
</tbody>
</table>

* Not available.
in Table 3.1.2. The change from 'weaner' to 'fattener' for the Mountmarle group, occurred at a pen mean live weight of 100 lbs. The 'fattener' diet had a lower protein content and a higher energy concentration than the 'weaner' diet as is recommended in the A.R.C. Nutrient Requirements (1967). M.L.C. groups received one diet throughout the experiment. Dietary MEs (Table 3.1.2) were calculated from book values of the total digestible nutrients (TDN) of the individual dietary constituents. The calculation assumes that the digestible energy of TDN is 4.4 kcal/g (A.R.C., 1967) and that ME is about 95% of digestible energy (Diggs et al., 1959).

Litters in experiments 4 and 5 supplied M.L.C. sib groups for test at the M.L.C. test station, Stirling. The sib pairs were a subplot treatment and the comparison of the M.L.C. and Mountmarle subplots is an environmental comparison of a National central test environment and alternative on farm test environments. The interactions in analyses of the three feeding levels are therefore genotype x environment rather than genotype x feeding level interactions.

The M.L.C. test normally consists of a castrate and gilt pair reared in controlled environment buildings. The test period is that used for the Mountmarle subplots, 601bs. to 2001bs. liveweight. The feeding regime is to-appetite and a single diet, with the ingredients and composition given in Tables 3.1.1. and 3.1.2. respectively, is fed in pellet form throughout the test period. No restriction is placed on the amount of pellets any pig may receive throughout the whole of the test, the pair being given as many pellets as they will clear up in
20-25 minutes, twice daily, with the daily ration increased once a week (Note, 1969). Sib pairs were usually transferred from Mountmarle to Stirling at the same time as sib entry to the A.B.R.O. experimental accommodation. Acclimatisation periods were therefore similar.

The Mountmarle diets were fed either ad libitum or to a scale. The scale was assumed to be a sub-appetite intake level and therefore is alternatively called restricted. With ad libitum feeding the diet is available to appetite at all times, allowing the pig to eat at will. The ad libitum sub plots had the diets fed as a dry meal through bulk hoppers at the front of the pen. Restricted pigs were fed dry meal in the permanent troughs.

Feed wastage for the ad lib. pigs was kept at a minimum by surveillance by the farm staff and spot checks by the author. Faulty hoppers were repaired or replaced as quickly as possible. In all cases of feed wastage in later experiments, the spoilt meal was removed, weighed and recorded.

The scale for the restricted feeding level had a minimum of 3lb. and a maximum of 5lb. per pig per day. Any pens not finishing the 3lb. level had stale feed removed and wastage recorded. Increments between the minimum and maximum levels were 1lb. per pig per day and were dictated by pen appetite. It was thought that a scale with a 5lb. maximum was similar to those in commercial practise and that it would provide a sufficient contrast to ad libitum intakes.

The feeding method for the restricted pigs varied somewhat between trials. Experiments 1 and 2 used a once daily feeding method. Feed wastage problems were encountered in experiment 2.
and water was added to the dry meal placed in the trough in an attempt to limit the loss of feed, but the efforts were not altogether successful. However, the subsequent simple expedient of splitting the restricted ration into 2 equal feeds limited feed wastage levels in experiment 3 and equal twice daily feeds were therefore used for experiments 4 and 5. Feeding time for experiments 1 and 2 was usually 06.30 hrs, and for experiments 3 to 5 06.30 and 15.30 hrs.

Experiment 1 was completed prior to the author's arrival at ABRO. Also staff changes at Mountmarle may have led to some variation in the interpretation of the scale increments. However, it was understood that for experiment 1 the increments, although dictated by pen appetite, was only implemented weekly. Experiment 2 was continued with the same incremental procedure although feed wastage created difficulties in ration adjustment. Subsequent to the implementation of twice daily feeding in experiment 3 the level of feed wastage for scale pigs was reduced and with feed intakes more accurately monitored, increments for subsequent experiments were made, not weekly, but as soon as dictated by pen appetite. The pen ration was incremented the day following the pen group eating the existing ration within one hour of the food being available. The changed emphasis in the pattern of feed intake gave further deviation from the M.L.C. 'to appetite' regime and the contrast between ad libitum, te-appetite and the Mountmarle scale in experiments 4 and 5 was likely to give three distinct levels of nutrient intake.

Health

Pigs were weighed monthly as a check on health status and any pig gaining less than 10lbs during a month was culled from
the experiment. In general health was good. Culls and casualties for each experiment are given in the materials section.

Character measurement and definition

Pigs were sold for commercial bacon production, experiments 1 and 2 to Messrs. Mitchells, Ayr and experiments 3 to 5 Mountmarle pigs to David A. Hall Ltd., Broxburn. Slaughter weight was about 1951bs. liveweight. Pigs were slaughtered in weekly batches on Thursdays and those for slaughter were determined by a weekly weighing the previous Wednesday. Pigs in experiment 1 were fasted from the evening prior to transport and prefasted and fasted slaughter weights were recorded. There were no prefasted weights for the later experiments. Split carcass measurements were recorded at the factories and economy of production data at Mountmarle.

For experiments 1 and 2 the pig carcasses were processed for Ayrshire bacon. Each pig was electrically stunned, bled to death, scalded and scraped, and then skinned. After cooling for approximately one hour, the carcass was weighed with head and feet on. Adjustment was made for evaporation loss as detailed by the Fatstock Guarantee Scheme. Split carcasses were then held in cold store overnight and next day each side was cut in two, perpendicular to the line of the back at the posterior edge of the head of the last rib. The bacon joint was then boned and rolled. Curing involved a stay in pickle of 2 days, after which the rolls were allowed to drain and then weighed. The roll weight will be called bacon weight. No bacon weights were available for experiment 2.
Split carcass measurements were taken in a hanging position immediately before the cutting of the side, i.e. after overnight cold storage. After the carcass was cut at the last rib a tracing was made of the interior cut surface. The tracing gave the area of the 'eye' muscle, Longissimus dorsi, and the fat depths 'C' and 'K' above the 'eye' muscle. The fat depths 'C' and 'K' are defined later.

Pigs in experiments 3 to 5 were processed for Wiltshire bacon and the carcass included the skin. Measurements were limited to those on the split carcass and the last rib tracing. Fat depths for these later experiments therefore included skin thickness while fat depths for the earlier trials did not. All carcass measurements were made on the left carcass side. The right side was used only if the left side was not available or was unsuitable.

Measurement details for M.L.C. pigs has been given by Cuthbertson (1968) and is as given for the Mountmarle pigs except that carcass length is the average of the lengths of both warm sides, carcass weight is the sum of the weights of head, chine bone and 2 x (the hindquarter, forequarter, kidney, flare fat, feet and m. psoas major of the left side) and split carcass backfat measurements are taken on the warm carcass. Eye muscle area is calculated from a photograph of the forequarter cut surface.

Details of carcass measurements and of the economy of production characters are listed below. Definitions, units and contractions are given.
Daily gain - average daily liveweight increase of the pig from the start of the test to the last liveweight, lbs./day (DG)

Feed conversion efficiency - the weight of meal consumed by a pen divided by the pen weight increment from the initial liveweight to the last liveweight lbs./lbs. (FCE)

Daily feed intake - average weight of meal consumed by the pig per day of test lbs./day. (DFI)

Prefasted liveweight lbs. (Prf. wt.)

Fasted liveweight (slaughter wt.) lbs. (Sl. wt.)

Carcass weight lbs. (Carc. wt.)

Bacon weight lbs. (Bacon)

Carcass length - taken on the cold suspended carcass, from the symphysis pubis to the anterior edge of the first rib, mm. (Length)

Backfat thickness, measures of fat depth, taken along the mid line of the back (excluding skin thickness in experiments 1 and 2, including skin thickness in experiments 3 to 5).

Shoulder - maximum depth at shoulder, mm. (Max.)

Mid-back - minimum depth in the middle of the back, mm (Mid.)

Loin 2 - depth over the middle of the rump muscle, the glutus medius, mm. (Loin)

Fat firmness - firmness of mid back fat estimated by thumb pressure, 1 = soft, 2 = average, 3 = hard (Fat score)

Streak thickness - in the middle of the flank, mm (Streak)

Measurements taken from the tracing of the anterior cut surface at the last rib.

Fat depth C - fat depth over the maximum depth of the eye muscle, mm. (C).
Fat depth $K$ = fat depth over the latero-dorsal corner of the eye muscle, mm. ($K$)

Eye muscle area = a planimeter area measure, sq.cm. (EMA)

In calculating feed conversion efficiencies a pen losing a pig was debited with all food consumed but credited with the weight gain of the pig withdrawn from the experiment.

**Analytical methods**

The experiments were factorial experiments with a split plot design. The partition of degrees of freedom for a completely random split plot design is given by Steel and Torrie (1960). If the genotypes are represented at '$a$' levels and there are '$r$' litters per genotype each fed at '$b$' levels, then the partition of the degrees of freedom is:

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotype</td>
<td>$a-1$</td>
</tr>
<tr>
<td>Error (a)</td>
<td>$a(r-1)$</td>
</tr>
<tr>
<td>Feeding level</td>
<td>$b-1$</td>
</tr>
<tr>
<td>Genotype x Feeding level</td>
<td>$(a-1)(b-1)$</td>
</tr>
<tr>
<td>Error (b)</td>
<td>$a(r-1)(b-1)$</td>
</tr>
<tr>
<td>Total</td>
<td>$a b r - 1$</td>
</tr>
</tbody>
</table>

The mean square due to feeding levels and to genotype x feeding level interactions are tested for significance against the error mean square within litters (pairs of pens) and the mean square for genotypes is tested for significance against the mean square due to litters within genotypes.

The advantage of split plot designs for factorial study of interaction is that relative to a factorial experiment not laid out as a split plot, there is increased precision for subplot comparisons, including the interaction component. Overall
precision of the experiment is not likely to be changed and there will be lower precision for whole plot comparisons (Steel and Torrie, 1960).

Initially most of the experiments had unequal numbers of litters of the various genotypes and there was also some loss of data during the experiments. Analysis was therefore completed with a least squares computer program (Harvey, 1968), using a single model fitting genotypes, litters within genotypes, feeding levels and the two factor interactions of genotype and feeding level. The whole plot error mean square was therefore the pooled sums of squares for litters, with the appropriate degrees of freedom as divisor. Subplot error sums of squares and mean squares were those given as 'residual' by the least squares programme.

It is appreciated that this method was approximate because, with unequal sub class frequencies, the whole plot effects should not be adjusted for the whole plot error effects (Harvey, 1968). The computing procedures for the programme applicable to split plot designs have been outlined by Harvey (1964). The procedure gives the entire analysis by complementary least squares analysis of progressively larger models. Appropriate error sums of squares for the whole and subplots are calculated from differences in the error terms of the analyses and sums of squares for main effects are obtained directly. When this was done essentially the same answers were obtained as from the single model analysis, as is to be expected when the degree of unbalance is not great. The single model procedures were therefore followed for the analyses and any inaccuracies will have little, if any, effect on the interpretation of interactions and genotype and feed effects.
Programme limitations complicated some analyses when, for example, more than two main effects were considered. The problem was overcome by running separate whole and split plot analyses. Where a separate whole analysis was carried out this was done on litter sums and the separate split plot analysis on subplot (feeding level) differences. This procedure leads to changes in the relative size of the whole plot and split plot mean squares but does not affect tests of significance or interpretation of the results.

Where the analyses necessitated estimation of missing subplot values, Anderson's (1946) method was used and for each estimated value one degree of freedom was subtracted from the residual sum of squares degrees of freedom (Steel and Torrie, 1960). The resulting estimate of the residual mean squares is unbiased, however the mean squares for the main effects and whole plot error will be biased upwards. In the analyses few values were estimated and the biases can be ignored (Steel and Torrie, 1960), although it is possible that the significance of feeding level effects may be overestimated.

**Correction for weight at slaughter and for sex**

Variation resulting from final weight and sex ratios differences was removed by applying corrections for both sources of variation. The methods of King (1957, 1963) were used and for weight at slaughter correction factors were within subplot regressions of the character on weight at slaughter. Slaughter weight corrections for the pen mean observations, FCE and DFI, were calculated as within cross, trial, feed subgroup regressions, after the effects of sex for DFI were eliminated.
by treating sex as a dummy variate. Table 3.1.3 gives the slaughter weight corrections calculated for experiment 1, experiment 2 and experiments 3 to 5.

The corrections for slaughter weight shown in Table 3.1.3, when significantly different from zero, were generally consistent and of similar magnitude to published estimates (King, 1957). Some inconsistencies were apparent between experiment 2 estimates and the other populations. However for internal use they were considered adequate and were applied regardless of statistical significance. Experiment 1 was adjusted to a slaughter weight of 193.0 lbs. and the remainder to a slaughter weight of 198.0 lbs.

The slaughter weight correction is a between pig regression and hence open to the criticisms put forward by Standal and Moen (1971) and by Hinkema (1972). These authors show that a correction for daily gain derived in this way penalises the faster growing and hence heavier pigs. No alternative correction method was possible with the available data and as the slaughter weight variation was large, the corrections for daily gain shown in Table 3.1.5 were applied despite their inherent inaccuracy.

Following the correction of data for slaughter weight variation, sex differences (castrate—gilt) were computed and applied to remove variation due to subplot sex ratio differences. The corrections applied are given in Table 3.1.4 and were calculated by within subplot comparisons of data with disproportionate sex ratios (Snedecor and Cochran, 1969). The estimates were generally consistent between populations, in keeping with accepted performance and in agreement with published estimates.
| Character | Experiment 1 | | | Experiment 2 | | | Experiments 3 to 5 | | |
|----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
|          | Correction  | S.E.        | Correction  | S.E.        | Correction  | S.E.        | Correction  | S.E.        |
| PCE      | 0.008       | 0.011       | -0.025      | 0.025       | -0.013      | 0.007       |             |             |
| DFI      | 0.058       | 0.020       | -0.200      | 0.353       | 0.018       | 0.004       |             |             |
| DG       | 0.005       | 0.001       | 0.009       | 0.003       | 0.008       | 0.001       |             |             |
| Prf. wt. | 0.665       | 0.030       | -          | -           | -           | -           |             |             |
| Crkt. wt. | 0.746      | 0.029       | 0.418       | 0.056       | 0.722       | 0.026       |             |             |
| Bacon    | 0.292       | 0.028       | -          | -           | -           | -           |             |             |
| Length   | 1.015       | 0.162       | 1.065       | 0.353       | 1.224       | 0.143       |             |             |
| Max      | 0.112       | 0.042       | 0.136       | 0.067       | 0.011       | 0.040       |             |             |
| Mid      | 0.057       | 0.032       | 0.011       | 0.058       | 0.025       | 0.029       |             |             |
| Loin     | 0.048       | 0.035       | 0.074       | 0.048       | 0.025       | 0.027       |             |             |
| C        | 0.108       | 0.035       | 0.099       | 0.072       | 0.028       | 0.032       |             |             |
| K        | 0.093       | 0.035       | 0.034       | 0.074       | 0.055       | 0.044       |             |             |
| BHA      | 0.069       | 0.031       | -0.016      | 0.055       | 0.086       | 0.024       |             |             |
| Streak   | 0.101       | 0.034       | -0.090      | 0.074       | 0.061       | 0.055       |             |             |
| Fatscore | -0.001      | 0.005       | 0.001       | 0.010       | 0.009       | 0.006       |             |             |

* Change for each lb. increase in slaughter weight.
<table>
<thead>
<tr>
<th>Character</th>
<th>Experiment 1</th>
<th>S.E.</th>
<th>Experiment 2</th>
<th>S.E.</th>
<th>Experiments 3 to 5</th>
<th>S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DG</td>
<td>0.05</td>
<td>0.01</td>
<td>0.06</td>
<td>0.02</td>
<td>0.13</td>
<td>0.01</td>
</tr>
<tr>
<td>Prf. wt.</td>
<td>0.77</td>
<td>0.30</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Crc. wt.</td>
<td>0.26</td>
<td>0.37</td>
<td>0.30</td>
<td>0.57</td>
<td>0.24</td>
<td>0.33</td>
</tr>
<tr>
<td>Bacon</td>
<td>0.36</td>
<td>0.28</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Length</td>
<td>-6.60</td>
<td>1.63</td>
<td>-6.83</td>
<td>4.01</td>
<td>-4.34</td>
<td>1.84</td>
</tr>
<tr>
<td>Max</td>
<td>4.12</td>
<td>0.41</td>
<td>3.05</td>
<td>0.72</td>
<td>3.63</td>
<td>0.32</td>
</tr>
<tr>
<td>Mid</td>
<td>2.72</td>
<td>0.32</td>
<td>3.86</td>
<td>0.65</td>
<td>4.30</td>
<td>0.37</td>
</tr>
<tr>
<td>Loin</td>
<td>3.67</td>
<td>0.37</td>
<td>3.50</td>
<td>0.54</td>
<td>4.62</td>
<td>0.35</td>
</tr>
<tr>
<td>C</td>
<td>5.01</td>
<td>0.35</td>
<td>6.78</td>
<td>0.75</td>
<td>6.06</td>
<td>0.42</td>
</tr>
<tr>
<td>K</td>
<td>5.30</td>
<td>0.34</td>
<td>5.25</td>
<td>0.67</td>
<td>7.22</td>
<td>0.56</td>
</tr>
<tr>
<td>BMA</td>
<td>-3.55</td>
<td>0.31</td>
<td>-2.89</td>
<td>0.63</td>
<td>-3.43</td>
<td>0.33</td>
</tr>
<tr>
<td>Streak</td>
<td>-0.25</td>
<td>0.34</td>
<td>-0.59</td>
<td>0.80</td>
<td>-0.31</td>
<td>0.57</td>
</tr>
<tr>
<td>Fatscore</td>
<td>0.06</td>
<td>0.05</td>
<td>0.54</td>
<td>0.12</td>
<td>0.05</td>
<td>0.06</td>
</tr>
</tbody>
</table>
The sex difference method was inappropriate for the pen mean characters, FCE and DFI, and no adjustment was made.

Within subplot regressions of characters on initial weight were computed after fitting regressions for slaughter weight and sex. Generally the regression coefficients were small, not statistically significantly different from zero, and if applied did not alter the last digit of the observation. Therefore no corrections were applied for initial weight differences.

Therefore, with a few exceptions, the observations analysed were pen means corrected to an equal sex ratio and to the same slaughter weight.

The experimental details and results for the five experiments follow. A brief discussion will follow each analysis and a general discussion of the genotype x feeding level interaction experiments is presented at the end of the chapter.

3.2 Experiment 1: Crosses of the Hampshire, Lacombe, Landrace, Large White, Pietrain and Wessex breeds.

Materials

Experiment 1 comprised three replicates, trials 1, 2 and 3, in which crossbred progeny were fed diets to a scale or ad libitum as described in 3.1. The progeny were sired by Hampshire (H), Pietrain (P), Lacombe (LC) and Large White (LW) boars and were out of LW, Wessex x LW (W x LW), Landrace, x LW (L x LW), LC x LW and H x LW, dams. There were no LC backcrosses. The litter were purebreds, 2 and 3 breed crosses and backcrosses. For brevity all genotypes will be termed crosses. The number of subplots for each cross is given in table 3.2.1.
Table 3.2.1. Experiment 1. Genotype and Feeding Level Subplot Numbers

<table>
<thead>
<tr>
<th>Sire</th>
<th>Dam</th>
<th>Feeding Level</th>
<th></th>
<th></th>
<th></th>
<th>Trials 1, 2 and 3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Scale</td>
<td>Adlib</td>
<td>Scale</td>
<td>Adlib</td>
<td>Scale</td>
</tr>
<tr>
<td>HAMPSHIRE(H)</td>
<td></td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>PIETRAIN(P)</td>
<td></td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>LACOMBE(LC)</td>
<td>LARGE WHITE</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>LARGE WHITE(LW)</td>
<td></td>
<td>-</td>
<td>-</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>H</td>
<td>WESSEX x LW</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>1</td>
</tr>
<tr>
<td>P</td>
<td></td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>LC</td>
<td>WESSEX x LW</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>LW</td>
<td>WESSEX x LW</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>4</td>
<td>1</td>
</tr>
<tr>
<td>H</td>
<td>LANDRACE x LW</td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>P</td>
<td></td>
<td>1</td>
<td>-</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>LC</td>
<td>LANDRACE x LW</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>LW</td>
<td>LANDRACE x LW</td>
<td>2</td>
<td>-</td>
<td>1</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>H</td>
<td>LACOMBE x LW</td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>P</td>
<td>LACOMBE x LW</td>
<td>3</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>-</td>
</tr>
<tr>
<td>LW</td>
<td>LACOMBE x LW</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>H</td>
<td>HAMPSHIRE x LW</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>P</td>
<td>HAMPSHIRE x LW</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>LC</td>
<td>HAMPSHIRE x LW</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>LW</td>
<td>HAMPSHIRE x LW</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
</tbody>
</table>
In each of the trials all parents of the crosses were outbred with the exception of the Hampshires. In trial 1, the 3 Hampshire sires were already inbred when imported, in trial 2 the 3 sires were about 17% inbred and in trial 3 the three sires were about 19% inbred.

Sire breeds were generally represented by 3 sires per trial. However 4 Pietrain boars in trial 2 and 2 Pietrain boars in trial 3 were used. For the combined trials 9 Hampshire, 6 Pietrain, 8 Lacoitbe and 9 Large White boars are represented. Dams had litters in only one trial.

The duration of the trials and the limits of the litter farrowing dates are given below:

<table>
<thead>
<tr>
<th>Trial</th>
<th>Duration</th>
<th>Litters farrowed</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>First</td>
</tr>
<tr>
<td>Trial 1</td>
<td>June - Nov. 1965</td>
<td>April 2nd April</td>
</tr>
<tr>
<td>Trial 2</td>
<td>Oct 1965 - April 1966</td>
<td>Aug. 10th Sept. 24th</td>
</tr>
<tr>
<td>Trial 3</td>
<td>Dec. 1965 - May 1966</td>
<td>Oct. 1st Nov. 13th</td>
</tr>
</tbody>
</table>

The number of pigs starting and finishing the experiment is given in Table 3,2.2 and the causes of loss are listed. Losses were evenly distributed over crosses and feeding levels.

Unfortunately all economy of production data for the first replicate were lost and results were therefore restricted to carcass characters. The combined analyses of trials 1, 2 and 3 therefore consider the carcass characters and the analyses of trials 2 and 3 the economy of production characters.

Methods

The analysis used a model fitting the main effects, trial, sire breed, dam breed and feeding level, together with their 2 and 3 factor interactions. Dam breed was a general term describing the dam genotypes. The analysis had separate runs
of the litter sums and subplot (feeding level) differences.

The resultant changes in the relative size of the whole and
split plot mean squares does not effect the tests of significance.

In the tables, whole and split plot error mean squares are
designated $E_w$ and $E_g$ respectively.

**Results**

Table 3.2.3 gives the mean squares for the sire (S, brd)
and dam (D, brd) breed model. The least squares means and
contrasts for the significant effects of interest are given in
tables 3.2.4 to 3.2.7.

Table 3.2.4 shows that the feeding level treatments gave
significantly different levels of dietary intake and with its
significantly different performance for all characters except
### Table 3.2.7  
**Experiment 1.** "Sire and Dam breed" model Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>BG</th>
<th>DFI</th>
<th>FCE</th>
<th>df</th>
<th>Prf. wt.</th>
<th>Erc. wt.</th>
<th>Bacon</th>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trial (T)</td>
<td>1</td>
<td>0.091***</td>
<td>0.135</td>
<td>0.468**</td>
<td>2</td>
<td>17.42*</td>
<td>8.74</td>
<td>6.76</td>
<td>1798.1***</td>
</tr>
<tr>
<td>S. brd</td>
<td>3</td>
<td>0.049</td>
<td>0.171</td>
<td>0.056</td>
<td>3</td>
<td>10.88</td>
<td>9.53</td>
<td>54.32***</td>
<td>9029.6***</td>
</tr>
<tr>
<td>D. brd</td>
<td>4</td>
<td>0.005</td>
<td>0.051</td>
<td>0.055</td>
<td>4</td>
<td>6.72</td>
<td>8.48</td>
<td>4.07</td>
<td>1068.2**</td>
</tr>
<tr>
<td>T x S. brd</td>
<td>3</td>
<td>0.014</td>
<td>0.166</td>
<td>0.151</td>
<td>6</td>
<td>6.98</td>
<td>6.55</td>
<td>6.78</td>
<td>413.1</td>
</tr>
<tr>
<td>T x D. brd</td>
<td>4</td>
<td>0.006</td>
<td>0.161</td>
<td>0.042</td>
<td>8</td>
<td>5.46</td>
<td>5.16</td>
<td>2.20</td>
<td>191.3</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>11</td>
<td>0.014</td>
<td>0.075</td>
<td>0.082</td>
<td>11</td>
<td>5.82</td>
<td>5.10</td>
<td>3.09</td>
<td>192.5</td>
</tr>
<tr>
<td>E</td>
<td>42</td>
<td>0.009</td>
<td>0.128</td>
<td>0.060</td>
<td>66</td>
<td>5.13</td>
<td>4.16</td>
<td>4.57</td>
<td>214.6</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>2.171***</td>
<td>47.465***</td>
<td>2.197***</td>
<td>1</td>
<td>191.76***</td>
<td>222.78***</td>
<td>148.89</td>
<td>1215.1</td>
</tr>
<tr>
<td>T x F</td>
<td>1</td>
<td>0.085</td>
<td>0.056</td>
<td>0.103</td>
<td>2</td>
<td>1.03</td>
<td>24.95</td>
<td>77.63</td>
<td>431.4</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>3</td>
<td>0.028</td>
<td>0.065</td>
<td>0.150</td>
<td>3</td>
<td>8.17</td>
<td>11.79</td>
<td>31.82</td>
<td>206.9</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>4</td>
<td>0.014</td>
<td>0.077</td>
<td>0.087</td>
<td>4</td>
<td>12.36</td>
<td>4.84</td>
<td>19.44</td>
<td>60.8</td>
</tr>
<tr>
<td>T x S. brd x F</td>
<td>3</td>
<td>0.009</td>
<td>0.060</td>
<td>0.061</td>
<td>6</td>
<td>5.19</td>
<td>2.85</td>
<td>56.84</td>
<td>117.2</td>
</tr>
<tr>
<td>T x D. brd x F</td>
<td>4</td>
<td>0.015</td>
<td>0.084</td>
<td>0.175</td>
<td>8</td>
<td>10.94</td>
<td>4.22</td>
<td>45.09</td>
<td>169.1</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>11</td>
<td>0.003</td>
<td>0.078</td>
<td>0.103</td>
<td>11</td>
<td>12.65</td>
<td>6.76</td>
<td>64.36</td>
<td>281.4</td>
</tr>
<tr>
<td>E</td>
<td>29</td>
<td>0.039</td>
<td>0.110</td>
<td>0.151</td>
<td>48</td>
<td>7.50</td>
<td>5.84</td>
<td>204.52</td>
<td>333.9</td>
</tr>
</tbody>
</table>

### Table 3.2.8  
**Trial (T)**

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Min.</th>
<th>Mid.</th>
<th>Loin.</th>
<th>C</th>
<th>K</th>
<th>EMA</th>
<th>Streak</th>
<th>Fat score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trial (T)</td>
<td>2</td>
<td>45.11*</td>
<td>11.16</td>
<td>57.67**</td>
<td>19.34</td>
<td>27.69</td>
<td>60.734*</td>
<td>22.57**</td>
<td>0.106</td>
</tr>
<tr>
<td>S. brd</td>
<td>3</td>
<td>16.45</td>
<td>5.23</td>
<td>40.90**</td>
<td>29.81</td>
<td>23.44</td>
<td>188.584***</td>
<td>11.013*</td>
<td>0.116</td>
</tr>
<tr>
<td>D. brd</td>
<td>4</td>
<td>5.42</td>
<td>6.57</td>
<td>7.86</td>
<td>7.39</td>
<td>6.24</td>
<td>12.949</td>
<td>5.789</td>
<td>0.374</td>
</tr>
<tr>
<td>T x S. brd</td>
<td>6</td>
<td>8.69</td>
<td>5.48</td>
<td>6.65</td>
<td>5.38</td>
<td>7.74</td>
<td>8.481</td>
<td>5.117</td>
<td>0.076</td>
</tr>
<tr>
<td>T x D. brd</td>
<td>8</td>
<td>17.89</td>
<td>5.95</td>
<td>16.03</td>
<td>10.86</td>
<td>11.08</td>
<td>8.018</td>
<td>4.929</td>
<td>0.082</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>11</td>
<td>5.73</td>
<td>4.83</td>
<td>5.26</td>
<td>4.83</td>
<td>2.74</td>
<td>5.930</td>
<td>5.586</td>
<td>0.074</td>
</tr>
<tr>
<td>E</td>
<td>66</td>
<td>11.75</td>
<td>7.40</td>
<td>9.39</td>
<td>9.75</td>
<td>11.31</td>
<td>8.400</td>
<td>5.227</td>
<td>0.152</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>340.72***</td>
<td>263.01***</td>
<td>221.14***</td>
<td>146.44***</td>
<td>337.39***</td>
<td>68.295*</td>
<td>34.386</td>
<td>8.066***</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>3</td>
<td>19.78</td>
<td>9.37</td>
<td>14.10</td>
<td>66.20**</td>
<td>21.77</td>
<td>2.142</td>
<td>9.561</td>
<td>0.345</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>4</td>
<td>34.42*</td>
<td>24.77</td>
<td>14.40</td>
<td>62.47**</td>
<td>10.39</td>
<td>17.977</td>
<td>15.982</td>
<td>1.563**</td>
</tr>
<tr>
<td>T x S. brd x F</td>
<td>6</td>
<td>7.77</td>
<td>5.04</td>
<td>5.73</td>
<td>8.15</td>
<td>13.91</td>
<td>9.704</td>
<td>5.026</td>
<td>0.354</td>
</tr>
<tr>
<td>T x D. brd x F</td>
<td>8</td>
<td>1.87</td>
<td>3.51</td>
<td>8.06</td>
<td>13.08</td>
<td>2.11</td>
<td>12.024</td>
<td>4.078</td>
<td>0.591</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>11</td>
<td>56.17**</td>
<td>18.58</td>
<td>14.06</td>
<td>26.16*</td>
<td>24.45</td>
<td>11.645</td>
<td>10.381</td>
<td>0.589</td>
</tr>
<tr>
<td>E</td>
<td>48</td>
<td>12.27</td>
<td>10.15</td>
<td>16.45</td>
<td>12.48</td>
<td>14.79</td>
<td>11.283</td>
<td>13.491</td>
<td>0.417</td>
</tr>
</tbody>
</table>
bacon weight, carcass length and streak thickness. With ad libitum feeding, daily feed intake was higher (30%), daily gain faster (21%).

<table>
<thead>
<tr>
<th>Character</th>
<th>Ad libitum-Restricted</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prf. wt. lbs.</td>
<td>1.6</td>
</tr>
<tr>
<td>Crc. wt. lbs</td>
<td>2.2</td>
</tr>
<tr>
<td>Max mm.</td>
<td>2.6</td>
</tr>
<tr>
<td>Mid mm.</td>
<td>2.4</td>
</tr>
<tr>
<td>Loin mm.</td>
<td>2.0</td>
</tr>
<tr>
<td>C mm.</td>
<td>2.0</td>
</tr>
<tr>
<td>K mm.</td>
<td>2.6</td>
</tr>
<tr>
<td>EMA sq.cm.</td>
<td>0.97</td>
</tr>
<tr>
<td>Fatscore pts.</td>
<td>-0.4</td>
</tr>
<tr>
<td>Trials 1, 2 and 3</td>
<td></td>
</tr>
<tr>
<td>DG lbs/day</td>
<td>0.26</td>
</tr>
<tr>
<td>FCE lbs/lbs</td>
<td>0.25</td>
</tr>
<tr>
<td>DFI lbs/day</td>
<td>1.23</td>
</tr>
</tbody>
</table>

and food conversion efficiency poorer (7%). The increased feed intake gave heavier prefasted and carcass weights, thicker fats at all sites (12-13%), a larger eye muscle area (4%) and a lower fat firmness score.

The significant sire breed effect means (table 3.2.5) show that the white breeds, LW and LC, and the coloured breeds, H and P, sire progeny with distinct performance levels at the same slaughter weight, with H and P sired progeny having heavier but shorter carcasses, more bacon weight, less fat depth and larger eye muscle area. The advantages were greater in the Pietrain sired progeny. Of the four sire breeds the LW gave the lightest carcass and bacon weights,
Table 3.2.5  Experiment 1. "Sire and Dam breed" model Sire Breed
Least squares means.

<table>
<thead>
<tr>
<th>Sire breed</th>
<th>Carc. wt  (lb)</th>
<th>Bacon  (lb)</th>
<th>Length  (mm)</th>
<th>Loin  (mm)</th>
<th>C  (mm)</th>
<th>EMA (sq. cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hampshire</td>
<td>151.5</td>
<td>93.7</td>
<td>761.5</td>
<td>18.4</td>
<td>17.0</td>
<td>27.46</td>
</tr>
<tr>
<td>Pietrain</td>
<td>152.5</td>
<td>95.9</td>
<td>748.2</td>
<td>16.4</td>
<td>15.9</td>
<td>30.52</td>
</tr>
<tr>
<td>Lacombe</td>
<td>150.8</td>
<td>92.9</td>
<td>790.9</td>
<td>18.7</td>
<td>18.5</td>
<td>24.20</td>
</tr>
<tr>
<td>Large White</td>
<td>148.9</td>
<td>91.7</td>
<td>794.7</td>
<td>20.4</td>
<td>18.6</td>
<td>23.50</td>
</tr>
</tbody>
</table>

the thickest fat depths and smallest eye muscle area.

Dam breed differences were found for carcass length, Large White (777.9 mm), W x LW (773.3 mm), LC x LW (775.6 mm) and L x LW (781.2 mm) gave progeny of similar length but the H x LW progeny (761.0 mm) were shorter. There were no other significant dam breed effects.

Few of the two and three factor genotype x feeding level interactions were statistically significant (table 3.2.3). The contrasts for the significant two factor genotype x feeding level interactions are given in tables 3.2.6 and 3.2.7.

Table 3.2.6  Experiment 1. "Sire and Dam breed" model Interaction
Contrasts. Ad libitum-Scale

<table>
<thead>
<tr>
<th>Sire breed x Feeding level interactions</th>
<th>C  (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hampshire</td>
<td>0.2</td>
</tr>
<tr>
<td>Pietrain</td>
<td>2.6</td>
</tr>
<tr>
<td>Lacombe</td>
<td>3.8</td>
</tr>
<tr>
<td>Large White</td>
<td>-0.0</td>
</tr>
</tbody>
</table>
### Table 2.2.6, cont.

**Dam breed x Feeding level interactions: Ad libitum-Scale contrasts**

<table>
<thead>
<tr>
<th>Dam breed</th>
<th>Max (mm)</th>
<th>C (mm)</th>
<th>Fat score (pts)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White (LW)</td>
<td>2.9</td>
<td>4.4</td>
<td>0.2</td>
</tr>
<tr>
<td>Wexsex x LW</td>
<td>3.6</td>
<td>3.1</td>
<td>0.5</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>-0.3</td>
<td>0.5</td>
<td>-0.5</td>
</tr>
<tr>
<td>Lacombe x LW</td>
<td>3.9</td>
<td>2.2</td>
<td>-0.6</td>
</tr>
<tr>
<td>Hampshire x LW</td>
<td>3.3</td>
<td>2.2</td>
<td>-0.6</td>
</tr>
</tbody>
</table>

The contrasts for 'C' reveal no consistent pattern of response to the ad libitum and restricted feeding levels. The S. brd x P contrasts show that H and LW sired progeny gave no change in fat thickness at C with ad libitum feeding, while P and LC sired progeny increased fat thickness at C by over 2.5 mm (table 3.2.6). Yet the contrast for H x (LC x LW) was -4.3 and for H x LW cross progeny + 4.6. Similarly the contrasts for P x (L x LW) were -0.3 and for P x LW + 6.6, (table 3.2.7).

### Table 3.2.7 Experiment 1. "Sire and Dam breed" model

**Sire breed x Dam breed x Feeding level interaction contrasts**

<table>
<thead>
<tr>
<th>Sire breed</th>
<th>Dam breed</th>
<th>Max (mm)</th>
<th>C (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hampshire x LW</td>
<td>W x LW</td>
<td>3.8</td>
<td>4.6</td>
</tr>
<tr>
<td></td>
<td>L x LW</td>
<td>5.1</td>
<td>2.1</td>
</tr>
<tr>
<td></td>
<td>LC x LW</td>
<td>-1.5</td>
<td>-1.2</td>
</tr>
<tr>
<td></td>
<td>H x LW</td>
<td>0.1</td>
<td>-0.3</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>W x LW</td>
<td>3.6</td>
<td>6.6</td>
</tr>
<tr>
<td></td>
<td>L x LW</td>
<td>4.1</td>
<td>5.3</td>
</tr>
<tr>
<td></td>
<td>LC x LW</td>
<td>-1.2</td>
<td>-0.3</td>
</tr>
<tr>
<td></td>
<td>H x LW</td>
<td>3.7</td>
<td>0.4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.9</td>
<td>1.1</td>
</tr>
</tbody>
</table>
Table 3.2.7 (cont.)

<table>
<thead>
<tr>
<th>Lineback</th>
<th>x LW</th>
<th>2.0</th>
<th>2.5</th>
</tr>
</thead>
<tbody>
<tr>
<td>W x LW</td>
<td>2.9</td>
<td>4.4</td>
<td></td>
</tr>
<tr>
<td>L x LW</td>
<td>6.2</td>
<td>6.0</td>
<td></td>
</tr>
<tr>
<td>H x LW</td>
<td>3.6</td>
<td>5.1</td>
<td></td>
</tr>
<tr>
<td>Large White x LW</td>
<td>2.3</td>
<td>4.1</td>
<td></td>
</tr>
<tr>
<td>W x LW</td>
<td>2.8</td>
<td>0.7</td>
<td></td>
</tr>
<tr>
<td>L x LW</td>
<td>-4.8</td>
<td>-6.4</td>
<td></td>
</tr>
<tr>
<td>LC x LW</td>
<td>4.7</td>
<td>41.7</td>
<td></td>
</tr>
<tr>
<td>H x LW</td>
<td>6.6</td>
<td>3.2</td>
<td></td>
</tr>
</tbody>
</table>

The tables also show that dam breeds often gave results which were not consistent with those of the sire breed, for example the progeny of LW dams gained 4.4 mm of fat at C and 2.9 mm at Max on ad libitum compared to restricted, while LW sired progeny gave no change at C (table 3.2.6). Similarly the progeny of LC x LW dams had a contrast of +1.1 mm and LC sired progeny a contrast of + 3.8 mm. These inconsistencies within the paternal and maternal breed performances suggest that the interaction for C was due to sampling error. Similar reasoning applies to the 2 and 3 factor interactions for Max.

The remaining interaction, D x F for fat score, shows a softening of fat firmness on ad libitum feeding for all progeny except those of LW dams (table 3.2.6). These had a slightly higher than average fat score. Later experiments also consider the response of the progeny of LW dams to ad libitum and restricted feeding and give further information for the fat score result.

Discussion

Experiment 1 has shown that genotype x feeding level interaction gave sources of variation which were generally not statistically significant. For the growth efficiency characters, DG, FCE and
DFI, and for carcass weight, the interaction mean square was seldom larger than the error mean square. There were, however, three carcass composition characters with significant genotype x feeding level interactions, backfat thickness at the shoulder (Max) and over the eye muscle (C) and fat firmness score.

Discussion of the fat depth interactions within the results section revealed inconsistent breed paternal and maternal responses and it was suggested that sampling error could therefore account for the interactions. Interactions within this body of data were therefore regarded as unimportant.

In the review of literature the determinants of the statistical and practical importance of interactions were mentioned as experimental design, the size of genotypic performance differences and the nutritional contrasts and their commercial relevance.

Experimental design for interaction studies has been discussed by Robertson (1959) and the population for experiment 1, 670 pigs, would appear adequate for the demonstration of any important interaction for the genotypes studied. Certainly the populations of other factorial interbreed experiments seldom exceed 100 pigs and the sire and dam breed subclass numbers for the combined trials are usually larger than those in comparable experiments. The absence of interactions would therefore not seem due to inadequacy of experimental design.

Differences for the sire breeds and crossbred dam genotypes studied were limited to carcass weight, bacon weight, carcass length, the fat depths loin and C, and eye muscle area. There were no genotype differences for the growth characters,
daily feed intake, food conversion efficiency and daily gain. However the sire and dam genotype means did support the qualitative breed differences, based on published estimates, given in Table 2.1. The present results show that Pietrains had the lowest and Lacombes the highest daily feed intake, that Pietrains had the least backfat and that Pietrains and Hampshires had advantages for eye muscle area and hence, in conjunction with other characters, presumably more carcass lean.

Despite these differences the crossbred populations responded proportionally to the feeding regimes. Ad libitum and the restricted scale feeding regimes caused no differential appetite response, the degree of restriction imposed by the scale regime being 30-33% for all sire breeds. Therefore within the postulated model, interaction could only occur if there was essential tissue gain variation. Direct measurement of lean was not made. However, the lack of consistent and substantial genotypic differences for fat depths suggests that variation for lean percentage of the crossbred progeny at a constant slaughter weight was small and as there were no significant genotypic effects for DG or FCE then the variation for essential tissue gain and efficiency of food conversion is also likely to have been small. It is therefore not surprising that interaction was an unimportant source of variation.

In contrast to the lack of genotypic effects, the influence of feeding regime on growth efficiency was large. Ad libitum compared to restricted gave a depression of 7% for food conversion efficiency and increases of 30% for daily feed intake, 21% for daily gain, 12-13% for fat depth and 4% for eye muscle area, all effects agreeing with the general conclusion of Braude's 1972 review. Only bacon weight, carcass length and streak thickness
were not affected by the contrast of feeding levels. Restricted feeding consistently improved Hampshire, Pietrain and Large White food conversion efficiency by 9-10% but as feed intake was reduced, liveweight gains decreased by 15-20%. The improvement in food conversion efficiency for Lacombes was less marked, 5%, although the percentage reduction in backfat thickness was consistently greater for the Lacombes than for the other breeds.

Superficially this suggests that the increase in efficiency for restricted fed Lacombes resulting from the energetic efficiency of lean, rather than fat, deposition, was largely counterbalanced by decreased efficiency because of reduced liveweight gain (and therefore increased maintenance costs). In addition feed intake restriction possibly depressed lean tissue growth as well as the contemporaneous fat deposition. Certainly eye muscle area was reduced more for Lacombes than for other breeds. Any lean tissue depression would suggest that the Lacombe's large appetite may be associated with a high nutrient intake threshold for essential tissue growth, though not necessarily at a competitive efficiency of food conversion.

The reasoning above assumes that indirect carcass composition characters gave an accurate prediction of tissue proportions. That some of the evidence was contradictory merely highlights the general uncertainty attached to indirect measurement of carcass composition, particularly with the variation in carcass dimensions found in these trials. For more definitive work carcass or joint dissection seems necessary. However in view of the direct relevance to dead weight grading of most of the characters, their use was both appropriate and adequate for the present study and it is suggested that the lack of interactions between these cross-
breds of diverse origin and the different feeding regimes for the characters studied confirms the validity of either feeding regime for the comparison of slaughter generation pigs of probable commercial merit.

A further important facet of the results is the indication of the apparent economic advantage accruing from the sub appetite feed intake levels for these potential commercial genotypes.

3.3 **Experiment 2: Crosses of the Hampshire, Landrace, Large White, Pietrain and Yorkshire breeds.**

In previous ABRO crossbreeding experiments (King, 1968), Hampshire and crossbred Hampshire/Pietrain boars, when compared with Large White boars, produced increases in the litter size of the females to which they were mated. Hampshire/Pietrain (HP) boars gave the larger effect. Further matings of HP boars compared to British Landrace and Large White boars produced the progeny used in experiments 2 to 5. Dams were genotypes being compared for litter productivity trials.

**Materials**

In experiment 2 the crossbred progeny of Landrace (L) and Hampshire/Pietrain sires and inbred rotation Large White (ILW), outbred Large White (OLW) and American Yorkshire × outbred Large White (YLW) dams were fed ad libitum and restricted levels. All sires and dams were bred at Mountmarle.

The litters were sired by 5 HP and 3 L boars and were born between 19th May and 16th June 1970. The first pens started tests on 29th July and the last pigs were slaughtered on 25th January 1971.

154 pigs started the experiment and 151 were slaughtered for bacon. Two pigs, one ad lib. and one restricted, were culled on
growth performance and another ad lib. pig died of gut oedema.

Five carcass records were not obtained at the bacon factory.
Therefore 146 records, 73 ad lib. and 73 restricted, were available for analysis.

The number of subplots for each genotype and feeding level is given in table 3.5.1.

Table 3.5.1. Genotype and Feeding level subplot numbers.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Feeding level</th>
<th>Sire</th>
<th>Dam</th>
<th>Restricted</th>
<th>Ad libitum</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td></td>
<td>ILW</td>
<td></td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GLW</td>
<td></td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>YLW</td>
<td></td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>L</td>
<td></td>
<td>ILW</td>
<td></td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GLW</td>
<td></td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>YLW</td>
<td></td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

The feeding levels, restricted and ad libitum were as described in Section 3.1.

Methods.

A Sire (S. brd) and Dam (D. brd) breed model was fitted to the data. Dam breed was a general term to describe the three dam strains. The model fitted the main effects, sire breed, dam breed and feeding level together with the 2 and 3 factor interactions of these effects. Fitting three main effects necessitated running separate whole and subplot analyses with the result that the relative sizes of the mean squares changed. Feeding level effects and the two and three factor interactions with sire and dam breed are given as ad libitum – restricted contrasts.
Results.

Table 3.3.2 gives the mean squares for the analysis. Means and contrasts for significant effects are given in table 3.3.3.

The feeding level treatments gave significantly different daily feed intakes, 5.19 lbs/day for ad libitum feeding and 4.07 lbs/day for restricted. The latter gave significantly slower live weight gains, lighter carcasses, thinner fat depths at all points and a thinner streak. While the feeding level effect for FCE was small, the result followed the trend observed in experiment 1, an improved efficiency with restricted feed intake. Restricted fed pigs also tended to be longer, to have marginally smaller eye muscle areas and comparable fat scores.

Sire breed effects were limited to carcass weight and length and eye muscle area, with HP carcasses heavier, shorter and with larger eye muscle area than Landrace carcasses (table 3.3.3). There were no significant sire breed effects for fat thickness. The only dam breed effect, for shoulder backfat thickness (Max), showed that the progeny of outbred LW dams had the thinnest fat at the shoulder, YLW progeny were intermediate and inbred rotation LW progeny had the thickest fat. The same rankings held for the other fat thicknesses but the differences were not significant.

There were no significant genotypic or interaction effects for the economy of production characters, although the D.G. sire breed x feeding level mean square approached significance. The ad libitum - restricted contrasts (table 3.3.4) show the uniform liveweight gain responses of the dam breeds and indicate the differential sire breed responses for gain and dam breed responses for food conversion efficiency.
Table 3.3.2. Experiment 2. "Sire and Dam breed" model: Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DG</th>
<th>FCE</th>
<th>DDI</th>
<th>Crvwt.</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>0.003</td>
<td>0.070</td>
<td>0.056</td>
<td>31.921**</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>0.005</td>
<td>0.036</td>
<td>0.007</td>
<td>4.070</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>2</td>
<td>0.001</td>
<td>0.060</td>
<td>0.075</td>
<td>4.261</td>
</tr>
<tr>
<td>Ew</td>
<td>14</td>
<td>0.006</td>
<td>0.066</td>
<td>0.177</td>
<td>2.561</td>
</tr>
</tbody>
</table>

Feeding level (F)  
<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Length</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>8168.5**</td>
<td>1969</td>
<td>4200</td>
<td>15515</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>278.5</td>
<td>25407*</td>
<td>7970</td>
<td>9780</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>2</td>
<td>158.5</td>
<td>0.661</td>
<td>0.266</td>
<td>2.622</td>
</tr>
<tr>
<td>Ew</td>
<td>14</td>
<td>139.4</td>
<td>4751</td>
<td>10473</td>
<td>9841</td>
</tr>
</tbody>
</table>

Feeding level (F)  
<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Length</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>79.2</td>
<td>4616</td>
<td>0.049</td>
<td>0.379</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>27.5</td>
<td>9402</td>
<td>20072</td>
<td>8726</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>2</td>
<td>123.1</td>
<td>3884</td>
<td>7777</td>
<td>21425</td>
</tr>
<tr>
<td>Ew</td>
<td>14</td>
<td>169.0</td>
<td>11087</td>
<td>12186</td>
<td>19120</td>
</tr>
</tbody>
</table>

Source                      | df | C      | K    | EMA   | Streak Fat score |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>3.386</td>
<td>13.819</td>
<td>37.080***</td>
<td>15.910 0.994</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>37.502</td>
<td>20.745</td>
<td>7.694</td>
<td>50.653 0.531</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>2</td>
<td>1.496</td>
<td>8.615</td>
<td>6.156</td>
<td>1.978 0.016</td>
</tr>
<tr>
<td>Ew</td>
<td>14</td>
<td>19.117</td>
<td>12.044</td>
<td>3.367</td>
<td>7.935 0.235</td>
</tr>
</tbody>
</table>

Feeding level (F)  
<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>C</th>
<th>K</th>
<th>EMA</th>
<th>Streak Fat score</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>3.386</td>
<td>13.819</td>
<td>37.080***</td>
<td>15.910 0.994</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>37.502</td>
<td>20.745</td>
<td>7.694</td>
<td>50.653 0.531</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>2</td>
<td>1.496</td>
<td>8.615</td>
<td>6.156</td>
<td>1.978 0.016</td>
</tr>
<tr>
<td>Ew</td>
<td>14</td>
<td>19.117</td>
<td>12.044</td>
<td>3.367</td>
<td>7.935 0.235</td>
</tr>
</tbody>
</table>

Note: * indicates significance at 0.05 level, ** at 0.01 level, *** at 0.001 level.
Table 3.3.3. Experiment 2. "Sire and Dam breed" model.

Significant effects means and contrasts.

<table>
<thead>
<tr>
<th>Sire breed</th>
<th>Cre. wt (lbs)</th>
<th>Character</th>
<th>Length (mm)</th>
<th>EMA (sq.cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td>146.9</td>
<td></td>
<td>767.3</td>
<td>30.94</td>
</tr>
<tr>
<td>Landrace</td>
<td>144.3</td>
<td></td>
<td>808.1</td>
<td>28.19</td>
</tr>
<tr>
<td>Dam breed</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inbred LW</td>
<td></td>
<td>Max (mm)</td>
<td>47.6</td>
<td></td>
</tr>
<tr>
<td>Outbred LW</td>
<td></td>
<td></td>
<td>45.7</td>
<td></td>
</tr>
<tr>
<td>Yorkshire x Outbred LW</td>
<td></td>
<td></td>
<td>45.4</td>
<td></td>
</tr>
</tbody>
</table>

Feeding level

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>DFI (lbs/day)</th>
<th>Cre. wt (lbs)</th>
<th>Max (mm)</th>
<th>Mid (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ad libitum-Restricted</td>
<td>0.25</td>
<td>0.92</td>
<td>6.1</td>
<td>2.8</td>
<td>4.4</td>
</tr>
<tr>
<td>Loin</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ad libitum-Restricted</td>
<td>2.5</td>
<td>3.2</td>
<td>3.4</td>
<td>1.7</td>
<td></td>
</tr>
</tbody>
</table>

D = brd x Feeding level contrasts

Fat score (pts)

<table>
<thead>
<tr>
<th></th>
<th>Ad libitum-Restricted</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inbred LW</td>
<td>0.2</td>
</tr>
<tr>
<td>Outbred LW</td>
<td>0.4</td>
</tr>
<tr>
<td>Yorkshire x Outbred LW</td>
<td>-0.4</td>
</tr>
</tbody>
</table>

Table 3.3.4. Experiment 2. "Sire and Dam breed" ad libitum restricted contrasts.

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>FCE (1lb/lb)</th>
<th>DFI (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td>0.19</td>
<td>0.19</td>
<td>0.88</td>
</tr>
<tr>
<td>L</td>
<td>0.31</td>
<td>-0.06</td>
<td>0.95</td>
</tr>
<tr>
<td>ILW</td>
<td>0.26</td>
<td>-0.05</td>
<td>0.82</td>
</tr>
<tr>
<td>OLM</td>
<td>0.21</td>
<td>0.07</td>
<td>0.79</td>
</tr>
<tr>
<td>YLM</td>
<td>0.27</td>
<td>0.18</td>
<td>1.15</td>
</tr>
</tbody>
</table>
The only genotype x feeding level interaction, a dam breed x feeding level interaction for fat score, resulted from the opposite responses of the OLW and YLW dams (table 5,5,3,3). With ad libitum feeding, the former gave a high score, a harder fat, and the latter a low score, a softer fat. The importance of the interaction will be better judged following the results of experiment 4 in which the same LW dam strains are again fed ad libitum and restricted levels.

Discussion

As in the previous experiment, litter subplots were fed either ad libitum or once daily according to a scale. Analysis of the thirteen characters gave only one genotype x feeding level interaction and in general, therefore, genotype x feeding level interaction was an unimportant source of variation.

The only interaction was a dam breed x feeding level interaction for fat score. Experiment 1 results suggested that in general ad libitum feeding gave lower fat scores, i.e., softer back fats, but that the progeny of the LW dams responded differentially by giving slightly higher fat firmness scores. That differential response is repeated here with the different LW strains. OLW dams, comparable with the LW dams of experiment 1, confirmed the earlier result showing firmer fats with ad libitum feeding and ILW dams gave a parallel result. However the YLW dams gave the reverse response, a firmer fat score with restricted feeding. As a result, ranking changed. No explanation for the interaction is immediately obvious. Experiment 4 provides further data on the fat score responses of LW strains to ad libitum and restricted feeding.

Although not statistically significant, the differential effects of feeding level on sire breed (table 5,5,4) are perhaps of
The differential responses occurred with a restriction of daily feed intake for both sire breeds of 21%, which gave fat thickness reductions of 13% for HP progeny and 16% for L progeny. There were parallel responses for other carcass characters. Although not significantly different, the changes in the efficiencies of food conversion which produced these small fat thickness differentials were opposite in direction. Contrary to accepted performance and to that observed in the earlier experiment and in this experiment for HP progeny, Landrace progeny showed no improvement in food conversion efficiency when feed intake was restricted.

These differential responses can be discussed within the growth concepts mentioned in section 2.2. It is possible, for example, that the Landrace restricted intake was below the breed's nutrient requirements for essential tissue growth. Therefore essential tissue gain was depressed, reducing the efficiency of food conversion and giving a slower daily gain. If, on the other hand, the Hampshire/Pietrain restricted intake met its own essential tissue nutrient requirements, HP essential tissue gain would not be depressed and, as feeding was sub appetite, contemporary fat deposition would be reduced. Consequently HP FCE is improved and daily gain less effected for HP than for Landrace and a differential response results.

Whether these observed differences are indicative of effects having practical importance is questioned by the lack of statistical significance and by the large variation observed within the Landrace restricted treatment. The poor food conversion efficiency of some subplots may have resulted from feed wastage. The relative importance of feed wastage and possible variation for essential tissue

...
nutrient requirement is uncertain. In the later experiments, 4 and 5, the restricted feeding was considerably tightened and there was little or no wastage. Results of these experiments will more accurately indicate probable physiological variation and any resulting interactions. It is apparent that any general conclusions from experiment 2 regarding the importance of genotype x feeding level interactions must be made with caution. Feed wastage may have influenced experimental results and population sizes, compared to those of experiment 1, were small. The results for economy of production characters indicated possible differential responses of the kind explicable by the growth concepts outlined in the introductory chapter. Whether these responses were a chance occurrence, or whether their lack of statistical significance was due to a small experimental population cannot be ascertained. However it is likely that more comparisons involving similar genotypes will reveal any recurring tendencies for genotype x feeding level interactions and will therefore confirm or disprove the conclusion drawn from experiments 1 and 2 that genotype x feeding level interaction was an unimportant source of variation. The sire breed comparison of Hampshire/Pietrain and a British White breed is therefore continued in experiments 3, 4 and 5 and a further comparison of Large White strain dams is reported in experiment 4.

3.4 Experiment 3. Crosses of the Hampshire, Landrace, Large White and Pietrain breeds

Experiment 3 was the first of a series of three experiments in which progeny sired by Hampshire/Pietrain and Large White boars were fed ad libitum or to a restricted scale. In the later experiments, numbers 4 and 5, the M.L.C. to appetite test environment gave a further subplot treatment.
**Materials.**

The population was a small sample of Hampshire/Pietrain x Landrace and Large White x Landrace progeny. The litters were from matings of HP and LW boars continuing the investigation of sire breed effect on litter productivity. Litters were born between 2nd and 22nd April 1971 and were sired by 4 HP and 2 LW boars. No HP boars were common to experiments 2 and 3.  

112 pigs were started on the experiment, the first pens on 30th June and the last on 27th July. The last pigs were slaughtered on 10th November 1971. One pig was culled from the experiment due to a rupture and another died from pulmonary failure. No carcass data were obtained for 2 ad libitum and 2 restricted pigs. 106 records, 55 restricted and 51 ad libitum, were therefore available for analysis. These were distributed as 12 restricted and 11 ad libitum subplots of HP x L and 5 restricted and 6 ad libitum subplots of LW x L.  

Feeding levels were again ad libitum and restricted as described in section 3.1 and the diets were as given in table 3.1.1 and 3.2.2. In contrast to earlier experiments, the restricted pigs were fed their ration split equally between two daily feeds. Increments from the scale minimum, 3 lbs., to the maximum, 5 lbs., were made weekly except for pens failing to consume their allocated ration.  

**Methods.**

As in experiment 2, the population size in this experiment suffered by comparison with experiment 1 and, on theoretical grounds is probably inadequate (Robertson, 1959). Consequently the power of the test of statistical significance for interaction will
be low, important interactions may not be detected and chance interactions may be recorded. As noted above the experiment was the first of a series comparing Hampshire/Pietrain and Large White sired progeny on ad libitum and restricted feeding. It is therefore possible to combine the data for analysis. The combined population will rectify any design deficiency and the increased power of the test for interaction will indicate any repeatable interaction.

The combined analysis is reported in section 3.7.

Results.

As a preliminary to the combined analysis, experiment 3 data was analysed fitting the main effects, cross and feeding level, together with their two factor interaction. There were no significant genotype x feeding level interactions. The mean squares and least squares means are tabulated in appendix II.

Discussion of the experiment will follow the analysis of the combined data for experiments 3, 4 and 5 (section 3.7).

3.5 Experiment 4. Crosses of the Hampshire, Large White, Pietrain and Yorkshire breeds.

Materials.

There were three subplots in experiment 4. In addition to the Mountmarle ad libitum and restricted subplots, litters were further split to provide castrate/gilt sib pairs for the MLC central testing programme at the Stirling station. The feeding level on the MLC test is to-appetite as described in Section 3.1 and although the MLC subplots provide contrasts of other environmental effects, the environmental source of variation will continue to be designated "feeding level".
Crossbred litters were born between 17th February and 30th March 1972 and were sired by three outbred Hampshire/Pietrain (HP) boars and three outbred Large White (LW) boars. Dam genotypes were three LW strains as in experiment 2, inbred rotation LW (ILW), outbred LW (OLW) and Yorkshire x outbred LW (YLW). No LW x OLW litters were represented.

There were 56 restricted, 48 ad libitum and 50 MLC fed pigs on the trial, the first pens of which started the experiment on 9th May. The last pig was slaughtered on November 27th. Of the original 134 pigs one dies and no carcass records were obtained for a further three. Analyses therefore considered 130 records, 55 for ad libitum feeding, 45 from restricted and 30 from the MLC regime. There were no streak thickness or fat score measurements for the MLC pigs.

The number of subplots for each strain cross and feeding level is given in Table 3.5.1.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Feeding level</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sire</td>
<td>Dam</td>
</tr>
<tr>
<td>HP</td>
<td>( ILW</td>
<td>6</td>
</tr>
<tr>
<td>HP</td>
<td>( OLW</td>
<td>2</td>
</tr>
<tr>
<td>HP</td>
<td>( YLW</td>
<td>3</td>
</tr>
<tr>
<td>LW</td>
<td>( ILW</td>
<td>3</td>
</tr>
<tr>
<td>LW</td>
<td>( YLW</td>
<td>2</td>
</tr>
</tbody>
</table>

Method.

Class sizes were equivalent to those in the previous experiment and are therefore probably inadequate. As explained
in section 3.4, these deficiencies can be overcome by combining experiments 3 to 5 in a sire breed comparison. The major comparison can therefore be made more accurately in the combined analysis, although some information is provided by analyses of the individual experiment.

In the combined model, dam genotypes will be confounded with experimental period. There will therefore be no indication of dam genotype x feeding level interaction as found in experiment 2 (section 3.3) for fat score. The Large White genotypes giving that result are again reported here and an analysis of the individual experiment may confirm the differential responses shown earlier. It is also possible that experiment 4 may indicate trends in the responses to the ad libitum, to appetite and restricted feeding levels.

To investigate these effects two analyses are presented, model I, a strain cross model with the three feeding levels, and model II, a sire and dam breed model with the ad libitum and restricted feeding levels. The fitting of sire and dam breeds necessitated running separate whole and subplot analyses and only two subplots could be included.

Results.

Model I: The mean squares for the strain cross model with the three feeding levels are presented in table 3.5.2 and the least squares means for the significant effects in table 3.5.3. Table 3.5.2 shows that there were no significant genotype x feeding level interactions and generally the interaction mean squares were smaller than the error mean squares. Of the genotype effects only the carcass weight, length and EMA differences were statistically significant, while the feeding level mean squares for all characters except mid and loin were significant.
Table 3.5.2. Experiment 4. "Strain Cross" model with three feeding levels. Mean squares.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DG</th>
<th>FCE</th>
<th>DFI</th>
<th>Crc.wt.</th>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>Str. Cross (C)</td>
<td>4</td>
<td>0.016</td>
<td>0.018</td>
<td>0.231</td>
<td>42.930**</td>
<td>5333.0***</td>
</tr>
<tr>
<td>Litters</td>
<td>11</td>
<td>0.015</td>
<td>0.020</td>
<td>0.168</td>
<td>6.613</td>
<td>95.5</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>2</td>
<td>0.060**</td>
<td>2.100***</td>
<td>8.042***</td>
<td>480.375***</td>
<td>485.3**</td>
</tr>
<tr>
<td>C x F</td>
<td>8</td>
<td>0.007</td>
<td>0.007</td>
<td>0.117</td>
<td>1.511</td>
<td>97.7</td>
</tr>
<tr>
<td>E_s</td>
<td>20</td>
<td>0.009</td>
<td>0.022</td>
<td>0.128</td>
<td>1.657</td>
<td>61.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
<th>C</th>
<th>K</th>
<th>EMA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Str. Cross (C)</td>
<td>4</td>
<td>31.655</td>
<td>25.545</td>
<td>20.706</td>
<td>23.527</td>
<td>50.200</td>
<td>53.205*</td>
</tr>
<tr>
<td>Litters</td>
<td>11</td>
<td>19.745</td>
<td>18.695</td>
<td>12.467</td>
<td>37.010</td>
<td>40.750</td>
<td>10.384</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>2</td>
<td>69.745**</td>
<td>3.946</td>
<td>9.500</td>
<td>83.772**</td>
<td>75.588**</td>
<td>51.595***</td>
</tr>
<tr>
<td>C x F</td>
<td>8</td>
<td>5.110</td>
<td>2.658</td>
<td>8.069</td>
<td>2.977</td>
<td>14.316</td>
<td>3.384</td>
</tr>
</tbody>
</table>

The Montmore ad libitum and restricted subplots and the MLC to appetite subplot gave three distinct feeding levels (table 3.5.3). The highest intake, ad libitum, gave the worst efficiency of food conversion and the fastest daily gain, while the lowest intake, restricted, had the best food conversion but the slowest daily gain. The MLC environment gave intermediate performance. Carcass characters had inconsistent feed effects, with ad libitum fed pigs having thicker backfat depths at the shoulder than restricted pigs but not at C and K. The MLC fed pigs had significantly thinner fat at C and K than either Montmore treatments but at the shoulder had a similar depth to the ad libitum fed pigs. MLC pigs also had the largest EMA and by far the heaviest carcass.

Genotype effects were less variable and the strain cross mean reflect the important influence of the sire breeds. HP crosses
Table 3.5.3. Experiment 4. "Strain Cross" model with three feeding levels. Cross and Feeding level least squares means.

<table>
<thead>
<tr>
<th>Strain Cross</th>
<th>Crc.wt. (lbs)</th>
<th>Character</th>
<th>EMA (sq.cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Outbred LW)</td>
<td>152.3</td>
<td>765.8</td>
<td>31.99</td>
</tr>
<tr>
<td>HP x (Inbred LW)</td>
<td>155.4</td>
<td>758.1</td>
<td>32.44</td>
</tr>
<tr>
<td>(Yorkshire/Outbred LW)</td>
<td>153.3</td>
<td>769.5</td>
<td>30.65</td>
</tr>
<tr>
<td>LW x (Inbred LW)</td>
<td>150.5</td>
<td>786.9</td>
<td>27.33</td>
</tr>
<tr>
<td>(Yorkshire/Outbred LW)</td>
<td>147.7</td>
<td>798.7</td>
<td>27.19</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Feeding level</th>
<th>DG (lbs/day)</th>
<th>FCE (lbs/1b)</th>
<th>DFI (lbs/day)</th>
<th>Crc.wt. (lbs)</th>
<th>Length (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Restricted</td>
<td>1.44</td>
<td>2.72</td>
<td>3.92</td>
<td>147.6</td>
<td>772.5</td>
</tr>
<tr>
<td>Ad libitum</td>
<td>1.57</td>
<td>3.46</td>
<td>5.45</td>
<td>148.4</td>
<td>783.0</td>
</tr>
<tr>
<td>MLC</td>
<td>1.54</td>
<td>2.78</td>
<td>4.27</td>
<td>158.4</td>
<td>771.9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Max (mm)</th>
<th>C (mm)</th>
<th>K (mm)</th>
<th>EMA (sq.cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Restricted</td>
<td>43.7</td>
<td>22.8</td>
<td>30.8</td>
</tr>
<tr>
<td>Ad libitum</td>
<td>46.6</td>
<td>22.8</td>
<td>39.8</td>
</tr>
<tr>
<td>MLC</td>
<td>46.7</td>
<td>18.4</td>
<td>26.7</td>
</tr>
</tbody>
</table>

had heavier and shorter carcasses with larger EMA than LW crosses. Influence of the LW strains was much smaller.

Model II. Possible interactions between feeding level (ad libitum and Mountmarle restricted) and sire and dam genotypes and the differences between sire breeds and between dam genotypes were investigated by fitting a sire and dam breed model (table 3.5.4). The change in the relative sizes of the whole and split plot mean squares was a result of the separate analyses of whole and split plot observations.

Again there were no significant two factor interactions, however the S, brd x D, brd x feeding level effects for Loin, K
## Table 5.5A. Experiment 1. Sire and Dam breed model: Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DG</th>
<th>FCE</th>
<th>DFI</th>
<th>Crc.wt.</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>0.030</td>
<td>0.002</td>
<td>0.389</td>
<td>65.100***</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>0.003</td>
<td>0.015</td>
<td>0.132</td>
<td>6.432</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>1</td>
<td>0.000</td>
<td>0.011</td>
<td>0.067</td>
<td>4.750</td>
</tr>
<tr>
<td>F</td>
<td>11</td>
<td>0.008</td>
<td>0.009</td>
<td>0.098</td>
<td>2.534</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>0.196*</td>
<td>4.696***</td>
<td>21.715***</td>
<td>3.484</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>1</td>
<td>0.072</td>
<td>0.004</td>
<td>0.306</td>
<td>3.000</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>2</td>
<td>0.028</td>
<td>0.026</td>
<td>0.597</td>
<td>0.584</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>1</td>
<td>0.005</td>
<td>0.083</td>
<td>0.455</td>
<td>0.801</td>
</tr>
<tr>
<td>E</td>
<td>11</td>
<td>0.022</td>
<td>0.051</td>
<td>0.376</td>
<td>3.107</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Length</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>2109.4***</td>
<td>5.333</td>
<td>1.172</td>
<td>7.363</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>305.3***</td>
<td>30.074</td>
<td>22.557</td>
<td>10.748</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>1</td>
<td>41.4</td>
<td>0.368</td>
<td>0.227</td>
<td>0.053</td>
</tr>
<tr>
<td>F</td>
<td>11</td>
<td>32.8</td>
<td>11.924</td>
<td>8.253</td>
<td>4.911</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>1265.6*</td>
<td>216.213**</td>
<td>0.879</td>
<td>5.835</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>1</td>
<td>379.7</td>
<td>27.452</td>
<td>0.775</td>
<td>10.641</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>2</td>
<td>49.3</td>
<td>16.375</td>
<td>5.661</td>
<td>43.158</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>1</td>
<td>7.2</td>
<td>26.255</td>
<td>5.267</td>
<td>55.041*</td>
</tr>
<tr>
<td>E</td>
<td>11</td>
<td>140.3</td>
<td>16.313</td>
<td>10.656</td>
<td>11.361</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>C</th>
<th>K</th>
<th>EMA</th>
<th>Streak Fat score</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. brd</td>
<td>1</td>
<td>0.827</td>
<td>0.563</td>
<td>65.380**</td>
<td>22.688</td>
</tr>
<tr>
<td>D. brd</td>
<td>2</td>
<td>16.331</td>
<td>46.755</td>
<td>0.700</td>
<td>16.113</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>1</td>
<td>0.422</td>
<td>0.068</td>
<td>2.306</td>
<td>1.541</td>
</tr>
<tr>
<td>F</td>
<td>11</td>
<td>16.889</td>
<td>24.615</td>
<td>5.475</td>
<td>7.939</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>0.490</td>
<td>5.464</td>
<td>45.775*</td>
<td>21.778</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>1</td>
<td>0.403</td>
<td>16.217</td>
<td>1.559</td>
<td>16.333</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>2</td>
<td>16.499</td>
<td>23.056</td>
<td>18.226</td>
<td>11.078</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>1</td>
<td>32.541</td>
<td>116.875**</td>
<td>37.683*</td>
<td>4.320</td>
</tr>
<tr>
<td>E</td>
<td>11</td>
<td>16.579</td>
<td>10.770</td>
<td>7.152</td>
<td>20.731</td>
</tr>
</tbody>
</table>
and EMA were significant. Table 3.5.5 lists the contrasts for the three factor interactions which show that whereas the crosses of HP with ILW and YLW and of LW with ILW were generally fatter at Loin and K with ad libitum feeding, the fat depths of HP with GLW and LW with YLW were reduced. Some responses for EMA were consistent with the fat depth interactions. Those sire and dam breed contributions giving reduction in fat depth with ad libitum feeding, HP x GLW and LW x YLW, had increased EMA, while LW x ILW had thicker fat depths with ad libitum feeding and a smaller EMA. The other genotypes gave smaller changes.

Table 3.5.6 gives the feeding level contrasts. Again the increased dietary intake with ad libitum feeding gave an improved daily liveweight gain but a depressed efficiency of food conversion.

Table 3.5.5. Experiment 4. Sire and Dam breed model. Ad libitum restricted contrasts for S\, brd x D\, brd x F interactions.

<table>
<thead>
<tr>
<th>Sire breed</th>
<th>Dam breed</th>
<th>Loin (mm)</th>
<th>K (mm)</th>
<th>EMA (sq.cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td>Outbred LW</td>
<td>-3.1</td>
<td>2.6</td>
<td>3.56</td>
</tr>
<tr>
<td>HP</td>
<td>Inbred LW</td>
<td>1.6</td>
<td>-0.3</td>
<td>1.58</td>
</tr>
<tr>
<td>HP</td>
<td>Yorkshire/outbred</td>
<td>2.4</td>
<td>4.1</td>
<td>0.56</td>
</tr>
<tr>
<td></td>
<td>LW</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Inbred LW</td>
<td>4.0</td>
<td>3.6</td>
<td>-1.44</td>
</tr>
<tr>
<td></td>
<td>Yorkshire/outbred</td>
<td>-3.8</td>
<td>-4.5</td>
<td>4.83</td>
</tr>
</tbody>
</table>

Ad libitum fed pigs also had thicker fat at the shoulder, longer carcasses and a larger EMA.

Sire breed means show that HP sired progeny had heavier but shorter carcasses and a larger eye muscle area. Of the dam breeds, YLW and OLW progeny were longer than the progeny of the inbred rotation Large Whites. Other dam breed differences were not
### Table 3.5.6. Experiment 4. Sire and Dam breed model. Main effect means and contrasts.

<table>
<thead>
<tr>
<th>Sire breed</th>
<th>CRC wt. (lbs)</th>
<th>Length (mm)</th>
<th>EMA (sq. cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td>149.7</td>
<td>767.6</td>
<td>30.81</td>
</tr>
<tr>
<td>LW</td>
<td>145.1</td>
<td>794.1</td>
<td>26.14</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Dam breed</th>
<th>Length (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Outbred LW</td>
<td>783.0</td>
</tr>
<tr>
<td>Inbred LW</td>
<td>772.8</td>
</tr>
<tr>
<td>Yorkshire/outbred LW</td>
<td>786.6</td>
</tr>
</tbody>
</table>

#### Feeding level contrasts

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>FCE (lb/lb)</th>
<th>DFI (lbs/day)</th>
<th>Length (mm)</th>
<th>Max (mm)</th>
<th>EMA (sq. cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ad libitum-Restricted</td>
<td>0.15</td>
<td>0.72</td>
<td>1.55</td>
<td>11.9</td>
<td>4.9</td>
<td>2.21</td>
</tr>
</tbody>
</table>

Significant, although fat depths indicated that ILW progeny were fattest and that generally YLW progeny had least fat.

### Discussion.

The HP/LW comparison was extended in this experiment to include sib pairs tested within the MLC central test program. Environmental contrasts therefore included nutritional, environmental complex and carcass evaluation factors and the Mountmarle comparison continued the feeding level interaction study.

No two factor interactions were found between strain cross and the three test environments, Mountmarle ad libitum, Mountmarle restricted and MLC to-appetite, or between sire and dam genotypes and the Mountmarle feeding levels. Distinct feed intake levels, growth performance and carcass production for the three environments and between the genotypic groups resulted, but there were no significant differential responses.
Although there were no significant two factor interactions in the two models, sire breed × dam breed × feeding level interactions were significant for loin, K and EMA. The comparable analysis for experiment 2 (with Landrace instead of Large White as the contrasting sire breed) showed no three factor interactions, and in view of the small dam breed populations and the inconsistent dam breed responses in experiments 2 and 4, the repeatability of the interactions is questionable and their practical importance doubtful.

Similar conclusions may be drawn about the dam breed × feeding level interaction for fat score in experiment 2. The interaction was not repeated in this experiment and the only measure of consistency between the fat score results was the negative contrast for the YLW dams. Fat score is a parameter seldom used by other workers and the results cannot be related to other experiments. Lush, Thomas, Cuthbertson and Beard (1936) have reported significant sire effects for fat firmness but they did not study possible interactions.

Genotypic effects were dominated by the sire breed effects for carcass weight, carcass length and eye muscle area. Despite these carcass composition differences, sire breed growth efficiency characters were not significantly different, although HP progeny had lower daily feed intake on all three regimes. The analyses have shown that the feed intake restriction (ad libitum compared to restricted) of about 40%, was similar for all genotypes and gave identical or very similar percentage changes for FCE and DG and for carcass composition as described by the split carcass and last rib characters.
Consideration of these feeding level effects shows that the
ad libitum regime, when compared to restricted feeding, gave
increases in carcass length and eye muscle area which suggest a
comparative improvement in fat free body growth. Coincident
with this possible improvement there were marginal increases in
fat depth (2 to 3%) significantly faster liveweight gains,
7 to 12%, and significant depression of FCE, 30%. These changes
suggest the following alternative conclusions:
1. the small increase in fat content produced by ad libitum
feeding has much higher energetic cost than the savings
in maintenance requirements accruing from faster liveweight
gains, or
2. the extent of carcass composition differences was not shown
by linear carcass measurements, or
3. a combination of 1. and 2.

Alternative 2. may result from variation in intramuscular
fat, variation in internal fat depots, e.g. flare fat and/or
variation in trimmed carcass lean/fat ratios not explained by
backfat variation. The present data provide no information on
the alternatives. However Martin, Fredeen, Weiss and Carson
(1972) found no genotypic variation in the proportion of fat in the
different fat depots and no variation for intramuscular fat,
although breed differences for intramuscular fat have been
reported by Jensen, Craig and Robison (1967) and Allen, Forrest,
Chapman, First, Bray and Briskey (1966). It has also been shown
that at 200 lbs. liveweight, subcutaneous fat comprises 30% and
internal fat depots 5% of total fat (Richmond and Berg, 1972).
It is therefore likely that the relative importance of variation
for internal body fat is small and, as split carcass fat depths are a direct measure of subcutaneous fat, any large variation in the major fat depot is likely to have been recorded.

An additional factor is the imprecise relationship between increases in carcass length and eye muscle area and the improvement in fat free body gain as area and length measures may not reflect a change in the weight of lean.

These uncertainties in the description and measurement of carcass composition changes suggest that a more detailed carcass analysis may have allowed a more categoric explanation of the substantial feeding level effects for food conversion efficiency. In addition, it is possible that genotypes exhibited, and feeding levels caused variation for characters, e.g. maintenance requirement, that were assumed constant within the metabolisable energy model (figure 2.2).

Because of these possibilities, and the limitations imposed by population size (of the dam breeds in particular), it is inappropriate to draw firm conclusions meantime. More definite indications of any differential responses, their practical importance and underlying causes, may be given by the combined analysis. The last experiment which contributes to the combined analysis is experiment 5 which completes the series of genotype x feeding level interaction experiments.


Materials.

In experiment 5 there were two replicates in which litter subplots were fed either ad libitum or restricted diets at
Mountmarle or to-appetite at MLC, Stirling. The litters were sired by Hampshire/Pietrain (HP) and Large White (LW) boars out of Duroc/Landrace (DL) and Large White/Landrace (LML) dams.

Farrowing and replicate periods did not overlap. The first replicate litters were born between 1st and 24th October 1971 and the second replicate litters between 4th and 26th April 1972. Replicate 1 covered the months December 1971 to May 1972 and replicate 2 June to November 1972.

A total of 367 pigs were allocated to the combined replicates and 352 records were obtained. In the first replicate 16 litters were allocated as 75 pigs on restricted intake, 69 pigs on ad libitum intake and 30 pigs on to-appetite feeding. The second replicate had 20 litters distributed as 78 restricted pigs, 76 ad libitum and 39 to-appetite. There was one death and one cull in the first replicate and 3 losses of carcasses records, leaving 169 complete production records. In the second replicate 3 HP sired pigs died of congenital heart failure and one LW sired pig died of haemorrhagic enteritis. The deaths were from both ad libitum and restricted feeding levels. Another 6 carcass records were not obtained at the bacon factory and 183 records were available for analysis. The number of subplots for each cross is given in Table 3.6.1.

Table 3.6.1. Experiment 5. Genotype and Feeding Level subplot numbers.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Replicate 1</th>
<th>Replicate 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>Feeding level</td>
<td>MLC</td>
</tr>
<tr>
<td></td>
<td>Restricted</td>
<td>Ad lib.</td>
</tr>
<tr>
<td>HP</td>
<td>DL</td>
<td>6</td>
</tr>
<tr>
<td>HP</td>
<td>LML</td>
<td>4</td>
</tr>
<tr>
<td>LW</td>
<td>DL</td>
<td>6</td>
</tr>
<tr>
<td>LW</td>
<td>LML</td>
<td>3</td>
</tr>
</tbody>
</table>
All parents were outbred. In replicate 1, 3 HP and 3 LW boars were used and in replicate 2, 3 HP and 2 LW boars. One HP boar was common to both replicates and in all 5 boars of each breed were represented. Fifteen of the dams were also common to both replicates. LW boars in this and earlier experiments were principally purchased from the Newcastle selection herd and were derived from an ad libitum testing regime. All other parent stock was ABRO bred.

Methods.

Models considering genotypic effects as crosses and as sire and dam breeds were fitted. The analysis of the cross model fitted all three subplot treatments. The three factor interaction, cross x replicate x feeding level, was not fitted. The Mountmarle results were used for the sire and dam breed model.

Results.

The mean squares for the cross model with three feeding levels are given in Table 3.6.2. The whole plot error mean square is designated $E_w$ and the subplot error, $E_s$.

Table 3.6.2. Experiment 3. "Cross" model with three feeding levels:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DF</th>
<th>FCE</th>
<th>DFI</th>
<th>Crc.wt.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>3</td>
<td>0.021</td>
<td>0.030</td>
<td>0.133</td>
<td>123.634***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>1</td>
<td>0.026</td>
<td>0.836***</td>
<td>0.865*</td>
<td>3.218</td>
</tr>
<tr>
<td>C x R</td>
<td>3</td>
<td>0.023</td>
<td>0.002</td>
<td>0.273</td>
<td>3.050</td>
</tr>
<tr>
<td>$E_w$</td>
<td>31</td>
<td>0.009</td>
<td>0.021</td>
<td>0.125</td>
<td>3.625</td>
</tr>
<tr>
<td>Feeding level(F)</td>
<td>2</td>
<td>0.232***</td>
<td>6.395</td>
<td>26.629***</td>
<td>360.348***</td>
</tr>
<tr>
<td>C x F</td>
<td>6</td>
<td>0.006</td>
<td>0.023</td>
<td>0.018</td>
<td>5.498</td>
</tr>
<tr>
<td>R x F</td>
<td>2</td>
<td>0.063**</td>
<td>0.215***</td>
<td>0.813***</td>
<td>2.636</td>
</tr>
<tr>
<td>$E_s$</td>
<td>64</td>
<td>0.011</td>
<td>0.017</td>
<td>0.102</td>
<td>3.153</td>
</tr>
</tbody>
</table>
Table 3.6.2. contd.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Length</th>
<th>Max</th>
<th>Mid</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>3</td>
<td>14640.7***</td>
<td>27.688</td>
<td>69.200**</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>1</td>
<td>666.0</td>
<td>480.780***</td>
<td>29.180</td>
</tr>
<tr>
<td>C x R</td>
<td>3</td>
<td>188.8</td>
<td>18.198</td>
<td>5.066</td>
</tr>
<tr>
<td>Ew</td>
<td>31</td>
<td>224.3</td>
<td>11.582</td>
<td>15.269</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>2</td>
<td>949.4**</td>
<td>265.945***</td>
<td>64.116***</td>
</tr>
<tr>
<td>C x F</td>
<td>6</td>
<td>60.5</td>
<td>8.163</td>
<td>15.666</td>
</tr>
<tr>
<td>R x F</td>
<td>2</td>
<td>222.9</td>
<td>21.517</td>
<td>10.050</td>
</tr>
<tr>
<td>E_E</td>
<td>64</td>
<td>155.2</td>
<td>8.496</td>
<td>7.593</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Loin</th>
<th>C</th>
<th>K</th>
<th>ENA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>3</td>
<td>28.253</td>
<td>35.418</td>
<td>6.451</td>
<td>159.259***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>1</td>
<td>2.771</td>
<td>3.032</td>
<td>0.002</td>
<td>51.620*</td>
</tr>
<tr>
<td>C x R</td>
<td>3</td>
<td>4.342</td>
<td>7.923</td>
<td>31.039</td>
<td>5.581</td>
</tr>
<tr>
<td>Ew</td>
<td>31</td>
<td>17.137</td>
<td>15.988</td>
<td>24.209</td>
<td>8.999</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>2</td>
<td>76.157***</td>
<td>166.705***</td>
<td>527.049***</td>
<td>51.423***</td>
</tr>
<tr>
<td>C x F</td>
<td>6</td>
<td>12.717</td>
<td>7.963</td>
<td>19.334</td>
<td>8.227</td>
</tr>
<tr>
<td>R x F</td>
<td>2</td>
<td>31.017*</td>
<td>9.828</td>
<td>52.345</td>
<td>18.337*</td>
</tr>
<tr>
<td>E_E</td>
<td>64</td>
<td>6.757</td>
<td>12.849</td>
<td>19.257</td>
<td>3.955</td>
</tr>
</tbody>
</table>

Although all characters gave significant feeding level (i.e. test environment) effects, there were no significant genotype x feeding level interactions. The only significant two factor interactions were replicate x feeding level interactions (table 3.6.3).

Table 3.6.3. Experiment 5. "Cross" model with three feeding levels; Interaction means.

<table>
<thead>
<tr>
<th>DG (lbs/day)</th>
<th>Replicate x Feeding level means</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Replicate 1</td>
</tr>
<tr>
<td>Restricted</td>
<td>1.41</td>
</tr>
<tr>
<td>Ad libitum</td>
<td>1.61</td>
</tr>
<tr>
<td>MLC</td>
<td>1.47</td>
</tr>
<tr>
<td></td>
<td>Loin (mm)</td>
</tr>
<tr>
<td>----------------</td>
<td>-----------</td>
</tr>
<tr>
<td></td>
<td>Replicate 1</td>
</tr>
<tr>
<td>Restricted</td>
<td>21.0</td>
</tr>
<tr>
<td>Ad libitum</td>
<td>24.3</td>
</tr>
<tr>
<td>MLC</td>
<td>21.3</td>
</tr>
</tbody>
</table>

Table 3.6.4 lists the significant main effect means and, as in experiment 4, the subplot treatments gave three distinct feed intake levels. The resulting FCEs for the MLC and restricted treatments were not different but ad libitum FCE was significantly inferior which resulted in significantly different means for daily gain. Carcass weights reflected the effects shown in experiment 4 with ad libitum and restricted weights similar and MLC carcasses 9 lbs. heavier. Ad libitum carcasses were the shortest and had the smallest eye muscle area and MLC carcasses were the longest and had the largest 'eye area. Fat thickness results were consistent for mid, C and K, with ad libitum pigs having the thickest and MLC pigs the thinnest fat. At the loin MLC pigs had thicker fat than the restricted fed pigs and at the shoulder the MLC and ad libitum samples had similar fat depths and restricted pigs thinner fat.

The cross effects given in table 3.6.4 indicate, as has been found in the previous experiments involving HP and LW sired progeny, that in general the differences appear attributable to sire breed effects. The cross means also suggest that LWL progeny give longer carcasses with less mid backfat and larger eye muscle areas than DL progeny. Cross effects were also significant for mid backfat thickness with HP DL progeny having most fat and LW sired crosses the least fat. Other fat depths were not significantly different but DL crosses were generally fatter than LWL crosses.
The effects of sire breed and dam genotypes and their possible interactions with ad libitum and restricted feeding levels were investigated in the sire and dam breed model (table 3.6.5). The relative change in the size of the mean squares results from the separate analyses of whole and split plot observations.

Again there were no interactions of sire breed or dam genotype with feeding level and the only interaction involving feeding level was with replicate for FCE (table 3.6.6).
Table 5.6.5. Experiment 5. "Sire and Dam breed" model. Mean squares (Mutton data only).

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Source</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Replicate (R)</strong></td>
<td>1</td>
<td>0.009</td>
<td>0.440***</td>
</tr>
<tr>
<td>S. brd</td>
<td>1</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>D. brd</td>
<td>1</td>
<td>0.000</td>
<td>0.001</td>
</tr>
<tr>
<td>R x S. brd</td>
<td>1</td>
<td>0.094**</td>
<td>0.001</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>1</td>
<td>0.036</td>
<td>0.035*</td>
</tr>
<tr>
<td>E_w</td>
<td>32</td>
<td>0.009</td>
<td>0.008</td>
</tr>
<tr>
<td><strong>Feeding level (F)</strong></td>
<td>1</td>
<td>0.925***</td>
<td>19.810***</td>
</tr>
<tr>
<td>R x F</td>
<td>1</td>
<td>0.030</td>
<td>0.642***</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>1</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>1</td>
<td>0.035</td>
<td>0.139</td>
</tr>
<tr>
<td>R x S. brd x F</td>
<td>1</td>
<td>0.013</td>
<td>0.062</td>
</tr>
<tr>
<td>R x D. brd x F</td>
<td>1</td>
<td>0.059</td>
<td>0.018</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>1</td>
<td>0.021</td>
<td>0.098</td>
</tr>
<tr>
<td><strong>E_s</strong></td>
<td>32</td>
<td>0.021</td>
<td>0.046</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Source</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Replicate (R)</strong></td>
<td>1</td>
<td>14.071</td>
<td>8.128</td>
</tr>
<tr>
<td>S. brd</td>
<td>1</td>
<td>12.576</td>
<td>0.569</td>
</tr>
<tr>
<td>D. brd</td>
<td>1</td>
<td>2.667</td>
<td>15.720</td>
</tr>
<tr>
<td>R x S. brd</td>
<td>1</td>
<td>0.209</td>
<td>0.325</td>
</tr>
<tr>
<td>R x D. brd</td>
<td>11</td>
<td>9.592</td>
<td>7.490</td>
</tr>
<tr>
<td>S. brd x D. brd</td>
<td>1</td>
<td>5.018</td>
<td>1.790</td>
</tr>
<tr>
<td>E_w</td>
<td>32</td>
<td>6.853</td>
<td>10.421</td>
</tr>
<tr>
<td><strong>Feeding level (F)</strong></td>
<td>1</td>
<td>298.082***</td>
<td>207.395**</td>
</tr>
<tr>
<td>R x F</td>
<td>1</td>
<td>8.362</td>
<td>0.065</td>
</tr>
<tr>
<td>S. brd x F</td>
<td>1</td>
<td>11.581</td>
<td>3.086</td>
</tr>
<tr>
<td>D. brd x F</td>
<td>1</td>
<td>0.006</td>
<td>8.712</td>
</tr>
<tr>
<td>R x S. brd x F</td>
<td>1</td>
<td>5.396</td>
<td>19.754</td>
</tr>
<tr>
<td>R x D. brd x F</td>
<td>1</td>
<td>1.824</td>
<td>5.261</td>
</tr>
<tr>
<td>S. brd x D. brd x F</td>
<td>1</td>
<td>32.257</td>
<td>16.341</td>
</tr>
<tr>
<td>E_s</td>
<td>32</td>
<td>14.615</td>
<td>25.562</td>
</tr>
</tbody>
</table>
Table 3.6.6. Experiment 5. "Sire and Dam breed" model:

Interaction means and contrasts (Mountmarle data only).

<table>
<thead>
<tr>
<th>S. brd x D. brd interaction means</th>
<th>Replicate x D. brd interaction means</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>FCE</strong> (lb/lb)</td>
<td><strong>Carc. wt.</strong> (lb)</td>
</tr>
<tr>
<td>HP</td>
<td>LW</td>
</tr>
<tr>
<td>DL</td>
<td>3.18</td>
</tr>
<tr>
<td>LVL</td>
<td>3.13</td>
</tr>
</tbody>
</table>

Replicate x Feeding level contrasts:
- Replicate 1: 0.61
- Replicate 2: 0.88

Other significant interactions were for S. brd x D. brd and Replicate x D. brd, (table 3.6.6). The carcass weight S. brd x D. brd interaction means show that while HP crosses were superior to LW crosses, dam breed rankings were dependent upon sire breed. For FCE, sire and dam level rankings reversed with the alternative parent breed. Reversed rankings are also shown in the replicate x dam breed interactions for DG and DFI and ranking of dam breeds was therefore dependent on both replicate and sire breed.

Table 3.6.7. Experiment 5. "Sire and Dam breed" model:

Main effect means and contrasts (Mountmarle data only).

<table>
<thead>
<tr>
<th>Replicate</th>
<th><strong>FCE</strong> (lb/lb)</th>
<th><strong>DFI</strong> (lbs/day)</th>
<th><strong>Length</strong> (mm)</th>
<th><strong>Max</strong> (mm)</th>
<th><strong>EM</strong> (mm)</th>
<th><strong>Streak</strong> (mm)</th>
<th><strong>Fat score</strong> (pts)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.27</td>
<td>4.94</td>
<td>777.6</td>
<td>45.5</td>
<td>30.64</td>
<td>19.6</td>
<td>2.4</td>
</tr>
<tr>
<td>2</td>
<td>3.04</td>
<td>4.60</td>
<td>784.6</td>
<td>40.4</td>
<td>28.42</td>
<td>23.1</td>
<td>2.7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sire breed</th>
<th><strong>Carc. wt.</strong> (lb)</th>
<th><strong>Length</strong> (mm)</th>
<th><strong>EM</strong> (mm)</th>
<th><strong>Streak</strong> (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HP</td>
<td>149.7</td>
<td>761.7</td>
<td>31.96</td>
<td>22.7</td>
</tr>
<tr>
<td>LW</td>
<td>145.4</td>
<td>800.5</td>
<td>27.10</td>
<td>20.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Dam breed</th>
<th><strong>Length</strong> (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DL</td>
<td>773.5</td>
</tr>
<tr>
<td>LVL</td>
<td>788.7</td>
</tr>
</tbody>
</table>
Table 3.6.7 contd.

**Feeding level contrasts**

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>FCE (lb/lb)</th>
<th>DFI (lbs/day)</th>
<th>Length (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ad libitum-Restricted</td>
<td>0.16</td>
<td>0.75</td>
<td>1.64</td>
<td>4.8</td>
</tr>
</tbody>
</table>

Max (mm) Mid (mm) Loin (mm) C (mm) K (mm)

<table>
<thead>
<tr>
<th></th>
<th>Max (mm)</th>
<th>Mid (mm)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
<th>K (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ad libitum-Restricted</td>
<td>4.8</td>
<td>1.8</td>
<td>2.9</td>
<td>2.4</td>
<td>3.0</td>
</tr>
</tbody>
</table>

**Discussion.**

Contributory genotypes to the final comparison of crossbreds within alternative test environments/feeding levels were the commercially dominant Large White and Landrace, Hampshire/Pietrain crossbred boars as a possible sire breed competitor and Duroc as a potential dam line constituent. It was suggested in chapter 2 that Pietrains and Durocs were examples of extreme genotypes for the characters appetite and essential tissue growth. Large Whites from the Newcastle herd (selected on ad libitum feeding) provided a further deviation from the probable high lean:low intake performance of the Hampshire/Pietrain progeny. The experiment therefore exposed genotypes of expected different performance to two feeding levels and a third test environment, and had a population size such that genotype x environment interactions likely to be economically important would also be statistically significant.

Despite these expected parent breed performances and the contrasting feed intake levels, there were no genotype x environment interactions and no trends within the results to indicate their possible occurrence in a larger experiment.
Therefore, in agreement with the earlier experiments, genotypic rankings were comparable for the test environments used.

Although there were no genotype x environment interactions several other two factor interactions were reported (table 3.6.6). Of these the s. brd x d. brd interactions for FCE and carcass weight, if repeatable, have considerable economic importance. The interactions show an accentuation of the HP sire breed superiority for carcass weight when crossed with LWL dams and indicate the cross's superior performance for FCE. A consistent feature of the crossbred comparisons has been the competitive performance of the HP sired progeny. The potential of a sire breed will be enhanced if it interacts advantageously with the dominant British commercial dam, LWL. Further comparisons are therefore needed to study the repeatability of the interactions and to substantiate any superiority of the HP x LWL crossbred.

Interactions of replicate with other main effects contributed the majority of the remaining interactions. The effect of sampling error between replicates was presumably large and other sources of replicate variation which may have contributed to replicate interaction effects were the variation due to sires within crosses, macroclimatic effects, the variation due to the arbitrary nature of the increments of the restricted and MLC feeding regimes and the variation due to observer difference. The reduced DFI in replicate 2 and the concomitant results may be attributed more feasibly to sampling error, sire differences and seasonal effects, while the arbitrary nature of the restricted feeding regimes is likely to have contributed to the replicate x feeding level interactions within the three feed model analysis.
Outwith the interactions previously discussed and in the absence of any genotype x test environment interaction the crossbred performances can be evaluated directly. Particularly noteworthy is the absence of genotypic effects, and especially the similar growth efficiency performance of the HP and LW sire breeds and the DL and LWL dams. As would be expected from the comparable growth data there were no genotypic effects for fat thickness. However, in agreement with earlier experiments, HP progeny had heavier carcasses with larger eye muscle areas than LWs. HP progeny also tended to have thinner fat at all points except the mid back and HP streaks were significantly thicker. Economic advantages for these characters therefore favour the HP and suggest some HP advantage for weight of carcass lean. However, the shorter HP carcass has disadvantages for bacon production and possibly for meat quality. Therefore, while the performance of the HP as a sire breed, and the DL as a dam breed suggest potential commercial merit, their productivity including, for example, measurement of meat quality and stress susceptibility, carcass proportions and lean distribution, requires further investigation.

Contrasting with the small genotypic effects, the comparison of Mountmarle and MLC environments produced marked differences in performance. Some of the effects in the three feed model e.g. carcass weight, length, eye muscle area and the inconsistent fat depths, were undoubtedly due to differences between the observations made on the Mountmarle population at a commercial bacon factory and the observations of the MLC carcass evaluation procedure. These differences will not have biased estimates of interaction or main effects but evaluation procedure and feeding
level variation is confounded and comparison of MLC to appetite with Mountmarle restricted and ad libitum feeding level effects for carcass composition is impossible.

For growth data it is apparent that the gradation of intakes followed the pattern expected: ad libitum, MLC and restricted, and FCEs deteriorated with increasing intake and liveweight gains followed DFI rankings. DFI feeding regime differentials were consistent for experiments 4 and 5 and indicate the proportional expression of appetite on each feeding system. In addition the absence of significant genotypic appetite and efficiency variation ensured that the maximum level imposed by the Mountmarle scale — 5 lbs/day — did not influence performance beyond the concomitant changes expected with the restriction, food conversion efficiency showed marked improvement and fatness was reduced. The economic advantages resulting are considerable and outweigh any financial loss resulting from slower daily gain. Therefore, in agreement with previous results, feeding level performances indicated an economic advantage in restricting feed intake and, as no genotype x feeding level interactions have been found, feeding level restriction can be recommended for all the genotypes studied.

The conclusions drawn from experiment 5 are again consistent with those drawn from earlier experiments: genotype x feeding level interaction is an unimportant source of variation, restricted feeding improves post-weaning performance and Hampshire/Pietrain sired progeny give growth efficiency and carcass characteristics comparable with Large White sired progeny.
Further discussion of the importance of genotype x feeding level interaction, of the Hampshire/Pietrain and Large White sire comparison and of the feeding level effects will follow the results of a combined analysis of experiments 3, 4 and 5.

3.7 Combined analysis of Experiments 3, 4 and 5: The post-weaning performance of Large White and Hampshire/Pietrain sired progeny on ad libitum and restricted feeding regimes.

As the individual experiments 3, 4 and 5 may have lacked sensitivity for important genotype x feeding level interactions, an analysis was performed of the combined data, thereby increasing the power of the tests of significance for interaction, sire breed and feeding level.

3.7.1 Materials and methods.

Populations, procedures and data collection were reported in the previous sections. Only the Mountmarle ad libitum and restricted subplot observations were used in this analysis and they comprised 300 progeny sired by 9 Hampshire/Pietrain (HP) boars and 188 sired by 7 Large White (LW) boars.

The HP boars were the progeny of H sires and P dams and were bred at ABRO from imported, or the progeny of imported, stock. The LW boars were either purchased high pointed performance tested board or were purchased from the Newcastle University selection herd or were their progeny. In either case the LW boars are likely to represent above average performance for the breed. The two sire breeds were mated to six different dam genotypes distributed over four time periods. These dam 'breeds' and time periods were confounded and were combined as eight 'breed'/period combinations.
The model fitted the main effects: breed of boar, dam 'breed'/period combinations, feeding method and sex, together with the two factor interactions of these effects. Three factor interactions were not fitted and individual observations were used. Food conversion efficiency and its derivative daily feed intake were pen observations but for the analysis they were used as if recorded on individual pigs. These assumptions, together with the intra-litter correlation of the litter mates, do not bias the contrasts of interest, although the significance of differences will have been overestimated.

The analysis considered the fixed character, slaughter weight, as well as the thirteen characters considered previously.

3.7.2 Results.

The mean squares for the analysis are given in table 3.7.1. The effect of particular interest, the sire breed x feeding level interaction, was not a significant source of variation for any character and the residual mean square was generally larger than the interaction mean square. As there were no sire breed x feeding level interaction and if the other interactions involving these main effects are ignored, the sire breed and feeding level means can be evaluated directly.

The means for the two feeding regimes, Table 3.7.2, show that distinct feeding levels resulted and that the higher intake of the ad libitum progeny gave faster but less efficient growth and produced carcasses of comparable size but with more fat. Feeding level did not affect the area of eye muscle nor the fat firmness score. There were no feed or sire breed effects for slaughter weight.
Table 5.7.1. Combined analysis of experiments 3, 4 and 5. Mean squares.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Source</th>
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</thead>
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<td>Mid</td>
<td>154.0***</td>
</tr>
<tr>
<td>Dam breed/Period (D)</td>
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<td>160.7***</td>
<td></td>
</tr>
<tr>
<td>Sex (Sx)</td>
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<td>1.46</td>
<td>2.2</td>
</tr>
<tr>
<td>Feeding level (F)</td>
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<td>3.716***</td>
<td></td>
</tr>
<tr>
<td>S x D</td>
<td>6</td>
<td>1.554***</td>
<td></td>
</tr>
<tr>
<td>S x Sx</td>
<td>1</td>
<td>0.716***</td>
<td></td>
</tr>
<tr>
<td>SS x F</td>
<td>1</td>
<td>0.012</td>
<td></td>
</tr>
<tr>
<td>D x Sx</td>
<td>7</td>
<td>17.525***</td>
<td></td>
</tr>
<tr>
<td>D x F</td>
<td>7</td>
<td>0.208</td>
<td></td>
</tr>
<tr>
<td>S x F</td>
<td>1</td>
<td>171.4**</td>
<td></td>
</tr>
<tr>
<td>Residual</td>
<td>454</td>
<td>154.0***</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Source</th>
<th>df</th>
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</thead>
<tbody>
<tr>
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<td>Mid</td>
<td>160.7***</td>
</tr>
<tr>
<td>Dam breed/Period (D)</td>
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<td>1.905***</td>
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</tr>
<tr>
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<td></td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>3.716***</td>
<td></td>
</tr>
<tr>
<td>S x D</td>
<td>6</td>
<td>1.554***</td>
<td></td>
</tr>
<tr>
<td>S x Sx</td>
<td>1</td>
<td>0.716***</td>
<td></td>
</tr>
<tr>
<td>SS x F</td>
<td>1</td>
<td>0.208</td>
<td></td>
</tr>
<tr>
<td>D x Sx</td>
<td>7</td>
<td>17.525***</td>
<td></td>
</tr>
<tr>
<td>D x F</td>
<td>7</td>
<td>0.208</td>
<td></td>
</tr>
<tr>
<td>S x F</td>
<td>1</td>
<td>171.4**</td>
<td></td>
</tr>
<tr>
<td>Residual</td>
<td>454</td>
<td>154.0***</td>
<td></td>
</tr>
</tbody>
</table>
Growth efficiency characters were not significantly different for the sire breeds although the HP sired progeny ate less, had the same efficiency of food conversion and therefore grew slightly more slowly. The HP progeny had a considerable advantage for carcass weight and although the carcass was shorter (3 cms), fat thicknesses were the same at the shoulder and on the last rib cut, were significantly less at the loin and significantly more at the mid back. In addition area of eye muscle was significantly greater for the HP progeny.

Lean et al. (1972) have shown that the shorter carcasses of Pietrain and Pietrain cross pigs with similar fat thicknesses and a larger E%A than Landrace pigs had higher weights of lean tissue and lower weights of fat and bone. From the similar characteristics shown by the HP carcasses compared to the LW carcasses, it is likely that the HP progeny had a higher carcass lean % than the LW progeny.

Fat firmness scores were not different for the sire breeds.

Commercial merit of the HP sires within particular market outlets will depend upon dead weight grading systems reflecting the advantages shown by the genotype's progeny. All progeny in the experiments were slaughtered for Wiltshire bacon production and routinely graded by the MLC. The grading standards were those in force at the start of the comparison in 1971 and were based on a range of carcass weights and back fat measurements taken at the loin, the shoulder and at 'C'. A minimum carcass length of 775 mm was required for the top grade (1). Increasing fatness devalued a carcass to grade 2 or 3. Table 3.7.3 gives the comparative grading results. There was some imbalance for subclass numbers but this should not seriously affect the comparison.
Table 5.7.2. Sire breed and feeding level least squares means and standard errors.

<table>
<thead>
<tr>
<th>Character</th>
<th>Large White</th>
<th></th>
<th>Hampshire/Pietrain</th>
<th></th>
</tr>
</thead>
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<tr>
<td></td>
<td>Mean</td>
<td>S.E.</td>
<td>Mean</td>
<td>S.E.</td>
</tr>
<tr>
<td>SI wt. lbs</td>
<td>194.5</td>
<td>0.47</td>
<td>194.6</td>
<td>0.34</td>
</tr>
<tr>
<td>DG lbs/day</td>
<td>1.47</td>
<td>0.01</td>
<td>1.45</td>
<td>0.01</td>
</tr>
<tr>
<td>FCE lb/lb</td>
<td>3.15</td>
<td>0.02</td>
<td>3.14</td>
<td>0.01</td>
</tr>
<tr>
<td>DFI lbs/day</td>
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<td>0.05</td>
<td>4.55</td>
<td>0.03</td>
</tr>
<tr>
<td>CRC wt. lb</td>
<td>143.2</td>
<td>0.42</td>
<td>147.1</td>
<td>0.31</td>
</tr>
<tr>
<td>C Llength mm</td>
<td>794.4</td>
<td>1.60</td>
<td>764.6</td>
<td>1.18</td>
</tr>
<tr>
<td>Max mm</td>
<td>44.0</td>
<td>0.45</td>
<td>45.1</td>
<td>0.33</td>
</tr>
<tr>
<td>Mid mm</td>
<td>22.2</td>
<td>0.36</td>
<td>23.6</td>
<td>0.27</td>
</tr>
<tr>
<td>Loin mm</td>
<td>21.9</td>
<td>0.34</td>
<td>20.6</td>
<td>0.25</td>
</tr>
<tr>
<td>C mm</td>
<td>22.4</td>
<td>0.40</td>
<td>22.0</td>
<td>0.30</td>
</tr>
<tr>
<td>K mm</td>
<td>29.5</td>
<td>0.33</td>
<td>29.2</td>
<td>0.39</td>
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<tr>
<td>EMA sq.cm</td>
<td>26.97</td>
<td>0.29</td>
<td>21.22</td>
<td>0.21</td>
</tr>
<tr>
<td>Streak mm</td>
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<td>0.47</td>
<td>22.0</td>
<td>0.35</td>
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<tr>
<td>Fat score pts</td>
<td>2.5</td>
<td>0.05</td>
<td>2.6</td>
<td>0.04</td>
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</table>

<table>
<thead>
<tr>
<th>Character</th>
<th>Restricted</th>
<th></th>
<th>Ad libitum</th>
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<tr>
<td></td>
<td>Mean</td>
<td>S.E.</td>
<td>Mean</td>
<td>S.E.</td>
</tr>
<tr>
<td>SI wt. lbs</td>
<td>195.1</td>
<td>0.42</td>
<td>194.0</td>
<td>0.44</td>
</tr>
<tr>
<td>DG lbs/day</td>
<td>1.39</td>
<td>0.01</td>
<td>1.53</td>
<td>0.01</td>
</tr>
<tr>
<td>FCE lb/lb</td>
<td>2.82</td>
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</tr>
<tr>
<td>DFI lbs/day</td>
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<tr>
<td>CRC wt. lb</td>
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<td>145.2</td>
<td>0.40</td>
</tr>
<tr>
<td>C Llength mm</td>
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<td>1.44</td>
<td>777.1</td>
<td>1.50</td>
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<tr>
<td>Max mm</td>
<td>41.6</td>
<td>0.41</td>
<td>45.4</td>
<td>0.43</td>
</tr>
<tr>
<td>Mid mm</td>
<td>22.3</td>
<td>0.33</td>
<td>23.5</td>
<td>0.34</td>
</tr>
<tr>
<td>Loin mm</td>
<td>20.7</td>
<td>0.30</td>
<td>21.9</td>
<td>0.32</td>
</tr>
<tr>
<td>C mm</td>
<td>21.5</td>
<td>0.36</td>
<td>22.9</td>
<td>0.38</td>
</tr>
<tr>
<td>K mm</td>
<td>28.1</td>
<td>0.47</td>
<td>30.4</td>
<td>0.49</td>
</tr>
<tr>
<td>EMA sq.cm</td>
<td>28.94</td>
<td>0.26</td>
<td>29.25</td>
<td>0.27</td>
</tr>
<tr>
<td>Streak mm</td>
<td>21.7</td>
<td>0.42</td>
<td>20.4</td>
<td>0.44</td>
</tr>
<tr>
<td>Fat score pts</td>
<td>2.6</td>
<td>0.04</td>
<td>2.5</td>
<td>0.05</td>
</tr>
</tbody>
</table>
Table 7.5.2. Experiments 3, 4 and 5. Sire breed/feeding level
Grading results.

<table>
<thead>
<tr>
<th>Breed of sire:</th>
<th>Hampshire/Pietrain</th>
<th>Large White</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Grade:</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Feeding regime</td>
<td>Percentage</td>
</tr>
<tr>
<td>Grade distribution</td>
<td>Restricted</td>
<td>28</td>
</tr>
<tr>
<td></td>
<td>with minimum length</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(Ad libitum)</td>
<td>18</td>
</tr>
<tr>
<td>Grade distribution</td>
<td>Restricted</td>
<td>65</td>
</tr>
<tr>
<td></td>
<td>without minimum</td>
<td></td>
</tr>
<tr>
<td></td>
<td>length requirement</td>
<td>37</td>
</tr>
</tbody>
</table>

The grading results gave no indication of interaction between feeding regime and sire breed. LW consistently produced a higher percentage of grade 1 carcasses and HP a higher percentage of carcasses in grade 2. Carcasses meeting the grade 1 requirements for fat depths but failing the minimum length requirement are graded 2. This necessarily penalised the shorter but possibly leaner HP population. In view of several findings showing that length adds little as an additional prediction of lean content (Buck et al., 1962; Cuthbertson and Pease, 1963) reclassification of the gradings, disregarding the length requirement seemed valid. The adjusted results removed the grading advantage of the LW sired progeny and an important genotype x environment interaction is demonstrated in which HP and LW sired progeny are the genotypes and grading standards with and without minimum length requirements are the environmental factors.

As genotype x nutrition interactions do not appear important for grading standards with or without the length requirement, an economic comparison of ad libitum and restricted feeding regimes becomes the straightforward comparison of growth
efficiencies and grading percentages. Growth efficiency means (Table 3.7.2) show that, for the post weaning production period (initial weight 60 lbs., final weight, 195 lbs.), restricted fed pigs took 9 days longer to reach slaughter weight but needed nearly 90 lbs. less feed, and grading results indicate that restricted feeding gave at least 20% more pigs in grade 1 (neglecting the HP pigs downgraded because of length). The grading improvement was drawn mainly from grade 3, which accentuates the economic benefits of restricted feeding and stresses the excess fat deposition associated with ad libitum feeding.

3.7.3 Discussion

The combined analysis indicates that genotype x feeding level interactions were unimportant within this body of data. Previous discussion attributed the lack of interactions to the absence of large genotypic variation for appetite and carcass lean and the proportional expression of breed appetite on the restricted feeding regimes. The present results follow that reasoning and therefore support the conclusion that genotype x feeding level interactions are unlikely to be important in comparisons of present genotypes considered competitive for the economic production of lean meat. Further discussion of the genotype x feeding level interaction experiments and their implications will follow in section 3.8.

In the absence of interaction between sire breed and feeding level, the main effects can be evaluated directly.
Sire breeds.

It has been shown that, at the same slaughter weight, HP sired progeny have growth efficiency characters comparable with those of LW sired progeny, a heavier carcass and apparent advantages for yield of lean meat. Lishman and Smith (1971) have shown similar HP advantages. The growth efficiency performance of HP progeny is therefore better than the mid parent value expected from the breed performances given in table 2.1 and indicates that the purebred performances underestimate crossbred performance.

The doubtful meat quality and stress resistance of pigs with Pietrain genes (MacDougall and Disney, 1972; Lister, 1969) was not investigated in the present study, although HP progeny tended to have a higher casualty rate than LW progeny. By contrast Curran et al. (1972) report that HP sired progeny gave a lower casualty rate compared to Landrace progeny and that no HP died in transit to the abattoir.

A commercial disadvantage of the HP sired progeny was their significantly shorter carcass which gave a substantial financial penalty within the bacon grading system. Curran et al. (1972) report a similar finding, which therefore indicates the necessity for market outlets which have no minimum length requirement.

Size of litters produced by the matings of sire breeds are usually of small importance. However matings of HP sires have been shown to improve litter size when compared to matings of LW sires (King, 1968). Recent evidence has confirmed the initial finding (King and Thorpe, 1973) and highlights the
overall merit of the HP as a possible competitive sire of slaughter generation pigs for the economic production of lean meat.

Feeding regimes.

The influence of feeding regime on slaughter performance agreed with the general conclusions of Braude's review (1972). The contrast of ad libitum and restricted feeding, with its concomitant energy and protein level differences gave increased growth rate and reduced carcass lean because energy increment increased live weight gain but not appreciably the deposition of lean tissue (Lodge et al., 1972). Expressed as characters within the analysis, growth rate and fat thicknesses are increased on ad libitum feeding but there are no feeding level effects for eye muscle area and carcass length. Thus while protein intakes can influence growth rate and carcass lean, the effects will be overridden by intakes of energy (Cooke et al., 1972).

The feeding regime comparison indicated that the appetites of both genotypes were such that fat deposition on ad libitum feeding exceeded acceptable commercial standards. With restricted feeding, reduced fat deposition gave a greater than 20% improvement in the number of grade 1 pigs which, combined with the improved FCE, gave a large economic advantage. Therefore, for most genotypes to produce a commercially acceptable product, restricted feed intake is required.

A discussion considering the results from all five genotype x feeding level interaction experiments is presented in section 3.8 and concludes the chapter.

3.8 Discussion.

One of the principal problems to be overcome by an
experimenter investigating genotype x environment interaction is the provision of an experimental population of sufficient size to ensure that differential responses of a magnitude likely to be economically important will also be statistically significant. The major objective of the five experiments reported here was the evaluation of the crossbred performance of exotic pig breeds in comparison with British breeds. The genotypes were not especially chosen for the study of genotype x environment interactions nor were the experiments especially designed to investigate the roles of appetite, lean gain and daily maintenance requirement in genotype x nutrition interactions. Nonetheless, as discussed in the review, the contributing breeds, as their performances became characterised, were found to show a wide variation in the characters appetite and lean gain and would have been thought likely to produce genotype x nutrition interactions when contrasting feeding levels were imposed.

To enable interactions to be estimated, the crossbred comparisons were designed as split plot factorials which, by imposing two, and later three, environmental factors on the crossbred genotype populations strained the available resources. However theoretical study (Robertson, 1959) indicated that minimal sub class sizes for the estimation of interaction were generally met and where some class sizes were sub optimal, for example the dam breed comparisons in experiments 2 and 4, the experiments provided preliminary information in interactions with dam genotypes but adequate estimation of interaction with sire breeds. When there were too few animals, the occasional significant interaction might have merely indicated the need for larger experiments, although the results showed no trends indicative of
differential responses likely to give more frequent interactions in larger experiments. However, to ensure that important interactions were not neglected through lack of experimental sensitivity, the combined data of experiments 3, 4 and 5 were analysed. The combined populations gave a greatly increased power for the significance test of interaction between sire breed and feeding level and, as has been discussed in section 3.7, the analysis gave no statistically significant interaction.

A further design feature of concern is the limited breed samples employed in these experiments. In particular, comparisons with the exotic breeds presented difficulties because of the small breeding populations of the recently imported breeds. To minimise the sampling error, efforts were made to use as many sires as possible for each breed in each comparison. The combined comparison of the Hampshire/Pietrain and Large White sire breeds for example had nine and seven sires respectively. The sample of their populations, while not large, should not have been unrepresentative. However had interactions been found it would have been difficult to generalise to the parent breeds from the samples used. Jensen (1974) has emphasised the need for defining the populations used in comparisons and it is suggested that for these comparisons the exotic breed samples can only be taken as representative of the available British population of the particular breed. To generalise the conclusions of the genotypic comparisons and the interaction findings to the total Pietrain or Hampshire populations is therefore not possible, especially as within breed variation will almost certainly give important sire x feeding level interaction.
Notwithstanding these possible limitations, the experiments gave consistent results (sections 3.2 to 3.7) and general conclusions can be drawn. Initially, remarks will be directed towards the characters studied, and for the major objective of the experiments, the comparison of crossbred genotypes, the traditional economic characters, daily gain, food conversion efficiency (which necessitated measuring daily feed intake) and fat depths were adequate to define the inter-related components of post weaning performance. The results of the bacon gradings, which determined the financial returns for the pig carcasses were presented in section 3.7. However the literature review indicated that, for the elucidation and prediction of interactions, it is necessary to study growth responses in terms of the physiological characters, tissue deposition rates, feed conversions and appetite. While the experiments were not designed to test this assertion, the characters measured did give a direct measure of appetite and an indirect measure of lean gain. Discussion of the results in terms of appetite and lean gain variation has therefore been possible, although as discussed earlier some caution has to be exercised in the prediction of carcass lean from indirect measurements made on carcasses of widely different dimensions.

The experimental results are summarised in table 3.8.1 and it can be seen that interaction was infrequently a significant source of variation. In the five experiments there were no statistically significant growth efficiency interactions and only occasional interactions for carcass composition characters. The latter were discussed earlier and, because of inconsistent maternal and paternal breed responses to the feeding level contrast, it was concluded that the interactions were most probably a result of sampling variation. Overall, therefore, the interactions
Table 3.8.1. Summary of the significant effects in the genotype x environment interaction experiments.

<table>
<thead>
<tr>
<th>Experiment No.</th>
<th>No. of Pigs</th>
<th>Genotype</th>
<th>Feeding regimes (F)</th>
<th>Daily gain</th>
<th>Daily feed intake</th>
<th>Feed conversion</th>
<th>Prefects</th>
<th>Growth rate</th>
<th>Shoulder</th>
<th>Hind fat</th>
<th>Fat finish</th>
<th>Fat fineness score</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>670</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Hampshire</td>
<td>Ad libitum</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>Pietrain</td>
<td>D</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lacombe</td>
<td>F</td>
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<td>Hampshire/</td>
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<td>Hampshire/</td>
<td>Ad libitum</td>
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* P < 5%
** P < 1%
*** P < 0.1%
na Measurements not available
C Crossbred genotypes of the breeds listed
were thought to have low repeatability from experiment to experiment and can be dismissed as having no practical significance.

Statistically significant genotypic differences in experiment 1 were limited to some backfat thicknesses, weight of carcass and eye muscle area and there were no genotype effects for the growth efficiency characters, daily feed intake, daily gain and food conversion efficiency. The absence of growth efficiency differences was unexpected and contrary to the evidence reported by the Ministry of Agriculture, Food and Fisheries (1970), although studies with crossbreds have found that, when crossed with the British white breeds, Hampshires and Pietrains often give growth efficiencies equivalent to or better than the purebred white breeds (Lishman and Smith, 1971; Lean et al., 1972; Smith et al., 1973). The estimates of the Hampshire and Pietrain purebred performances derived from their two and three breed crosses in experiment 1 are likely therefore to have been overestimated, just as their purebred performances given qualitatively in table 2.1 will have underestimated, their crossbred growth efficiency performance.

The possibility that the crossbred performance for growth efficiency of these breeds can exceed the average of the purebred parents was borne out when the Hampshire/Pietrain sires were compared with the British white breeds, Large White and Landrace in matings with dam genotypes derived from the Large White, Landrace and Duroc breeds. Again there were no genotypic effects for daily gain, food conversion efficiency or daily feed intake but there were consistent differences between genotypes for carcass weight, carcass length and eye muscle area. As discussed in
section 3.7, these differences suggested some Hampshire/Pietrain advantage for carcass lean and the comparison with Large White showed that the crossbred was a competitive sire for the economic production of lean meat.

Growth concepts suggested a rationalisation of genotype x feeding level interaction which, for interactions to occur, necessitated differential expression and suppression of appetite variation. Within the present data, the probability of genotype x feeding level interaction was therefore limited by the lack of significant genotypic effects for appetite. Furthermore the three environments gave proportional expression to the small genotypic appetite differences. Ad libitum feeding gave full expression of appetite, the Mountmarle scale was dependent on and gave expression to appetite within the scale's minimum and maximum levels, and the NFC to-appetite regime gave expression to genotypic appetite variation within twice daily twenty minute feeding periods.

The experiments can therefore be criticised for not imposing other feeding regimes, notably feeding to a time scale, which would give no expression of appetite variation and which are or could be used commercially or in selection programmes. The generality of the conclusion that genotype x feeding level interaction is unimportant may therefore be questioned. However, the experiments have shown that not only were there no genotypic effects for growth efficiency characters but also that carcass composition differences between e.g. the Hampshire/Pietrain and Large White sire breeds, were small. The genotypes were therefore unlikely to give feeding level interactions even on feeding regimes, e.g. a time scale, which totally suppressed appetite variation.
Further points to be raised in the discussion of the genotype x feeding level interaction experiments include the relevance of interbreed interaction study to the choice of intra-bred selection environments, suggestions for further genotype x environment interaction experiments and the conclusions drawn from the experiments about the roles of appetite, lean gain and daily maintenance requirement in genotype x nutrition interaction. These topics will be left to the final chapter so that the conclusions drawn from the protein level experiment can be included.

The genotype x protein level interaction experiment is described in chapter 4.
CHAPTER 4

INTERACTION BETWEEN GENOTYPE AND PROTEIN LEVEL
FOR POST-WEANING PERFORMANCE AT TWO SLAUGHTER WEIGHTS

Among the many factors which may lead to interactions, the quality of the diet and in particular the protein concentration, is one which attracts attention. The importation of the Pietrain breed to Britain in the 1960s provided a situation in which it was thought that this very lean breed (table 2.1) might require different quantities of dietary protein than the existing British breeds, Landrace, Wessex and Essex. There was therefore the possibility of important genotype x protein level interaction at commercial levels of dietary protein concentration and breed comparisons of the Pietrain and British pig breeds would need to consider possible genotype x protein level interactions.

When imported, the commercial application of the Pietrain was thought to be limited to pork (130 lbs) and heavy hog (260 lbs) slaughter weight production because, among other factors, bacon grading requires a minimum carcass length which exceeds that used for the Pietrain. Ad libitum feeding is used extensively in pork and heavy hog production emphasising the producer's economic gain from high growth rates and increased throughput. In addition the relationship between productive energy and 'essential tissue' growth curves (figure 2.2) shows that ad libitum feeding is likely to lead to comparatively little excess carcass fat at a pork slaughter weight, although this will not be true at heavy hog weight.

It was against this production background that in 1964-1967 the Pig Industry Development Authority (PIDA) financed a crossbred comparison of pigs of the Pietrain, Landrace, Essex and Wessex
breeds, when fed *ad libitum* for slaughter at pork and heavy hog weights. The factorial comparison had a split plot design so that half of each litter could be fed a high protein ration and half a low protein ration and possible genotype x protein level interactions investigated.

Analysis of some of the experimental data has been reported by King (1972a). A more comprehensive analysis of genotype x protein level interaction is reported here.

4.1 Materials and methods

Genotypes

The parent breeds of the different genotypes were:

<table>
<thead>
<tr>
<th>Sire</th>
<th>Dam</th>
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<tr>
<td>Large White (LW) x LW</td>
<td>(LW)</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>(ELW)</td>
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<tr>
<td>Pietrain x LW</td>
<td>(PLW)</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>(LLW)</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>(WLW)</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>(LWW)</td>
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Essex, Wessex and Landrace boars were purchased from herds which, by an examination of pedigrees, were found to make a major contribution to the breed's population in Britain (Appendix III lists contributing herds). The Pietrain boars were a direct importation from Belgium and a small herd of Pietrain sows was kept to maintain the pure breed. The sire breeds, other than Pietrain, represented the major British breeds at the time and boars were assumed representative of their breed populations.

The Large White dams were drawn from the University College of North Wales, Bangor, control herds. The herd size was maintained at 16 boars and 32 sows with replacements being
chosen at random subject to the restriction that each boar should be replaced by a son and each sow by a daughter
(Cook et al., 1971). The mating procedure is described by Watson (1968) and is such that genetic changes over the years are minimised. The herd can therefore provide stock of relatively constant genetic merit.

The reciprocal cross of the Wessex $\delta^X$ Large White $\phi$ mating, i.e. Large White $\delta^X$ Wessex $\phi$, was included in the experiment on the basis of evidence from a 1960 PIDA survey. 1500 herds were surveyed and the majority, 905, had purebred sows of which 24% were Wessex and 4% Essex. Therefore the Wessex dam rather than the Essex was a major contributor of pure and crossbred progeny and warranted comparison of its crossbred progeny. Its inclusion gave a direct contrast of $W \delta^X LW \phi$ and $LW \delta^X W \phi$ progeny and measured any deviation of the commercially unorthodox cross.

Each genotype was represented by progeny sired by 7, 8 or 9 boars. The dams started the experiment as gilts and were retained for 3 or 4 parities. At each of the slaughter weights there were 1, 2 or 3 litters sired by each boar and the basic design was replicated eight times. In this way, each replicate had 4 or 5 litters for each genotype with half slaughtered at pork weight and half at heavy hog weight. The experiment totalled 806 pork pigs in 220 subplots and 752 heavy hog pigs in 209 subplots. Of these, 447 of the pork pigs and 423 of the heavy hog pigs were dissected.

Mating, farrowing and pre-weaning management

The experiment was carried out at PIDA's Pig Research Station, Stockton-on-Forest, Yorkshire, hereafter referred to
as Stockton.

Batch mating and farrowing were practised. Litters were introduced to creep feed at 10 days of age and males were castrated and all pigs weighed at 3 wks. of age. As the post-weaning period was to be in outdoor wooden huts, creep heating was switched off at about 25 days to start the hardening off process. A gradual transition from creep pellets to a 'growing' diet started at about 6 wks. of age. Weaning was at 56 days and live weights were recorded at this stage.

Experimental housing

The experiment was a factorial comparison of split plot design with a litter as the whole plot and the protein level factors as the subplot treatments. A whole plot was therefore housed in two finishing pens (outdoor wooden huts), with each pen containing a subplot of 3 or 4 pigs depending on litter size. Subplots were balanced as far as possible for sex ratios and initial liveweight. Where pigs were surplus to experimental requirements they were removed on a heaviest/lightest basis so that the pigs left for selection were those nearest the litter mean. Litters were allocated at random to either pork or heavy hog slaughter weights.

Nutrition

The experimental diets were compounded to provide, in combination, high and low concentrations of protein. The feeding patterns were:
Slaughter Dietary Post-weaning period
weight protein level 30-130 lbs 130-260 lbs

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<tr>
<td>Pork</td>
<td>High</td>
<td>Diet A (19.7% protein)</td>
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<tr>
<td></td>
<td>Low</td>
<td>Diet E (16.0% protein)</td>
<td>-</td>
</tr>
<tr>
<td>Heavy hog</td>
<td>High</td>
<td>Diet A (18.7% protein) Diet E (16.0% protein)</td>
<td>-</td>
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<tr>
<td></td>
<td>Low</td>
<td>Diet E (16.0% protein) Diet E (13.7% protein)</td>
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The experimental diets were fed ad libitum and the test period began at a pen mean liveweight of 50 lbs. The change of diet for heavy hog pigs was at a pen mean liveweight of 130 lbs, a procedure approximating to commercial practise. Dietary components and calculated chemical composition are given in Tables 4.1.1 and 4.1.2.

### Table 4.1.1. Dietary components (percentages of air dry weight)

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<tr>
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<th>A₁</th>
<th>E₁</th>
<th>E₂</th>
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<tr>
<td>Barley meal</td>
<td>60.0</td>
<td>65.0</td>
<td>70.0</td>
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<tr>
<td>Fine wheat feed</td>
<td>25.0</td>
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<td>25.0</td>
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<tr>
<td>White fish meal</td>
<td>10.0</td>
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<tr>
<td>Soya bean meal</td>
<td>5.0</td>
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(all with mineral and vitamin supplement)

### Table 4.1.2. Diets - calculated chemical composition (percentages of air dry weight).

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<tr>
<td>Protein</td>
<td>18.7</td>
<td>16.0</td>
<td>13.7</td>
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<tr>
<td>Lysine</td>
<td>0.92</td>
<td>0.71</td>
<td>0.53</td>
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<tr>
<td>Total digestible nutrients</td>
<td>68.5</td>
<td>68.8</td>
<td>68.9</td>
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<tr>
<td>Metabolisable energy (kcal/lb)</td>
<td>1.30</td>
<td>1.31</td>
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Total digestible nutrient (TDN) values (table 6.1.2) were calculated from 'book' values of the TDNs for dietary components. Calculation of metabolisable energy (ME) assumes that the digestible energy of TDN is 4.4 kcal/g. (A.R.C., 1967)
and that ME is about 95% of digestible energy (Diggs et al., 1959). Diet A₁ was the standard progeny test ration with 18.7% protein fed at PIDA (subsequently MLC) test stations until 1971.

The diets fed to heavy hogs in the finishing period (130-260 lbs liveweight) had lower protein contents than the growing period (50-130 lbs liveweight) diets. This is usual commercial practise and the contrast of high and low protein levels reflected the range of recommended protein levels at that time.

It will be noted that the diets were, for all intents and purposes, isocaloric. The diets were fed ad libitum and energy intake differences will therefore only be due to genotypic variation for appetite. It is presumed that dietary protein concentration has no effect on appetite. Dietary intake, within genotypes, is generally to a constant daily digestible energy intake (Cole, Hardy and Lewis, 1972).

Protein:lysine ratios were not constant in the three diets. The concentration of lysine increased relative to the decline in protein concentration and the change in protein concentration was therefore accompanied by changes in protein quality. For convenience the dietary protein changes will be described as changes in dietary protein concentration.

Health

Throughout the experiment health was generally good and no infections likely to affect performances were recorded.
Character measurement and definition

Near slaughter weight pigs were weighed weekly, and when
porkers exceeded a live weight of 125 lbs and heavy hogs 255 lbs,
they were slaughtered that afternoon at the commercial slaughter-
house of Messrs. Woods of Mirfield.

All carcasses provided the conventional linear measurements
and, in addition, a random castrate/gilt pair from each subplot
was dissected by the PIDA dissection unit, Sherburn-in-Elmet.
The following account of the measurement and definition of
economy of production and carcass composition characters is
therefore applicable to all pigs in the experiment, while the
dissection characters apply to approximately half of the pigs.

Carcass assessment procedure is detailed below. The
location of some carcass measurements and joint divisions are
shown in figures 4.1.1 and 4.1.2.

First day

1. Pigs passed through the usual factory procedures of
   stunning, sticking, scalding, dehairing and mechanical scraping
   and evisceration.

2. The sternum of the pig was sawn through the centre.

3. Carcasses were split into two sides by chopping down through
   the centre of the vertebral column from the ham to the atlas.

4. The Ministry cold dead (carcass) weight was recorded.

5. pH measurements at 90 mins. post mortem were taken in the
   adductor muscle of the left side. Five readings were taken,
   3 with a calomel electrode in one position, and 2 in a different
   position. Ambient temperatures were recorded.

6. The heads of all pigs were removed completely by a cut at
   right angles to the back at the level of the atlas, and weighed.
7. The carcasses were left in a chillroom overnight.

Second day

8. The length of the left and right sides were taken from the notch of the anterior edge of the first rib to the anterior edge of the symphysis pubis. The average was recorded.

9. The depth of the left sides were taken in the region of the shoulder.

10. The depth of the subcutaneous fat and skin of the left side in the midline of the back was measured at the following points: shoulder, mid back, loin 2 (see fig. 4.1.1).

11. The left side of the carcass was placed on a table and straightened and on those left sides to be dissected, a line was drawn from the notch on the first rib to the anterior edge of the symphysis pubis. The line marked the division between back and streak (see fig. 4.1.2). While the side was lying on the table, the flare fat and kidney were removed carefully from those pigs not to be dissected and the weights of each was recorded separately.

The left side of each carcass was cut at right angles to the back at the level of the posterior edge of the head of the last rib. In replicates 6, 7 and 8 the forequarter and hindquarter (+ psoas minor) were weighed and recorded.

12. The following measurements were taken on the anterior cut surface of the carcass: A, B, C, K, J, E and D (see fig. 6.1.1). A tracing was taken of the anterior cut surface and the 'eye' muscle area measured from the tracing by planimeter.

13. A subjective assessment of the condition of the freshly exposed cross section of the eye muscle was made and categorised as follows:
LENGTH

DEPTH

LOIN 2

MIDBACK

SHOULDER

CUT SIDE

FIGURE 4.1 PIG CARCASS SHOWING THE LOCATION OF SOME CARCASS MEASUREMENTS
FIGURE 4.2 PIG CARCASS SHOWING DIVISION INTO JOINTS.
a. Normal—normal colour and texture with no exudation.
b. Wet—normal colour and texture but showing signs of watery exudation.
c. Pale—pale colour but normal texture and no exudation.
d. Dry—normal colour, coarse texture and unusually dry.
e. Wet and pale—pale in colour with coarse texture showing exudation or a spongy consistency.
f. Dry and pale—pale in colour with coarse texture and unusually dry.

14. An estimate of the colour of the eye muscle cross section was obtained by using a modified EEL Smoke Stain Reflectometer set to 50 on a grey Formica panel (British Standard 2660, 9-096) (see MacDougall et al., 1969).

15. The left side of all pigs to be dissected was marked clearly and placed in a chillroom until they could be dissected.

**Dissection**

The fore and hind quarters to be dissected were split into four standardised commercial joints, shoulder, back, streak and ham (figure 4.1.2). Jointing prior to dissection gave ease of handling, but more particularly, provided detailed information on the comparative yield of the cuts. The ham joint was removed by a cut at right angles to the line of the back at the anterior edge of the symphysis pubis and the shoulder joint by a cut at right angles to the line of the back at the posterior edge of the head of the fourth rib. The division between the back and streak joints was the line drawn from the notch of the first rib to the anterior edge of the symphysis pubis (second day, para 11). For the analyses the subjoints of the back and streak joints were disregarded.
Individual joints were dissected into muscle, subcutaneous fat, intermuscular fat, bone, skin and glands. Fat was classified as subcutaneous until it reached the same level as the adjacent peripheral muscles. The remaining mass was divided into lean, intermuscular fat, bone and a remainder consisting of tendon, glands and major blood vessels. Tissue weights within joints were recorded and the tissue weights for the side were therefore the sum of the relevant tissue weights in each joint. Weights of tissues within the head, tail and feet were not included. These were included in the Ministry carcass weight. The weight of psoas muscle was included in the lean tissue weight of the back joint. Variation for psoas muscle weight was not examined.

Dissection varied slightly during the experiment, e.g. some of the earlier dissected pigs included feet dissection data, while the majority did not. Small corrections, derived by averaging tissue weights for the feet dissections, were subtracted from the relevant tissue weights of the earlier pigs. Any inaccuracy resulting from the correction is likely to be negligible.

In the analyses a distinction is made between carcass weight as a character and carcass weight as the basis for calculation of joint and tissue percentages of carcass weight. The character carcass weight is the Ministry cold dead (carcass) weight. Carcass weight for percentage derivation is the sum of the weights of lean tissue, subcutaneous fat, intermuscular fat, bone, skin and glands, plus the weight of the head, flare fat, kidney and feet. Expressing tissue percentages as a proportion of the sum of component tissues reduces any inaccuracy resulting from moisture loss during dissection.
Other possible sources of error in the measurement of split carcass and dissection traits include inaccuracies in carcass splitting, any carcass bilateral asymmetry and differences between dissectors. Cuthbertson (1968) dismisses the last two factors as important sources of error but comments upon the difficulty in accurately splitting carcasses. However, unless the differences due to main effects for carcass shape and length were sufficient to influence the splitting and/or jointing of carcasses then important inaccuracies are unlikely to have occurred.

Carcass and dissection characters are listed below. Definitions are not given except where it is thought the text requires amplification. Contractions and units follow the character named:

- Carcass weight: lbs (Carc. wt.)
- Carcass length: mm (Length)
- Carcass depth: mm (Depth)
- Backfat thicknesses - Shoulder mm (Max)
- Midback mm (Mid)
- Loin = 2 mm (Loin)
- 'C' mm (C)
- 'K' mm (K)
- 'J' fat depth = maximum depth of third layer of fat mm (J)
- Streak 'E' = fat depth of belly mm (E)
- Streak 'D' = depth of muscle and interspersed fat over E mm (D)
- Eye muscle 'A' = maximum width of eye muscle mm (A)
- Eye muscle 'B' = maximum depth of eye muscle perpendicular to A mm (B)
- Eye muscle area sq. cm. (EMA)
Eye muscle colour - an EEL reflectometer reading, is a measure of brightness component of colour and higher value recorded, greater the reflectance and therefore the lighter the colour.

Eye muscle condition* - a subjective assessment within one of six categories: normal, wet, pale, dry, pale and wet, pale and dry (given in the analyses as 1-6 respectively).

pH*  
Fore quarter weight* lbs (Foreq)  
Hind quarter weight* lbs (Hindq)

* These characters had large numbers of missing values. The subpopulations formed by pigs with observations for these characters were analysed as for characters with no missing values.

Shoulder % ** (Sh%)  
Back % (Back %)  
Streak % (Strk %)  
Ham % (Ham %)  
Lean % (Lean %)  
Fat % (Fat %)  
Subcutaneous fat % (Scf %)  
Intermuscular fat % (Imf %)  
Bone % (Bone %)  
Lean % (Sh, B, Str, H(Lean %
Subcutaneous fat % of Shoulder, Back (Scf %
Intermuscular fat % Streak and Ham. (Imf %
Bone % (Bone %)

The carcass and dissection characters listed represent different populations. All pigs were measured for the characters carcass weight to eye muscle colour. Eye muscle conditions, pH, fore and hind quarter were, however, only measured on subpopulations within the experiment. Dissected pigs provided observations for the characters shoulder % to bone % of shoulder.

Of the economy of production characters, feed conversion

** All percentages, unless otherwise stated, are of carcass weight as defined in the text.
efficiency (FCE) was measured on a pen basis. Food added to the ad libitum hopper was summed and the remainder at the end of the test subtracted to give the weight of meal consumed by the pen. A pen losing a pig during the experiment was debited with all food consumed but credited with the weight gain of the pig withdrawn from the experiment. Daily gain (DG) on test was an individual observation and the product of the pen mean DG and FCE gave daily feed intake (DFI). Daily gain of the carcass weight (CDG) was also calculated.

It was suggested that relative rates of lean and fat tissue deposition, as dictated by appetite and 'essential tissue' variation, are the underlying causes of interaction. The examination of tissue level growth and efficiency characters was therefore a logical extension of the analysis. The characters considered are defined below.

So that pen mean observations of tissue dietary conversion ratios and tissue growth rates could be calculated, lean and fat tissue percentages of non-dissected pigs were predicted using multiple regression equations of carcass measurements using the method described by Conniffe and Moran (1972). The analyses deriving the multiple regression equations are reported in Appendix III.

The liveweight, carcass weight and tissue weight economy of production characters are defined below. Their units and contractions are given:

Daily gain = average daily liveweight gain from the start of the test to the last live weight. 1bs/day (DG)

Feed conversion efficiency = the weight of meal consumed by a pen divided by the pen weight increment from the initial to final live weight 1bs/1bs (FCE)
Daily feed intake = average weight of meal consumed by the pen per day of test 1 lb/day (DFI)

Carcass daily gain = average daily gain of carcass weight from start of the test to the final carcass weight 1 lb/day (CDG)

Lean tissue growth rate = average daily gain of lean tissue on test 1 lb/day (LTGR)

Fatty tissue deposition rate = average daily deposition of fatty tissue on test 1 lb/day (FTDR)

Fat free body growth rate = average daily gain of fat free carcass weight on test 1 lb/day (FFBGR)

Lean tissue food conversion = the weight of meal consumed by a pen divided by the pen lean tissue weight increment on test 1 lb/lb (LTFC)

The calculation of tissue gains assumed an initial carcass weight of 32.5 lbs, an initial lean tissue weight of 17.5 lbs and an initial fatty tissue weight of 8.5 lbs. The values were derived from the data of Richmond and Berg (1971a) and Cuthbertson (1972). It was assumed that genotypic differences for initial weights were likely to contribute only negligible bias to derived characters.

Analytical methods

The experiment was conducted in a split plot design, litters making up the whole plots and protein levels the subplot treatments. The experiment had eight replicates and was repeated for each of two slaughter weights. Analyses were carried out within slaughter weights.

Three least squares analyses of variance are reported:

Analysis I describes the economy of production, split carcass and meat quality characters measured on all pigs or on sub-populations. Cross, replicate, protein level and sex (castrate or gilt) are included as main effects, together with their two factor interactions.
Analysis II applied the same model to those characters specific to the dissected population.

Analysis III describes pen mean observations with sex effects excluded. Main effects were cross, replicate and protein level and their two factor interactions.

No three factor interactions were fitted in the analyses which were completed with a least squares computer programme (Harvey, 1968). Programme procedures for split plot designs were discussed in 'Analytical methods', section 3.1.

Limitations of programme matrix store necessitated a modification of the procedure. The nested effect, litter within crosses and replicates, which is the whole plot error term, was omitted from initial analyses, run 1. In run 2 main effects were absorbed and litters fitted nested within the absorbed crosses and replicates. Litter sums of squares and mean squares were derived from run 2. Subtracting litter sums of squares from run 1 residual sums of squares gave the subplot error sums of squares and, by dividing by their degrees of freedom, the subplot error mean square. The complete analysis of variance was now available and the whole plot mean squares, crosses, replicates and their interaction, were tested for significance against the litter mean square and the subplot effects, protein level, sex and their interactions, were tested for significance against the subplot error mean square.

Corrections for weight at slaughter and for sex

As noted in Chapter 3, variation in weight at slaughter will occur with weekly slaughterings and additional variation in observed characters will therefore result. Similarly
subplot sex ratio differences will bias observed pen mean characters. Differences of final weight and sex ratio were removed by applying appropriate corrections calculated by the methods described in section 3.1. No correction was made for variation in initial weight as it was considered unlikely to give any important increase in experimental precision.

Corrections were applied whether or not they were significantly different from zero. Pork and heavy hog populations were corrected to 134 lbs and 257 lbs respectively. The standard deviations of slaughter weight were 4.7 lbs for pork and 5.0 lbs for heavy hogs. Applying the corrections shown in tables 4.1.3 and 4.1.4 therefore gave only small and often no change to most observed characters. In general most corrections were larger for pork pigs than for heavy hogs.

No comparable estimates are reported in the literature. However the corrections are consistent with extrapolations of published estimates for pigs slaughtered at 200 lbs (King, 1957) and were considered adequate for the adjustment of the data. All further analyses were based on the corrected data.

Of the pen mean characters considered in analysis III all but FCE and DFI and their derivative LTFC were calculated as means of slaughter weight corrected observations. The slaughter weight correction analysis was not applicable to the pen mean observations FCE and DFI and no correction was made. It was thought that the precision of analysis III would not be seriously affected.
<table>
<thead>
<tr>
<th>Character</th>
<th>Pork Correction*</th>
<th>S.E.</th>
<th>Heavy hog Correction*</th>
<th>S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily gain lbs/day</td>
<td>0.012</td>
<td>0.001</td>
<td>0.014</td>
<td>0.001</td>
</tr>
<tr>
<td>Carcass daily gain lbs/day</td>
<td>0.018</td>
<td>0.001</td>
<td>0.011</td>
<td>0.001</td>
</tr>
<tr>
<td>Carcass weight lbs</td>
<td>0.754</td>
<td>0.019</td>
<td>0.565</td>
<td>0.027</td>
</tr>
<tr>
<td>Length mm</td>
<td>1.375</td>
<td>0.116</td>
<td>0.957</td>
<td>0.153</td>
</tr>
<tr>
<td>Depth mm</td>
<td>0.432</td>
<td>0.076</td>
<td>0.352</td>
<td>0.090</td>
</tr>
<tr>
<td>Neck mm</td>
<td>0.140</td>
<td>0.032</td>
<td>0.104</td>
<td>0.043</td>
</tr>
<tr>
<td>Mid mm</td>
<td>0.126</td>
<td>0.022</td>
<td>0.076</td>
<td>0.034</td>
</tr>
<tr>
<td>Loin mm</td>
<td>0.153</td>
<td>0.027</td>
<td>0.105</td>
<td>0.041</td>
</tr>
<tr>
<td>C mm</td>
<td>0.082</td>
<td>0.020</td>
<td>0.057</td>
<td>0.036</td>
</tr>
<tr>
<td>K mm</td>
<td>0.161</td>
<td>0.026</td>
<td>0.110</td>
<td>0.038</td>
</tr>
<tr>
<td>J mm</td>
<td>0.086</td>
<td>0.009</td>
<td>0.039</td>
<td>0.018</td>
</tr>
<tr>
<td>E mm</td>
<td>0.037</td>
<td>0.011</td>
<td>-0.005</td>
<td>0.018</td>
</tr>
<tr>
<td>D mm</td>
<td>0.015</td>
<td>0.021</td>
<td>-0.008</td>
<td>0.032</td>
</tr>
<tr>
<td>A mm</td>
<td>0.130</td>
<td>0.033</td>
<td>-0.092</td>
<td>0.038</td>
</tr>
<tr>
<td>B mm</td>
<td>0.167</td>
<td>0.028</td>
<td>0.096</td>
<td>0.037</td>
</tr>
<tr>
<td>EMA sq.cm</td>
<td>0.104</td>
<td>0.015</td>
<td>0.046</td>
<td>0.023</td>
</tr>
<tr>
<td>Encolour pts</td>
<td>-0.002</td>
<td>0.004</td>
<td>-0.003</td>
<td>0.005</td>
</tr>
<tr>
<td>EEncondition pts</td>
<td>0.004</td>
<td>0.005</td>
<td>-0.012</td>
<td>0.015</td>
</tr>
<tr>
<td>pH units</td>
<td>0.002</td>
<td>0.003</td>
<td>0.009</td>
<td>0.004</td>
</tr>
<tr>
<td>Forequarter lbs</td>
<td>0.166</td>
<td>0.013</td>
<td>0.125</td>
<td>0.035</td>
</tr>
<tr>
<td>Hindquarter lbs</td>
<td>0.139</td>
<td>0.011</td>
<td>0.127</td>
<td>0.027</td>
</tr>
</tbody>
</table>

* Change for each lb increase in slaughter weight.
### Table 4.1.4. Analysis II. Corrections for slaughter weight.

<table>
<thead>
<tr>
<th>Character</th>
<th>Pork Correction*</th>
<th>S.E.</th>
<th>Heavy hog Correction*</th>
<th>S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lean %</td>
<td>-0.053</td>
<td>0.031</td>
<td>-0.013</td>
<td>0.031</td>
</tr>
<tr>
<td>Fat %</td>
<td>0.098</td>
<td>0.033</td>
<td>0.037</td>
<td>0.036</td>
</tr>
<tr>
<td>Subcut. fat %</td>
<td>0.073</td>
<td>0.030</td>
<td>0.026</td>
<td>0.032</td>
</tr>
<tr>
<td>Intermuscle, fat %</td>
<td>0.026</td>
<td>0.008</td>
<td>0.012</td>
<td>0.008</td>
</tr>
<tr>
<td>Bone %</td>
<td>-0.014</td>
<td>0.009</td>
<td>0.002</td>
<td>0.008</td>
</tr>
<tr>
<td>Shoulder %</td>
<td>0.003</td>
<td>0.012</td>
<td>0.019</td>
<td>0.010</td>
</tr>
<tr>
<td>Back %</td>
<td>0.019</td>
<td>0.015</td>
<td>-0.004</td>
<td>0.014</td>
</tr>
<tr>
<td>Streak %</td>
<td>0.009</td>
<td>0.012</td>
<td>0.002</td>
<td>0.011</td>
</tr>
<tr>
<td>Ham %</td>
<td>-0.003</td>
<td>0.010</td>
<td>0.002</td>
<td>0.009</td>
</tr>
<tr>
<td>Shoulder lean %</td>
<td>-0.080</td>
<td>0.035</td>
<td>-0.041</td>
<td>0.033</td>
</tr>
<tr>
<td>subcut. fat %</td>
<td>0.052</td>
<td>0.031</td>
<td>0.022</td>
<td>0.032</td>
</tr>
<tr>
<td>intermuscle, fat %</td>
<td>0.035</td>
<td>0.016</td>
<td>0.018</td>
<td>0.014</td>
</tr>
<tr>
<td>bone %</td>
<td>-0.008</td>
<td>0.013</td>
<td>0.011</td>
<td>0.013</td>
</tr>
<tr>
<td>Back lean %</td>
<td>-0.095</td>
<td>0.043</td>
<td>-0.054</td>
<td>0.042</td>
</tr>
<tr>
<td>subcut. fat %</td>
<td>0.100</td>
<td>0.046</td>
<td>0.041</td>
<td>0.046</td>
</tr>
<tr>
<td>intermuscle, fat %</td>
<td>0.027</td>
<td>0.010</td>
<td>0.014</td>
<td>0.011</td>
</tr>
<tr>
<td>bone %</td>
<td>-0.024</td>
<td>0.016</td>
<td>-0.013</td>
<td>0.012</td>
</tr>
<tr>
<td>Streak lean %</td>
<td>-0.056</td>
<td>0.046</td>
<td>-0.026</td>
<td>0.041</td>
</tr>
<tr>
<td>subcut. fat %</td>
<td>0.072</td>
<td>0.048</td>
<td>0.029</td>
<td>0.022</td>
</tr>
<tr>
<td>intermuscle, fat %</td>
<td>0.027</td>
<td>0.015</td>
<td>0.011</td>
<td>0.015</td>
</tr>
<tr>
<td>bone %</td>
<td>-0.021</td>
<td>0.008</td>
<td>-0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>Ham lean %</td>
<td>-0.073</td>
<td>0.030</td>
<td>-0.003</td>
<td>0.032</td>
</tr>
<tr>
<td>subcut. fat %</td>
<td>0.080</td>
<td>0.030</td>
<td>0.006</td>
<td>0.034</td>
</tr>
<tr>
<td>intermuscle, fat %</td>
<td>0.021</td>
<td>0.008</td>
<td>-0.001</td>
<td>0.006</td>
</tr>
<tr>
<td>bone %</td>
<td>-0.026</td>
<td>0.012</td>
<td>0.003</td>
<td>0.008</td>
</tr>
</tbody>
</table>

* Change for each lb increase in slaughterweight.
As pen mean observations may be biased by sex ratio differences, corrections were calculated as described in Section 3.1 (Snedecor and Cochran, 1969). The correction was applicable to DG and CDG only.

### Pork

<table>
<thead>
<tr>
<th></th>
<th>Castrate-</th>
<th>S.E.</th>
<th>Gilt</th>
<th>S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily gain</td>
<td>0.14</td>
<td>0.01</td>
<td>0.12</td>
<td>0.01</td>
</tr>
<tr>
<td>Carcass daily gain</td>
<td>0.10</td>
<td>0.01</td>
<td>0.11</td>
<td>0.01</td>
</tr>
</tbody>
</table>

The derived pen mean tissue percentages and growth rates had no sex ratio imbalance (Appendix IV) and the method was not applicable to the observed pen means FCE and DFI. As in Chapter 3, these characters were not corrected, and as only a small proportion of pens had imbalanced sex ratios it is thought that any bias is unlikely to have an important influence on analysis III results.

The results of each analysis for both slaughter weights are presented in Section 4.2.

#### Results

**Analysis I - Pork**

The least squares analysis of variance for the pork economy of production, split carcass and meat quality characters is given in table 4.2.1.

### Interaction effects

Cross x protein level interaction for all characters but pH was an unimportant source of variation with the mean square generally smaller than the residual mean square. The subclass means for the pH interaction (Table 4.2.2) show that LW, E and the V reciprocal crosses gave higher pH readings on the low protein diet, L a marginal deviation and P a large reduction. Cross ranking changes resulted.
Table 4.2.1. Pork Analysis I Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DG</th>
<th>CDG</th>
<th>Crv. wt.</th>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>0.588***</td>
<td>0.258***</td>
<td>156.31***</td>
<td>14970.3***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.194**</td>
<td>0.055</td>
<td>60.04***</td>
<td>1533.7</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>0.074</td>
<td>0.049</td>
<td>8.13</td>
<td>667.1</td>
</tr>
<tr>
<td>Litters</td>
<td>63</td>
<td>0.055</td>
<td>0.036</td>
<td>10.49</td>
<td>759.5</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.044</td>
<td>0.079*</td>
<td>12.46*</td>
<td>375.0</td>
</tr>
<tr>
<td>Sex (S)</td>
<td>1</td>
<td>3.129***</td>
<td>1.516***</td>
<td>279.39***</td>
<td>7838.3***</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.016</td>
<td>0.011</td>
<td>3.14</td>
<td>90.7</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.017</td>
<td>0.021</td>
<td>10.30</td>
<td>109.2</td>
</tr>
<tr>
<td>C x S</td>
<td>5</td>
<td>0.055**</td>
<td>0.065**</td>
<td>1.64</td>
<td>85.0</td>
</tr>
<tr>
<td>R x S</td>
<td>7</td>
<td>0.043**</td>
<td>0.059**</td>
<td>1.64</td>
<td>85.0</td>
</tr>
<tr>
<td>P x S</td>
<td>1</td>
<td>0.086*</td>
<td>0.003</td>
<td>19.30</td>
<td>139.3</td>
</tr>
<tr>
<td>Residual</td>
<td>668</td>
<td>0.015</td>
<td>0.017</td>
<td>5.42</td>
<td>167.6</td>
</tr>
</tbody>
</table>

(* P ≤ 0.05  ** P ≤ 0.01  *** P ≤ 0.001 in this and subsequent tables)

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Depth</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>687.7**</td>
<td>284.48***</td>
<td>97.30**</td>
<td>467.04***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>3948.3***</td>
<td>129.93***</td>
<td>62.47*</td>
<td>148.82</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>198.7</td>
<td>27.20</td>
<td>27.72</td>
<td>45.42</td>
</tr>
<tr>
<td>Litters</td>
<td>63</td>
<td>146.7</td>
<td>29.37</td>
<td>23.59</td>
<td>38.70</td>
</tr>
<tr>
<td>Protein level (R)</td>
<td>1</td>
<td>4.6</td>
<td>35.12</td>
<td>2.94</td>
<td>71.65**</td>
</tr>
<tr>
<td>Sex (S)</td>
<td>1</td>
<td>4.3</td>
<td>508.50***</td>
<td>316.79***</td>
<td>221.71***</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>40.8</td>
<td>8.89</td>
<td>4.64</td>
<td>3.07</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>58.0</td>
<td>17.92</td>
<td>6.24</td>
<td>4.35</td>
</tr>
<tr>
<td>C x S</td>
<td>5</td>
<td>150.2</td>
<td>27.71</td>
<td>4.06</td>
<td>20.55*</td>
</tr>
<tr>
<td>R x S</td>
<td>7</td>
<td>91.9</td>
<td>24.14</td>
<td>5.19</td>
<td>9.87</td>
</tr>
<tr>
<td>P x S</td>
<td>1</td>
<td>9.7</td>
<td>1.83</td>
<td>3.17*</td>
<td>6.69</td>
</tr>
<tr>
<td>Residual</td>
<td>668</td>
<td>70.9</td>
<td>12.98</td>
<td>6.33</td>
<td>8.82</td>
</tr>
</tbody>
</table>
### Table 4.2.1. contd.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>C</th>
<th>K</th>
<th>J</th>
<th>A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>296.50***</td>
<td>305.64***</td>
<td>22.49***</td>
<td>480.31***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>85.20**</td>
<td>136.34**</td>
<td>22.67***</td>
<td>135.61***</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>33.10</td>
<td>53.94</td>
<td>4.21</td>
<td>49.32*</td>
</tr>
<tr>
<td>Litters</td>
<td>65</td>
<td>24.21</td>
<td>40.45</td>
<td>3.01</td>
<td>28.35</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>25.52*</td>
<td>29.41</td>
<td>3.18</td>
<td>70.29*</td>
</tr>
<tr>
<td>Sex (S)</td>
<td>1</td>
<td>694.56***</td>
<td>1752.36***</td>
<td>87.54***</td>
<td>1429.76***</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>3.11</td>
<td>8.48</td>
<td>1.13</td>
<td>17.98</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>4.50</td>
<td>6.37</td>
<td>1.26</td>
<td>40.70**</td>
</tr>
<tr>
<td>C x S</td>
<td>5</td>
<td>14.06*</td>
<td>23.54**</td>
<td>3.67**</td>
<td>14.41</td>
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<tr>
<td>R x S</td>
<td>7</td>
<td>7.20</td>
<td>19.01*</td>
<td>0.54</td>
<td>11.65</td>
</tr>
<tr>
<td>P x S</td>
<td>1</td>
<td>0.25</td>
<td>20.59</td>
<td>0.16</td>
<td>4.31</td>
</tr>
<tr>
<td>Residual</td>
<td>668</td>
<td>5.05</td>
<td>8.04</td>
<td>0.92</td>
<td>14.08</td>
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</table>

<table>
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<th>D</th>
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<th>EMScol</th>
<th>E</th>
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<td>432.86***</td>
<td>0.528</td>
<td>23.90***</td>
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<td>187.31***</td>
<td>10.73</td>
<td>2.148***</td>
<td>87.05***</td>
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<td>19.40</td>
<td>15.68</td>
<td>0.581*</td>
<td>7.10*</td>
</tr>
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<td>Litters</td>
<td>65</td>
<td>24.29</td>
<td>11.72</td>
<td>0.295</td>
<td>4.19</td>
</tr>
<tr>
<td>Protein level (P)</td>
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<td>50.53*</td>
<td>26.13**</td>
<td>0.006</td>
<td>0.24</td>
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<td>1329.24***</td>
<td>667.51***</td>
<td>2.912***</td>
<td>73.87***</td>
</tr>
<tr>
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<td>7.33</td>
<td>5.28</td>
<td>0.111</td>
<td>1.13</td>
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<tr>
<td>R x P</td>
<td>7</td>
<td>10.56</td>
<td>2.86</td>
<td>0.374</td>
<td>1.32</td>
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<tr>
<td>C x S</td>
<td>5</td>
<td>5.92</td>
<td>2.50</td>
<td>0.576*</td>
<td>2.13</td>
</tr>
<tr>
<td>R x S</td>
<td>7</td>
<td>14.77</td>
<td>3.29</td>
<td>0.140</td>
<td>1.43</td>
</tr>
<tr>
<td>P x S</td>
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<td>1.31</td>
<td>2.39</td>
<td>0.079</td>
<td>0.11</td>
</tr>
<tr>
<td>Residual</td>
<td>668</td>
<td>9.40</td>
<td>2.76</td>
<td>0.234</td>
<td>1.60</td>
</tr>
<tr>
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<td>df</td>
<td>D</td>
<td>df</td>
<td>Foreq.</td>
<td>Hindq.</td>
</tr>
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<td>--------------------------</td>
<td>----</td>
<td>-------</td>
<td>----</td>
<td>---------</td>
<td>--------</td>
</tr>
<tr>
<td>Crvss (C)</td>
<td>5</td>
<td>27.36</td>
<td>5</td>
<td>4.461*</td>
<td>2.892</td>
</tr>
<tr>
<td>Replicate (R)</td>
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<td>106.94***</td>
<td>2</td>
<td>0.740</td>
<td>1.519</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>14.09</td>
<td>10</td>
<td>1.958</td>
<td>0.795</td>
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<tr>
<td>Litters</td>
<td>63</td>
<td>15.24</td>
<td>24</td>
<td>1.577</td>
<td>1.849</td>
</tr>
<tr>
<td>Protein level (P)</td>
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<td>5.10</td>
<td>1</td>
<td>1.819</td>
<td>0.357</td>
</tr>
<tr>
<td>Sex (S)</td>
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<td>13.51</td>
<td>1</td>
<td>18.723***</td>
<td>15.966***</td>
</tr>
<tr>
<td>C x P</td>
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<td>6.00</td>
<td>5</td>
<td>1.219</td>
<td>1.564</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>6.29</td>
<td>2</td>
<td>0.463</td>
<td>0.248</td>
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<td>C x S</td>
<td>5</td>
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<td>5</td>
<td>1.202</td>
<td>0.441</td>
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<tr>
<td>R x S</td>
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<td>5.33</td>
<td>2</td>
<td>1.149</td>
<td>0.003</td>
</tr>
<tr>
<td>P x S</td>
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<td>4.21</td>
<td>1</td>
<td>0.236</td>
<td>0.690</td>
</tr>
<tr>
<td>Residual</td>
<td>668</td>
<td>5.81</td>
<td>237</td>
<td>1.054</td>
<td>0.806</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>pH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
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<td>0.144</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>6.330***</td>
</tr>
<tr>
<td>C x R</td>
<td>33</td>
<td>0.090</td>
</tr>
<tr>
<td>Litters</td>
<td>59</td>
<td>0.151</td>
</tr>
<tr>
<td>Protein level (P)</td>
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<td>0.029</td>
</tr>
<tr>
<td>Sex (S)</td>
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<td>0.011</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.251*</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.052</td>
</tr>
<tr>
<td>C x S</td>
<td>5</td>
<td>0.063</td>
</tr>
<tr>
<td>R x S</td>
<td>7</td>
<td>0.078</td>
</tr>
<tr>
<td>P x S</td>
<td>1</td>
<td>0.001</td>
</tr>
<tr>
<td>Residual</td>
<td>378</td>
<td>0.078</td>
</tr>
</tbody>
</table>

Protein x sex interactions followed the pattern of cross x protein interactions in that most mean squares were smaller than the residual mean square. Subclass means for the significant interactions, BG and M1, are given in Table 4.2.2. Neither interaction gave a rank change. Castrates gained liveweight faster and had greater depth of fat at the mid back than gilts but the differences were smaller on the high protein diet. The
lack of substantiating interactions for other fat depths suggests that the midback interaction was a random effect.

Table 4.2.2. P.0.1 Analysis I. Cross x Protein level and Protein level x Sex Interactions.

<table>
<thead>
<tr>
<th>pI</th>
<th>Cross x Protein Level Interaction</th>
<th>Protein level x Sex Interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Low</td>
<td>High</td>
</tr>
<tr>
<td>LW</td>
<td>6.32</td>
<td>6.35</td>
</tr>
<tr>
<td>MLW</td>
<td>6.32</td>
<td>6.44</td>
</tr>
<tr>
<td>PLW</td>
<td>6.36</td>
<td>6.48</td>
</tr>
<tr>
<td>LLW</td>
<td>6.33</td>
<td>6.32</td>
</tr>
<tr>
<td>ELW</td>
<td>6.23</td>
<td>6.36</td>
</tr>
<tr>
<td>LW</td>
<td>6.39</td>
<td>6.42</td>
</tr>
</tbody>
</table>

The cross x sex interactions presented in Table 4.2.3 are consistent in result and indicate the differential responses of the LW cross. In contrast to the proportional sex differences of the other crosses, LW had minimal castrate/gilt differences for live and carcass gain and larger differences for the fat depths. The differential sex responses gave rank changes in DG, CDG, Loin, C, K and J. Similar, although less consistent results emerged for EMcol, in which the sex difference for LW was nearly twice the size of other sex differences. Pietrain pigs showed a reverse trend with castrates recording higher EMcol values than the gilts. The differential responses of the cross sexes gave rank changes.

The interactions of replicate and the other main effects can be attributed to individual boar differences which were not fitted in the model and to seasonal, environmental and sampling variation. Any sire x sex interaction will have contributed to the replicate x sex interaction. The replicate interactions will not be described further.
Table 4.2.5.  Pork Analysis I.  Cross x Sex Interactions

<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lbs/day)</th>
<th>CDG (lbs/day)</th>
<th>ENkol (pts)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW</td>
<td>1.67</td>
<td>1.51</td>
<td>0.16</td>
</tr>
<tr>
<td>WLW</td>
<td>1.76</td>
<td>1.62</td>
<td>0.14</td>
</tr>
<tr>
<td>PLW</td>
<td>1.58</td>
<td>1.47</td>
<td>0.11</td>
</tr>
<tr>
<td>LLW</td>
<td>1.79</td>
<td>1.64</td>
<td>0.15</td>
</tr>
<tr>
<td>BLW</td>
<td>1.75</td>
<td>1.56</td>
<td>0.17</td>
</tr>
<tr>
<td>LW</td>
<td>1.64</td>
<td>1.59</td>
<td>0.05</td>
</tr>
</tbody>
</table>

Loin  C  K  J
----  --  --  --
LW  14.1  13.0  1.1  12.8  10.8  2.0  18.0  14.8  3.2  2.5  2.0  0.5
WLW 18.4  18.0  0.4  15.4  14.1  1.5  20.1  18.2  1.9  3.4  3.0  0.4
PLW 13.4  13.0  0.4  11.7  10.2  1.5  16.0  13.5  2.5  2.5  2.0  0.5
LLW 15.0  14.2  0.8  13.4  12.0  1.4  18.3  15.5  2.8  3.1  2.5  0.6
BLW 17.4  16.0  1.4  14.3  12.0  2.5  19.0  15.2  3.8  3.5  2.5  1.2
LW  17.6  15.1  2.5  16.2  15.1  3.1  20.3  16.2  4.1  3.6  2.6  1.0

(* Castrate  ** Gilt in this and subsequent tables)

Protein level

Although the performance of all characters was advantageously affected by the high protein level, responses were generally small and only the responses for the characters given in table 4.2.4 reached statistical significance.

Table 4.3.4.  Pork Analysis I.  Protein level effects.

High-Low contrasts

<table>
<thead>
<tr>
<th>CDG (lbs/day)</th>
<th>Cre.Wt (lbs)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
<th>A (mm)</th>
<th>B (mm)</th>
<th>ENkol (sq.cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>High-Low</td>
<td>0.02</td>
<td>0.25</td>
<td>-0.6</td>
<td>-0.4</td>
<td>0.6</td>
<td>0.5</td>
</tr>
</tbody>
</table>

The contrasts show that high protein compared to low protein fed pigs gained carcass weight faster, gave a heavier carcass, with less fat at Loin and C and had a deeper, wider and larger area of eye muscle.
Cross

The differences between crosses were larger than the responses to change in protein level. The significant differences are given as deviations from the LW controls in table 4.3.5. The contrasts indicate that Pietrain crosses gained live and carcass weight more slowly than LWs but produced a heavier carcass with more fore quarter. The Pietrain cross carcass was much shorter but no deeper than the LW and had less fat at all points except the mid back. Its eye muscle was much larger.

In contrast to the Pietrain cross, Landrace sired pigs gained live and carcass weight faster than the LW but produced a lighter carcass of comparable length and depth. The Landrace cross progeny had heavier fore quarters than the LW controls. Only at the shoulder was the Landrace back fat thickness thinner than that of the LW. Eye muscle measurements were similar. The Essex cross pigs were not as fast growing as the Landrace sired pigs but were faster than the LW and produced a carcass of similar weight, length and width to that of the LW. The carcass had, however, consistently thicker fat and although the eye muscle was wider than the LW the area was no greater.

The performances of the Wessex reciprocal crosses were similar, although W sired pigs tended to grow more quickly than the progeny of W dams. The latter's growth was the same as the LW controls. The carcasses of the reciprocal crosses were lighter, shorter and deeper than the LW carcasses and had deeper fat thicknesses and smaller eye muscles. There was a tendency for LW x W pigs to have less fat and a deeper, larger eye muscle than the W x LW cross.
Table 4.2.5. Pork Analysis I. Cross effects.
Table 4.2.6. Pork Analysis I. Sex Effects.

Cross effects from Large White controls.

<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lb/day)</th>
<th>CDG (lb/day)</th>
<th>Crc.wt. (lb)</th>
<th>Foreq. (lb)</th>
<th>Length (mm)</th>
<th>Depth (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.10</td>
<td>0.06</td>
<td>-1.6</td>
<td>0.1</td>
<td>-9.0</td>
<td>5.6</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.07</td>
<td>-0.05</td>
<td>1.5</td>
<td>0.5</td>
<td>-27.3</td>
<td>0.8</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.12</td>
<td>0.10</td>
<td>-0.8</td>
<td>0.4</td>
<td>3.9</td>
<td>-0.8</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.05</td>
<td>0.04</td>
<td>-0.6</td>
<td>0.7</td>
<td>-2.3</td>
<td>1.7</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.02</td>
<td>0.00</td>
<td>-1.1</td>
<td>-0.1</td>
<td>-12.1</td>
<td>5.5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Max (mm)</th>
<th>Mid (mm)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
<th>K (mm)</th>
<th>J (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>2.5</td>
<td>2.4</td>
<td>4.6</td>
<td>3.0</td>
<td>2.7</td>
<td>0.9</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-1.2</td>
<td>0.9</td>
<td>-0.4</td>
<td>-0.8</td>
<td>-1.7</td>
<td>-0.1</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>-1.0</td>
<td>0.1</td>
<td>1.0</td>
<td>0.9</td>
<td>0.5</td>
<td>0.5</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>1.4</td>
<td>1.6</td>
<td>3.1</td>
<td>1.6</td>
<td>0.7</td>
<td>0.6</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>1.7</td>
<td>1.6</td>
<td>2.8</td>
<td>2.9</td>
<td>1.8</td>
<td>0.9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>A (mm)</th>
<th>B (mm)</th>
<th>EMA (sq.cm)</th>
<th>E (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-0.5</td>
<td>-1.5</td>
<td>-0.8</td>
<td>0.8</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>4.5</td>
<td>6.6</td>
<td>4.2</td>
<td>-0.1</td>
</tr>
<tr>
<td>Landrace x LW</td>
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<td>0.0</td>
<td>0.1</td>
<td>0.6</td>
</tr>
<tr>
<td>Essex x LW</td>
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<td>0.0</td>
<td>0.4</td>
<td>0.3</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-0.6</td>
<td>-0.7</td>
<td>-0.2</td>
<td>1.0</td>
</tr>
</tbody>
</table>

Table 4.2.6 gives the significant sex effect contrasts. The influence of sex (castrate-gilt) was greater than the contrast of protein levels. Castrates gained live and carcass weight faster than gilts, but at the same slaughter weight gave a lighter and shorter carcass with more fat at all points and a smaller eye muscle.
with a lower eye muscle colour score. The lower score represents a darker colour.

Replicate and replicate interaction contrasts will not be presented, but will be discussed later.

As the subjective categories of eye muscle condition do not fully satisfy the assumptions necessary for an analysis of variance, the EM cond results are also presented as percentages (table 4.2.7). No pale, dry or pale and dry eye muscles were recorded.

Overall the incidence of abnormal eye muscle conditions was low, about 5% of the total observations (Table 4.2.7). Within the low level of incidence, differences between crosses are apparent, Pietrain crosses (PLW) contributing half of all the abnormal observations and Landrace crosses (LLW) a quarter, and only the Pietrains having pale, wet eye muscles. The results also suggest a protein level effect, the high protein diet giving 7.6% abnormalities whereas there were only 2.8% on the low protein diet. A slightly larger difference was shown by the sexes, gilts having 10.5% abnormalities and castrates only 1.2%.

Replicate effects did not seem important. In view of the small number of observations the main effect results can only be regarded as preliminary, however it does appear that there are cross and sex differences and possibly an increased incidence of abnormalities due to the high protein diet.

The repeatability of the two factor subclass effects in tables 4.2.8, 4.2.9 and 4.2.10 can also be questioned because of the limited number of observations. Nevertheless some possible interaction effects are indicated, e.g. table 4.2.8 shows a possible cross x protein level interaction, all crosses except
Table 4.2.7. Pork Analysis I. Percentage of carcasses within each class of main effect occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th>Breed/Group</th>
<th>No. of Observations</th>
<th>Normal</th>
<th>Wet</th>
<th>Pale/Wet</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>51</td>
<td>98.0</td>
<td>2.0</td>
<td>-</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>58</td>
<td>98.3</td>
<td>1.7</td>
<td>-</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>55</td>
<td>83.6</td>
<td>14.5</td>
<td>1.8</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>52</td>
<td>90.6</td>
<td>9.4</td>
<td>-</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>44</td>
<td>95.4</td>
<td>4.6</td>
<td>-</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>56</td>
<td>100.0</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Replicate 6</td>
<td>87</td>
<td>93.1</td>
<td>6.9</td>
<td>-</td>
</tr>
<tr>
<td>7</td>
<td>104</td>
<td>92.3</td>
<td>7.7</td>
<td>-</td>
</tr>
<tr>
<td>8</td>
<td>105</td>
<td>98.1</td>
<td>1.9</td>
<td>-</td>
</tr>
<tr>
<td>High Protein</td>
<td>153</td>
<td>92.2</td>
<td>7.8</td>
<td>-</td>
</tr>
<tr>
<td>Low protein</td>
<td>143</td>
<td>97.2</td>
<td>2.1</td>
<td>0.7</td>
</tr>
<tr>
<td>Castrate</td>
<td>163</td>
<td>98.8</td>
<td>0.6</td>
<td>0.6</td>
</tr>
<tr>
<td>Gilt</td>
<td>153</td>
<td>89.5</td>
<td>10.5</td>
<td>-</td>
</tr>
</tbody>
</table>

ELW and LW having more abnormalities on high protein than on low protein. The data in Table 4.2.9 represent a possible cross x sex interaction with only the PLW having any abnormal castrates.

The sex x protein level results in Table 4.2.10 follow the earlier trends, gilts fed high protein having by far the greatest incidence of abnormalities, followed by the low protein fed gilts.

In general therefore the results suggest that the PLW and LLW crosses, the gilts and the high protein fed pigs and combinations of these, give a higher incidence of abnormal eye muscle conditions. The abnormal conditions in this population of pork pigs are limited to pale and pale and wet. Owing to the restricted size of the observed populations the results can only be regarded as preliminary and require further investigation with larger numbers.
### Table 4.2.8. Pork Analysis I. Percentage of carcasses within each cross x protein level subclass occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th></th>
<th>High protein</th>
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<th>Low protein</th>
<th></th>
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</thead>
<tbody>
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<td>Pale/Wet</td>
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<td>Pietrain x LW</td>
<td>77.6</td>
<td>22.6</td>
<td></td>
<td>91.7</td>
</tr>
<tr>
<td>Landrace x LW</td>
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<td>13.3</td>
<td></td>
<td>94.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>96.0</td>
<td>4.0</td>
<td></td>
<td>94.7</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>100.0</td>
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<td></td>
<td>100.0</td>
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</table>

### Table 4.2.9. Pork Analysis I. Percentage of carcasses within each cross x sex subclass occurring in eye muscle condition categories.

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<thead>
<tr>
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<tbody>
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<td>Normal</td>
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</tr>
<tr>
<td>Large White</td>
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<td></td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>100.0</td>
<td></td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>96.5</td>
<td>2.9</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>100.0</td>
<td></td>
</tr>
<tr>
<td>Essex x LW</td>
<td>100.0</td>
<td></td>
</tr>
<tr>
<td>LW x Wessex</td>
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</table>

### Table 4.2.10. Pork Analysis I. Percentage of carcasses within each sex x protein level subclass occurring in eye muscle condition categories.

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<th>Castrate</th>
<th>Gilt</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Normal</td>
<td>Wet</td>
</tr>
<tr>
<td>High protein</td>
<td>98.8</td>
<td>1.2</td>
</tr>
<tr>
<td>Low protein</td>
<td>98.8</td>
<td></td>
</tr>
</tbody>
</table>
Analysis 2. Heavy hog

The least squares analysis of variance for the heavy hog economy of production, split carcass and meat quality character is given in table 4.2.11.

Interaction effects

Twenty two significant interactions were observed, the majority of which were cross x sex interactions (table 4.2.11). Few of the heavy hog interactions were the same as those found in the pork analysis, but common to both were sex x replicate interactions for K and cross x sex interactions for loin, C, K and J. The replicate interactions can be attributed to effects such as sire differences, not fitted in the model. The replicate effects will not be described further.

Cross x protein level interactions were significant for weight of hind quarter and loin backfat thickness. The hind quarter interaction was not repeated for the fore quarter or carcass weights, although the cross responses to protein level for hind quarter were consistent with those for fore quarter. The hind quarter subclass means giving the interaction are listed below:

<table>
<thead>
<tr>
<th></th>
<th>High protein</th>
<th>Low protein</th>
<th>HP-LP</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW x LW</td>
<td>40.1</td>
<td>39.8</td>
<td>0.3</td>
</tr>
<tr>
<td>W x LW</td>
<td>38.9</td>
<td>40.3</td>
<td>-1.4</td>
</tr>
<tr>
<td>P x LW</td>
<td>41.1</td>
<td>39.6</td>
<td>1.5</td>
</tr>
<tr>
<td>L x LW</td>
<td>40.5</td>
<td>39.4</td>
<td>1.1</td>
</tr>
<tr>
<td>E x LW</td>
<td>41.6</td>
<td>39.7</td>
<td>1.9</td>
</tr>
<tr>
<td>LW x W</td>
<td>37.9</td>
<td>40.1</td>
<td>-2.2</td>
</tr>
</tbody>
</table>

In contrast to the similar LW hind quarter weights on the high and low protein levels, the Wessex reciprocal crosses had heavier hind quarters when fed a low protein regime and Pietrain, Landrace and Essex progeny had heavier hind quarter weights with the high protein regime. Forequarter responses to the protein levels were
consistent in direction with the hind quarter results but there were marked inconsistencies between the quarter and carcass weight responses for some crosses. Further inconsistencies occurred between carcass weight results for the fore/hind quarter population and the total experimental population. These highlight the presence of sampling error and it is probable that the hind quarter cross x protein level interaction can be attributed to sampling error.

Examination of joint weights as a percentage of carcass weight (Analysis II) will clarify any possible differential effects of protein level on carcass proportions.

The loin backfat thickness cross x protein level interaction was remarkable in that the extreme differential responses were those of the Wessex reciprocal crosses. The W x LW progeny gave reduced loin fat thickness with high protein while the LW x W cross gave increased fat thickness with high protein.

<table>
<thead>
<tr>
<th></th>
<th>High protein</th>
<th>Low protein</th>
<th>HP-LP</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW</td>
<td>28.8</td>
<td>28.9</td>
<td>-0.1</td>
</tr>
<tr>
<td>W x LW</td>
<td>34.0</td>
<td>35.1</td>
<td>-1.1</td>
</tr>
<tr>
<td>P x LW</td>
<td>27.7</td>
<td>26.9</td>
<td>0.8</td>
</tr>
<tr>
<td>L x LW</td>
<td>39.9</td>
<td>30.2</td>
<td>-0.3</td>
</tr>
<tr>
<td>E x LW</td>
<td>34.9</td>
<td>33.7</td>
<td>1.2</td>
</tr>
<tr>
<td>LW x W</td>
<td>35.0</td>
<td>31.9</td>
<td>3.1</td>
</tr>
</tbody>
</table>

The means show that the differential cross responses gave rank changes among the fatter crosses, W, E and LW, but that the crosses with the thinnest fat depth gave generally small, inconsistent fat thickness changes with the different protein regimes, changes which were insufficient to give rank changes.

The loin interaction was not substantiated by any other fat thickness cross x protein level interaction and considering the lack of protein level effects for the split carcass and other analysis I characters,
Table 4.2.11. Heavy Hog Analysis I Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>LG</th>
<th>CDG</th>
<th>Crv.wt.</th>
<th>Length</th>
<th>Depth</th>
<th>Max</th>
<th>Mid</th>
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<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>0.884***</td>
<td>0.460***</td>
<td>262.75***</td>
<td>2179.1***</td>
<td>485.5***</td>
<td>248.7*</td>
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<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.112</td>
<td>0.102</td>
<td>135.12***</td>
<td>1842.1*</td>
<td>118.6</td>
<td>169.0*</td>
<td></td>
</tr>
<tr>
<td>C x R</td>
<td>34</td>
<td>0.123*</td>
<td>0.088*</td>
<td>20.06</td>
<td>1514.5</td>
<td>117.0</td>
<td>40.3</td>
<td></td>
</tr>
<tr>
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<td>0.049</td>
<td>23.85</td>
<td>806.5</td>
<td>95.8</td>
<td>75.9</td>
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<tr>
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<td>0.008</td>
<td>2.06</td>
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<td>20.9</td>
<td>8.7</td>
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<tr>
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<td>1.768***</td>
<td>190.38***</td>
<td>6447.8***</td>
<td>3319.7***</td>
<td>2463.6***</td>
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<td>0.013</td>
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<td>80.9</td>
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<td>0.023</td>
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<td>148.1***</td>
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<td>0.020</td>
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<td>0.014</td>
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<th>J</th>
<th>A</th>
<th>B</th>
<th>EMA</th>
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<td>41.8</td>
<td>33.58</td>
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<tr>
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<td>34.71</td>
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<td>40.1</td>
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<td>20.5</td>
<td>11.5</td>
<td>1.59</td>
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<tr>
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<td>10.5</td>
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<td>70.0**</td>
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<td>24.1</td>
<td>20.01*</td>
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<td>25.6</td>
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<td>5.51</td>
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Table 4.2.11 (contd.)

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<td>2.767</td>
<td>5.095*</td>
</tr>
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<td>148.89***</td>
<td>80.32*</td>
<td>2</td>
<td>96.510***</td>
<td>6.408</td>
<td>8.251*</td>
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<td>10.015</td>
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<td>16.39</td>
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<td>1.816</td>
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<td>5.735</td>
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<td>Litters</td>
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</tr>
<tr>
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<tr>
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<tr>
<td>R x P</td>
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<td>0.156</td>
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<tr>
<td>C x S</td>
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</tr>
<tr>
<td>R x S</td>
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<td>0.057</td>
</tr>
<tr>
<td>P x S</td>
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<td>0.002</td>
</tr>
<tr>
<td>Residual</td>
<td>389</td>
<td>0.106</td>
</tr>
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</table>
the absence of interactions is hardly surprising. It is therefore suggested that the loin interaction is a random effect and that cross x protein level interaction for the heavy hog analysis I characters, as for pork, is an unimportant source of variation.

The sex x protein level interactions for DG and mid backfat observed at pork weight were not repeated at the heavier slaughter weight and no significant sex x protein level interactions were found. The pork cross x sex interactions for fat thicknesses were, however, repeated for heavy hogs. The subclass means for the significant effects are given in Table 4.2.12.

The fat depth interactions were changes in rank due to a consistently larger sex difference for the LW cross. This reiterates the pork result (table 4.2.3) and is observed again for length. While there were no heavy hog interactions to substantiate the pork DG, CDG and Bskel results, the heavy hog population gave an interaction for carcass weight. In general castrates gave heavier carcasses but the WLW castrate-gilt difference was small and negative, and the LW difference was also small. The differences gave rank changes. Rank change interactions for A and EMA occurred because the WLW sex differences were proportionately smaller. There were no pork cross x sex interactions for these characters, or for hind quarter weight, which at heavy hog weights gave rank changes for crosses between sexes. Large sex differences for the W and E crosses gave a complete reversal of rankings with their castrates having the lightest hind quarters but their gilts the heaviest. The limited population of this last result makes it particularly prone to sampling error.
Table 4.2.12. Heavy hog Analysis I. Cross x Sex Interactions.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Crc. wt. (lbs)</th>
<th>Hind quarter (lbs)</th>
<th>Length (mm)</th>
</tr>
</thead>
<tbody>
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<td>♂</td>
<td>♀</td>
<td>♂ - ♀</td>
</tr>
<tr>
<td>LW</td>
<td>205.2</td>
<td>204.7</td>
<td>0.5</td>
</tr>
<tr>
<td>WLV</td>
<td>203.7</td>
<td>203.9</td>
<td>-0.2</td>
</tr>
<tr>
<td>PLW</td>
<td>206.5</td>
<td>206.5</td>
<td>2.2</td>
</tr>
<tr>
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<td>204.2</td>
<td>1.6</td>
</tr>
<tr>
<td>ELW</td>
<td>204.3</td>
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<tr>
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<td>204.7</td>
<td>203.4</td>
<td>1.3</td>
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<table>
<thead>
<tr>
<th>Cross</th>
<th>Max (mm)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
</tr>
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<tbody>
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<td>♂</td>
<td>♀</td>
<td>♂ - ♀</td>
</tr>
<tr>
<td>LW</td>
<td>54.6</td>
<td>50.1</td>
<td>4.5</td>
</tr>
<tr>
<td>WLV</td>
<td>54.1</td>
<td>52.2</td>
<td>1.9</td>
</tr>
<tr>
<td>PLW</td>
<td>52.5</td>
<td>46.7</td>
<td>5.8</td>
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<tr>
<td>LLW</td>
<td>50.8</td>
<td>48.2</td>
<td>2.6</td>
</tr>
<tr>
<td>ELW</td>
<td>55.2</td>
<td>51.3</td>
<td>3.9</td>
</tr>
<tr>
<td>LWW</td>
<td>58.5</td>
<td>50.3</td>
<td>8.2</td>
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</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>K (mm)</th>
<th>J (mm)</th>
<th>A (mm)</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>♂</td>
<td>♀</td>
<td>♂ - ♀</td>
</tr>
<tr>
<td>LW</td>
<td>37.4</td>
<td>29.1</td>
<td>8.3</td>
</tr>
<tr>
<td>WLV</td>
<td>37.5</td>
<td>31.0</td>
<td>6.5</td>
</tr>
<tr>
<td>PLW</td>
<td>34.2</td>
<td>25.7</td>
<td>8.5</td>
</tr>
<tr>
<td>LLW</td>
<td>35.7</td>
<td>29.1</td>
<td>6.6</td>
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<tr>
<td>ELW</td>
<td>36.8</td>
<td>30.9</td>
<td>5.9</td>
</tr>
<tr>
<td>LWW</td>
<td>40.0</td>
<td>30.0</td>
<td>10.0</td>
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</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>EMA (sq. cm.)</th>
<th>E (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>♂</td>
<td>♀</td>
</tr>
<tr>
<td>LW</td>
<td>29.25</td>
<td>33.02</td>
</tr>
<tr>
<td>WLV</td>
<td>29.41</td>
<td>31.58</td>
</tr>
<tr>
<td>PLW</td>
<td>35.19</td>
<td>39.27</td>
</tr>
<tr>
<td>LLW</td>
<td>34.45</td>
<td>34.45</td>
</tr>
<tr>
<td>ELW</td>
<td>29.01</td>
<td>32.17</td>
</tr>
<tr>
<td>LWW</td>
<td>27.47</td>
<td>31.94</td>
</tr>
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</table>
### Table 4.2.15. Heavy Hog Analysis I. Main effect contrasts.

**Cross effects: Deviations from Large White controls.**

<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lbs/day)</th>
<th>CDG (lbs/day)</th>
<th>CRC.wt. (lbs)</th>
<th>Length (mm)</th>
<th>Depth (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.07</td>
<td>0.05</td>
<td>-1.3</td>
<td>-8.3</td>
<td>5.2</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.16</td>
<td>-0.12</td>
<td>2.6</td>
<td>-32.3</td>
<td>-2.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.03</td>
<td>0.04</td>
<td>0.0</td>
<td>5.5</td>
<td>-4.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.04</td>
<td>0.02</td>
<td>-0.8</td>
<td>0.7</td>
<td>-2.5</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.03</td>
<td>0.02</td>
<td>-0.9</td>
<td>-4.6</td>
<td>6.5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Max (mm)</th>
<th>Mid (mm)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
<th>K (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.8</td>
<td>3.2</td>
<td>5.7</td>
<td>2.8</td>
<td>1.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-2.8</td>
<td>2.2</td>
<td>-1.5</td>
<td>-2.1</td>
<td>-3.3</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>-2.8</td>
<td>1.1</td>
<td>1.2</td>
<td>0.2</td>
<td>-0.9</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.9</td>
<td>4.6</td>
<td>5.5</td>
<td>2.4</td>
<td>0.6</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>2.1</td>
<td>2.7</td>
<td>4.6</td>
<td>5.5</td>
<td>1.7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>J (mm)</th>
<th>A (mm)</th>
<th>B (mm)</th>
<th>EMA (sq.cm)</th>
<th>E (mm)</th>
<th>D (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>1.1</td>
<td>-0.8</td>
<td>-0.5</td>
<td>-0.6</td>
<td>1.2</td>
<td>1.6</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.4</td>
<td>5.4</td>
<td>7.7</td>
<td>6.1</td>
<td>-0.4</td>
<td>0.9</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.6</td>
<td>2.7</td>
<td>2.2</td>
<td>1.6</td>
<td>0.3</td>
<td>0.4</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>1.7</td>
<td>0.4</td>
<td>-0.7</td>
<td>-0.5</td>
<td>-0.1</td>
<td>-1.3</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>1.8</td>
<td>-1.2</td>
<td>-1.5</td>
<td>-1.4</td>
<td>1.3</td>
<td>0.7</td>
</tr>
</tbody>
</table>

**Sex effects: Castrate - Gilt contrasts**

<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lbs/day)</th>
<th>CDG (lbs/day)</th>
<th>CRC.wt. (lbs)</th>
<th>Foreq. (lb)</th>
<th>Length (mm)</th>
<th>Depth (mm)</th>
<th>Max (mm)</th>
<th>Mid (mm)</th>
<th>Loin (mm)</th>
<th>C (mm)</th>
<th>K (mm)</th>
<th>J (mm)</th>
<th>A (mm)</th>
<th>B (mm)</th>
<th>EMA (sq.cm)</th>
<th>E (mm)</th>
<th>D (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>0.11</td>
<td>0.10</td>
<td>1.1</td>
<td>1.2</td>
<td>-6.2</td>
<td>1.8</td>
<td>4.5</td>
<td>5.8</td>
<td>4.7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>C (mm)</th>
<th>K (mm)</th>
<th>J (mm)</th>
<th>A (mm)</th>
<th>B (mm)</th>
<th>EMA (sq.cm)</th>
<th>E (mm)</th>
<th>D (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>6.3</td>
<td>7.6</td>
<td>2.2</td>
<td>-3.9</td>
<td>-4.1</td>
<td>-5.5</td>
<td>1.8</td>
<td>0.6</td>
</tr>
</tbody>
</table>

**Protein level effects: High-Low contrasts**

<table>
<thead>
<tr>
<th>Cross</th>
<th>K (mm)</th>
<th>A (mm)</th>
<th>E (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>High-Low</td>
<td>0.7</td>
<td>-0.7</td>
<td>0.4</td>
</tr>
</tbody>
</table>
An explanation of these cross x sex interactions may be forthcoming from the tissue character results of analysis II.

**Protein level**

The influence of protein level was minimal with only K, A and E significantly altered by protein level, high protein giving more fat at K and E and a reduced width of eye muscle (table 4.2.13). At pork weight, protein level had no effect on E and the responses to increased dietary protein concentration at K and A for heavy hogs is the reverse found at pork weight. No consistent trend was shown by the remaining heavy hog characters.

**Cross**

In contrast to the minimal protein level effect, there were significant cross differences for growth and carcass characters but not for the meat quality characters, 

$\text{EICOL}$ and pH. The main effects for $\text{EICOND}$ will be given later (tables 4.2.14 to 4.2.17).

The cross contrasts (table 4.2.13) follow the pattern observed at the lighter slaughter weight. Compared to the LW controls the W reciprocal crosses gained live and carcass weight faster but produced a lighter, shorter but deeper carcass with thicker fat at all points, a smaller eye muscle and a thicker streak. As at pork weight the MLW cross grew faster than the LW cross and, except at the loin and C, had more fat and a smaller eye muscle.

The slower growth rate of Pietrain cross pigs to pork weight was repeated and emphasised at the heavier slaughter weight. The heavier, shorter Pietrain carcass had less fat at all points except the midback and a much larger eye muscle.

LLVs had advantages for growth rate and although the carcass was longer and shallower it weighed the same as the controls, and
as at pork weight the shoulder fat was thinner. All other fat
depths except K were thicker, but the eye muscle was larger.

E crosses grew faster than the LW controls but gave a
lighter, fatter carcass with a marginally smaller eye muscle,
a performance similar to that at pork weight except for the
comparative reduction in eye muscle size.

Fore and hind quarter weights, recorded on a subpopulation,
were not different between crosses. However the sensitivity of
the test was low as the subpopulation carcass weights showed no
significant cross effect despite the highly significant difference
shown in the analysis of the total population. Fore quarter
weights indicated that LW had the heaviest fore quarter and Pietrain
cross the heaviest hind quarter. Other differences were small.
Joints as a percentage of carcass weight are given in analysis II.

The pork pH cross x protein level interaction was not
repeated at heavy hog weight and although pH values were higher,
cross rankings were generally similar to overall pork rankings.
The Pietrain and Landrace crosses had the lowest pH values.

Sex

All heavy hog sex differences (table 4.2.13) were consistent
with pork differences except that for carcass weight. As at
pork weight castrates were faster growing, had thicker fat depths,
a thicker streak and a smaller eye muscle. However heavy hog
castrates gave a heavier carcass than gilts, whereas at pork
weight gilts were heavier.

The eye muscle condition results are presented in tables 4.2.14
to 4.2.17. No pale or pale and dry eye muscles were observed.
Results for cross, replicate, protein level and sex are given in
table 4.2.14.
Table 4.2.14. Heavy Hog Analysis I. Percentage of carcasses within each class of main effect occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th></th>
<th>No. of Observations</th>
<th>Normal</th>
<th>Wet</th>
<th>Pale</th>
<th>Pale/Wet</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>32</td>
<td>90.6</td>
<td>6.3</td>
<td>-</td>
<td>3.1</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>47</td>
<td>80.9</td>
<td>12.8</td>
<td>2.1</td>
<td>4.2</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>53</td>
<td>62.3</td>
<td>24.5</td>
<td>-</td>
<td>13.2</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>41</td>
<td>58.5</td>
<td>19.5</td>
<td>-</td>
<td>22.0</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>46</td>
<td>82.6</td>
<td>10.9</td>
<td>-</td>
<td>6.5</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>48</td>
<td>83.3</td>
<td>14.6</td>
<td>-</td>
<td>2.1</td>
</tr>
<tr>
<td>Replicate 6</td>
<td>65</td>
<td>52.3</td>
<td>29.2</td>
<td>1.5</td>
<td>16.9</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>80.2</td>
<td>10.4</td>
<td>-</td>
<td>9.4</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>86.5</td>
<td>11.5</td>
<td>-</td>
<td>2.0</td>
</tr>
<tr>
<td>High protein</td>
<td>130</td>
<td>77.7</td>
<td>16.2</td>
<td>0.8</td>
<td>5.3</td>
</tr>
<tr>
<td>Low protein</td>
<td>137</td>
<td>73.7</td>
<td>14.6</td>
<td>-</td>
<td>11.7</td>
</tr>
<tr>
<td>Castrate</td>
<td>130</td>
<td>80.8</td>
<td>10.0</td>
<td>-</td>
<td>9.2</td>
</tr>
<tr>
<td>Gilt</td>
<td>137</td>
<td>70.8</td>
<td>20.4</td>
<td>0.7</td>
<td>8.0</td>
</tr>
</tbody>
</table>

Protein level appears to have little influence on the incidence of heavy hog abnormalities (25-30%) or on the abnormal category observed. However a tendency for gilts to show more abnormalities, particularly wet eye muscles, than castrates is indicated and a possible sire effect may be inferred from the larger incidence of abnormalities in replicate 6.

Observations for crosses are limited, however the Pietrain and Landrace pigs show twice the abnormalities of the other genotypes, and of the remainder the LW controls had the lowest incidence. Within the high abnormal incidence Landrace had equal numbers of the wet and pale and wet categories while Pietrain had twice as many wet as pale and wet eye muscles. The difference between wet and pale and wet may be difficult to score.
### Table 4.2.15. Heavy Hog Analysis I. Percentage of carcasses within each cross x protein level subclass occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th>Protein Level</th>
<th>Subclass</th>
<th>Normal</th>
<th>Wet</th>
<th>Pale</th>
<th>Pale/Wet</th>
<th>Normal</th>
<th>Wet</th>
<th>Pale</th>
<th>Pale/Wet</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Large White</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>93.8</td>
<td>-</td>
<td>-</td>
<td>6.2</td>
<td>87.5</td>
<td>12.5</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td></td>
<td>72.0</td>
<td>20.0</td>
<td>4.0</td>
<td>4.0</td>
<td>90.9</td>
<td>4.5</td>
<td>-</td>
<td>4.5</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td></td>
<td>76.0</td>
<td>20.0</td>
<td>-</td>
<td>4.0</td>
<td>50.0</td>
<td>28.6</td>
<td>12.8</td>
<td>21.4</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td></td>
<td>61.1</td>
<td>22.2</td>
<td>-</td>
<td>16.7</td>
<td>56.5</td>
<td>17.4</td>
<td>-</td>
<td>26.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td></td>
<td>82.6</td>
<td>13.0</td>
<td>-</td>
<td>-</td>
<td>82.6</td>
<td>8.7</td>
<td>-</td>
<td>8.7</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td></td>
<td>82.6</td>
<td>17.4</td>
<td>-</td>
<td>-</td>
<td>84.0</td>
<td>12.0</td>
<td>-</td>
<td>4.0</td>
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</tbody>
</table>

### Table 4.2.16. Heavy Hog Analysis I. Percentage of carcasses within each cross x sex subclass occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th>Sex x Protein Level</th>
<th>Castrate</th>
<th>Gilt</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal</td>
<td>Wet</td>
<td>Pale</td>
</tr>
<tr>
<td>Large White</td>
<td>94.4</td>
<td>5.6</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>82.4</td>
<td>11.8</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>60.7</td>
<td>21.4</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>64.5</td>
<td>7.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>82.6</td>
<td>8.7</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>96.2</td>
<td>3.8</td>
</tr>
</tbody>
</table>

### Table 4.2.17. Heavy Hog Analysis I. Percentage of carcasses within each sex x protein level subclass occurring in eye muscle condition categories.

<table>
<thead>
<tr>
<th>Protein Level</th>
<th>Castrate</th>
<th>Gilt</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal</td>
<td>Wet</td>
<td>Pale</td>
</tr>
<tr>
<td>High</td>
<td>80.0</td>
<td>13.3</td>
</tr>
<tr>
<td>Low</td>
<td>79.4</td>
<td>7.4</td>
</tr>
</tbody>
</table>
Within the small populations observed, the sensitivity for interactions is obviously low. Table 4.2.15 presents the cross x protein level subclass incidence. If the distinction between the wet and pale/wet categories is ignored, the results can broadly be taken to indicate that LW, L, E and LW have similar abnormal incidence on both protein levels, but that the WLW cross has an increased incidence of abnormalities on high protein and that Pietrains have an increased incidence on low protein. However with small subclass numbers the likelihood of sampling error is high.

The presentation of cross x sex subclass incidence (table 4.2.16) has the same provisions expressed above. Again the results suggest a possible interaction, for while Wessex, Pietrain and Essex crosses have similar abnormal incidence for each sex, LW, Landrace and especially LW have greater incidence of gilt than castrate abnormalities. A further possible interaction, sex x protein level, is indicated in table 4.2.17. Gilt normal eye muscles were less frequent on the low protein diet but castrates were not affected by protein level. The reverse response for gilts was found at pork weight, high protein gilts giving higher incidence of abnormalities.

Comparison of the pork and heavy hog results reveals other contradictions, e.g. the increased incidence of abnormalities with the high protein diet at pork weight was not repeated at the heavier weight. However at both weights abnormalities were more frequent for the Pietrain and Landrace crosses and for gilts compared to castrates. The effect of protein level was less marked and inconsistent. The most obvious effect was, however, a slaughter weight difference. Overall incidence for abnormal categories at pork weight was about 5%, but at heavy hog weight the incidence was about 25%.
Analysis II - Pork

The least squares analysis of variance for the pork dissection characters is given in table 4.2.18.

Interaction effects

Table 4.2.18 shows that the interaction of primary interest, cross x protein level, gave no significant effects and that usually its mean square was smaller than the residual mean square.

Of the remaining interactions, there were only 3 of interest, cross x sex interactions for LTGR and FFBG and a protein level x sex interaction for carcass weight. The latter was not significant in the analysis (I) of the total population and can probably be attributed to sampling error.

The cross x sex interactions were interrelated and superficially are correlated with the observed cross x sex interactions in analysis I. The subclass means for LTGR, FFBG and the differences between them are given below. These show that whereas LW had a large sex difference for LTGR, the castrates and gilts of other genotypes had similar rates of lean tissue growth. The sex difference of FFBG for LW progeny was large and negative while the other genotypes had large positive castrate-gilt contrasts.

| Cross | LTGR (lbs/day) | | | | FFGR (lbs/day) | | | |
|-------|----------------|---------| | | | | | |
|       | $\bar{x}$ | $\bar{\phi}$ | $\bar{x} - \bar{\phi}$ | | | $\bar{x}$ | $\bar{\phi}$ | $\bar{x} - \bar{\phi}$ |
| LW    | 0.614 | 0.610 | 0.004 | | 1.064 | 1.025 | 0.039 |
| MLW   | 0.590 | 0.587 | 0.003 | | 1.066 | 1.027 | 0.039 |
| PLW   | 0.659 | 0.657 | 0.002 | | 1.069 | 1.045 | 0.024 |
| LLW   | 0.667 | 0.652 | 0.015 | | 1.148 | 1.088 | 0.060 |
| ELM   | 0.626 | 0.611 | 0.015 | | 0.083 | 1.032 | 0.051 |
| LW    | 0.561 | 0.612 | -0.061 | | 0.993 | 1.038 | -0.045 |

<table>
<thead>
<tr>
<th>Cross</th>
<th>FFBG - LTGR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\bar{x}$</td>
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Table 4.2.18. Pork Analysis II Mean Squares

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<td>0.027</td>
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<td>0.003</td>
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Table 4.2.13. (contd.) Pork Analysis II Mean Squares

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<th>Subcut. fat %</th>
<th>Intramus. fat %</th>
<th>Bone %</th>
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<td>136.32***</td>
<td>115.27***</td>
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<td>524.52***</td>
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<th>Streak %</th>
<th>Ham %</th>
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<tbody>
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<td>10.656**</td>
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<td>29.890***</td>
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<td>R x P</td>
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Table 4.2.18. (contd.) Pork Analysis II Mean Squares

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<th>Shoulder IMF %</th>
<th>Shoulder Bone %</th>
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<th>Back Scf %</th>
<th>Back IMF %</th>
<th>Back Bone %</th>
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<th>Streak IMF %</th>
<th>Streak Bone %</th>
<th>Ham Lean %</th>
<th>Ham Scf %</th>
<th>Ham IMF %</th>
<th>Ham Bone %</th>
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<td>8.549***</td>
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<td>1.80***</td>
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<td>5.7</td>
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</table>
The difference between LGGR and FFBGR is the rate of growth of carcass bone, skin etc. The derived means, show the similar rates of bone etc. gain for the LWW sexes and the faster rate for castrates compared to gilts of the other genotypes. Overall, therefore, LWW castrates produce lean more quickly than the gilts but have equivalent production rates of other essential tissues. The 'general' rule, however, is for the sexes to have similar LTGRs but for castrates to produce the remaining essential carcass tissues more quickly than gilts. The interactions can therefore be solely attributed to the exceptional behaviour of the LWW cross. The reciprocal cross, W x LW, followed the general rule in its growth processes.

There were no cross x sex interactions for FTDR, lean or fat percentages despite the fat depth interactions observed in analysis I. It is therefore difficult to explain the fat depth interactions by the present results, despite their superficial consistency in that LWW gilts gained lean tissue faster than the castrates and, relative to other genotypes, gave thinner backfats.

Protein level

The number of characters showing significant protein level effects was considerable and performance was generally affected advantageously by the higher protein level regime (table 4.2.19). As in analysis I DG gave an advantageous but insignificant response to increased protein level. However the component tissue growth rates, LTGR and FTDR were significantly improved and reduced respectively by the high dietary protein level. High protein also gave a heavier carcass with increased lean and decreased fat percentages. The reduction in fat was mainly from the subcutaneous depots. High protein significantly increased the bone percentage by 0.1%, although joint bone percentages were not generally significantly
Table 4.2.19. Pork Analysis II. Protein level effects.

High-low contrasts.

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<th>LTGR (lb/day)</th>
<th>FTDR (lbs/day)</th>
<th>FFDR (lbs/day)</th>
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<td></td>
</tr>
<tr>
<td>Scf %</td>
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<td>-1.1</td>
<td>-0.2</td>
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</tr>
<tr>
<td>Imf %</td>
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</tr>
<tr>
<td>Bone %</td>
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Shoulder

<table>
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<th>Imf %</th>
<th>Bone %</th>
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<td>Lean %</td>
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Back

<table>
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<tr>
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<td>Lean %</td>
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<td>-0.8</td>
<td>-0.1</td>
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</table>

Streak

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Scf %</th>
<th>Imf %</th>
<th>Bone %</th>
</tr>
</thead>
<tbody>
<tr>
<td>High-Low</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Ham

affected by protein level. The joint weights as a percentage of carcass weight were not influenced by protein level but the joint lean, subcutaneous and intermuscular fat percentages followed the significant responses shown by their carcass totals.

Cross

Significant cross effects are presented in table 4.2.20 as deviations from the performance of the Large White controls. Cross had a larger influence on analysis II characters than protein level.

Of the genotypes the Pietrain cross performance deviated most from that of the controls. The Pietrain crosses gained live and carcass weight more slowly but had a superior LTGR and were the only group to have a negative FTDR contrast. These differences gave a superior FFDR. The heavier Pietrain carcass had 3.2% more lean, 2.1% less fat and 0.7% less bone than the controls. The decrease in fat percentage was mainly from the subcutaneous depots.
Table 4.2.20.  

Pork Analysis II. Cross effects. Deviations from Large White controls.

<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lbs/day)</th>
<th>CDG (lbs/day)</th>
<th>Cross Vt. (lbs)</th>
<th>LTGR (lbs/day)</th>
<th>PTGR (lbs/day)</th>
<th>FFBGR (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.09</td>
<td>0.05</td>
<td>-1.6</td>
<td>-0.023</td>
<td>0.048</td>
<td>0.002</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.08</td>
<td>-0.03</td>
<td>1.6</td>
<td>0.046</td>
<td>-0.044</td>
<td>0.012</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.10</td>
<td>0.10</td>
<td>-0.4</td>
<td>0.047</td>
<td>0.023</td>
<td>0.074</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.05</td>
<td>0.04</td>
<td>-0.6</td>
<td>0.007</td>
<td>0.026</td>
<td>0.013</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.02</td>
<td>-0.01</td>
<td>-0.3</td>
<td>-0.026</td>
<td>0.023</td>
<td>-0.029</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Fat %</th>
<th>Scf %</th>
<th>Bone %</th>
<th>Sh %</th>
<th>Back %</th>
<th>Str %</th>
<th>Ham %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-2.2</td>
<td>1.3</td>
<td>1.4</td>
<td>-0.4</td>
<td>-0.5</td>
<td>0.5</td>
<td>0.6</td>
<td>-1.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.2</td>
<td>-2.1</td>
<td>-2.1</td>
<td>-0.7</td>
<td>-0.2</td>
<td>-0.5</td>
<td>0.5</td>
<td>0.8</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.1</td>
<td>0.1</td>
<td>0.2</td>
<td>-0.3</td>
<td>-0.8</td>
<td>0.4</td>
<td>0.2</td>
<td>0.2</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-0.5</td>
<td>0.3</td>
<td>0.7</td>
<td>-0.6</td>
<td>-0.4</td>
<td>0.5</td>
<td>0.3</td>
<td>-0.5</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-1.3</td>
<td>1.4</td>
<td>1.2</td>
<td>-0.5</td>
<td>-0.1</td>
<td>0.3</td>
<td>0.3</td>
<td>-0.7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Bone %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Fat %</th>
<th>Lean %</th>
<th>Fat %</th>
<th>Bone %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-1.0</td>
<td>0.1</td>
<td>-0.2</td>
<td>-2.9</td>
<td>2.9</td>
<td>0.5</td>
<td>0.5</td>
<td>-1.0</td>
<td></td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.0</td>
<td>-2.2</td>
<td>-1.1</td>
<td>4.1</td>
<td>-3.6</td>
<td>-0.0</td>
<td>-0.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>1.3</td>
<td>-1.4</td>
<td>-0.1</td>
<td>0.0</td>
<td>0.2</td>
<td>0.0</td>
<td>-0.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.3</td>
<td>-0.4</td>
<td>-0.5</td>
<td>-0.5</td>
<td>1.1</td>
<td>0.2</td>
<td>-1.1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-0.5</td>
<td>0.2</td>
<td>-0.5</td>
<td>-1.7</td>
<td>2.1</td>
<td>0.4</td>
<td>-1.1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Bone %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-3.0</td>
<td>2.0</td>
<td>-2.1</td>
<td>1.4</td>
<td>-0.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.2</td>
<td>-3.2</td>
<td>2.3</td>
<td>-1.2</td>
<td>-1.2</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>4.4</td>
<td>1.3</td>
<td>-0.9</td>
<td>0.8</td>
<td>-0.3</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-1.2</td>
<td>1.1</td>
<td>-1.0</td>
<td>1.3</td>
<td>-0.5</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-2.8</td>
<td>2.7</td>
<td>-0.8</td>
<td>0.7</td>
<td>-0.4</td>
</tr>
</tbody>
</table>
Carcass proportion contrasts show the Pietrain crosses to have smaller shoulders and backs and larger proportions of streak and ham. The back and ham contrasts were the extreme values observed. Tissue percentage contrasts within joints generally reflected the overall tissue comparison. The back joint, although proportionally smaller, had the largest advantages for lean and fat percentage.

In contrast to the Pietrain, the Landrace cross gained live and carcass weight faster than the controls and had a LTGR comparable with that of the Pietrain cross. However the Landrace cross deposited fat at nearly 0.07 lbs/day faster than the Pietrain cross. The resulting carcass was 0.4 lbs lighter than, and had similar tissue percentages to, the controls. Of all the genotypes Landrace had the smallest shoulder joint percentage and had a 0.4% advantage for back and streak and a 0.2% advantage for ham compared to the controls. Back tissue percentages reflected the overall carcass composition but shoulder had a higher and streak a lower lean percentage. Fat percentages showed the reverse trend.

The dissected Essex crosses gained gross weight faster than the controls, had an equivalent LTGR and a faster deposition of fat. A lighter carcass resulted with smaller lean and bone percentages and increased fat percentage. Essex crosses had smaller shoulder and ham percentages than the LW controls and larger back and streak proportions. Essex joint tissue percentages were not always consistent with carcass tissue percentages. While the streak and ham had lower lean and higher fat percentage than the controls the shoulder had more lean and less fat. Back lean and fat percentages were equivalent to the controls.
The performance of the Wessex reciprocal crosses confirmed the analysis I results in that W sired pigs tended to grow more quickly than the progeny of W dams, with both giving carcasses lighter than the control LWs. Despite their difference in liveweight gain LTGRs were similar, about 0.025 lbs/day less than the controls. FTGRs were both greater, with W sired pigs deviating by twice as much from the control performance. W x LW therefore had carcasses with less lean and more fat than the LW x W cross. Joint proportions were similar and joint tissue percentages reflected total carcass composition.

All joint and tissue characters have, so far, been expressed as percentages of carcass weight. The comparison of tissue percentages within different carcass weights and the varying joint proportions of the carcass weights may, however, mask cross effects for tissue and joint weights. The weights calculated from the significant 'percentage' characters of analysis II are therefore presented in table 4.2.21. All results apply to a slaughter weight of 134 lbs.

The tissue weights show that the Pietrain cross progeny produced more weight of lean and less fat than the other genotypes. With the exception of the LW controls, cross differences for bone weight were small. Joint weights at the constant live slaughter weight indicate that Pietrains gave the heaviest and Wessex the lightest 'shoulder' joint, Pietrains the lightest and Essex the heaviest 'back' joint, Pietrains the heaviest and Large White the lightest 'streaks' and Pietrains the heaviest and Wessex the lightest 'hams'. The results show that
Table 4.2.21.  Pork Cross tissue and joint weights (lbs) at 134 lbs liveweight.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Cross wt.</th>
<th>Lean</th>
<th>Fat</th>
<th>Scf</th>
<th>Bone</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW x LW</td>
<td>100.6</td>
<td>48.7</td>
<td>25.4</td>
<td>19.1</td>
<td>9.6</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>99.0</td>
<td>45.7</td>
<td>24.8</td>
<td>20.2</td>
<td>9.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>102.2</td>
<td>52.7</td>
<td>21.7</td>
<td>17.3</td>
<td>8.9</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>100.1</td>
<td>46.5</td>
<td>23.4</td>
<td>19.1</td>
<td>9.2</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>100.0</td>
<td>47.9</td>
<td>24.1</td>
<td>19.6</td>
<td>8.9</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>99.3</td>
<td>46.8</td>
<td>24.5</td>
<td>20.0</td>
<td>8.9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Shoulder</th>
<th>Back</th>
<th>Streak</th>
<th>Ham</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW x LW</td>
<td>26.3</td>
<td>26.1</td>
<td>13.9</td>
<td>19.3</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>25.3</td>
<td>26.1</td>
<td>14.3</td>
<td>18.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>26.5</td>
<td>26.0</td>
<td>14.6</td>
<td>20.6</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>25.4</td>
<td>26.3</td>
<td>14.2</td>
<td>19.4</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>25.8</td>
<td>26.4</td>
<td>14.1</td>
<td>18.7</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>25.8</td>
<td>26.1</td>
<td>14.0</td>
<td>18.4</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean</th>
<th>Scf</th>
<th>Bone</th>
<th>Lean</th>
<th>Scf</th>
<th>IMF</th>
<th>Bone</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW x LW</td>
<td>14.9</td>
<td>4.9</td>
<td>3.5</td>
<td>13.9</td>
<td>6.8</td>
<td>1.0</td>
<td>3.5</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>14.0</td>
<td>4.8</td>
<td>3.4</td>
<td>13.2</td>
<td>7.5</td>
<td>1.1</td>
<td>3.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>15.8</td>
<td>4.4</td>
<td>3.3</td>
<td>15.0</td>
<td>5.8</td>
<td>1.0</td>
<td>3.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>14.7</td>
<td>4.4</td>
<td>3.4</td>
<td>14.0</td>
<td>6.9</td>
<td>1.0</td>
<td>3.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>14.7</td>
<td>4.7</td>
<td>3.3</td>
<td>13.9</td>
<td>7.2</td>
<td>1.1</td>
<td>3.0</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>14.4</td>
<td>4.9</td>
<td>3.3</td>
<td>13.5</td>
<td>7.3</td>
<td>1.1</td>
<td>3.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean</th>
<th>Scf</th>
<th>Lean</th>
<th>Scf</th>
<th>Bone</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW x LW</td>
<td>7.3</td>
<td>4.5</td>
<td>12.7</td>
<td>3.1</td>
<td>2.1</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>7.0</td>
<td>4.7</td>
<td>11.5</td>
<td>3.2</td>
<td>1.9</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>8.1</td>
<td>4.0</td>
<td>13.9</td>
<td>3.0</td>
<td>2.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>7.2</td>
<td>4.6</td>
<td>12.6</td>
<td>3.3</td>
<td>2.0</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>7.2</td>
<td>4.5</td>
<td>12.1</td>
<td>3.2</td>
<td>1.9</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>6.9</td>
<td>4.7</td>
<td>12.0</td>
<td>3.1</td>
<td>1.9</td>
</tr>
</tbody>
</table>
Pietrains gave the most weight of lean and least of fat in each joint and, with the exception of the ham, the least weight of bone.

**Sex**

Significant sex effect contrasts are given in table 4.2.22. Notable, however is the absence of any sex difference for LTR and differences for daily and carcass gain are explained by differences for non-carcass growth and fat deposition. These differences produced castrate carcasses with 2.3% less lean, 2.3% more fat and marginally less bone than gilt carcasses and having small but significantly heavier shoulder and lighter ham proportions. Shoulder and ham tissue %s reflected total tissue results but the gilt advantages were more evident in the back and less in the streak joints.

**Table 4.2.22. Pork Analysis II. Sex effects. Castrate-Gilt contrasts.**

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>CDG (lbs/day)</th>
<th>Crc wt (lbs)</th>
<th>FTDR (lbs/day)</th>
<th>FFBGR (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>0.14</td>
<td>0.09</td>
<td>-1.5</td>
<td>0.063</td>
<td>0.028</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Fat %</th>
<th>Scf %</th>
<th>Imf %</th>
<th>Bone %</th>
<th>Sh %</th>
<th>Ham %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>-2.3</td>
<td>2.3</td>
<td>1.7</td>
<td>0.6</td>
<td>-0.1</td>
<td>0.3</td>
<td>-0.4</td>
</tr>
</tbody>
</table>

**Shoulder**

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Scf %</th>
<th>Imf %</th>
<th>Bone %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>-2.6</td>
<td>1.9</td>
<td>1.0</td>
<td>-0.2</td>
</tr>
</tbody>
</table>

**Back**

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Scf %</th>
<th>Imf %</th>
<th>Bone %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>-3.5</td>
<td>3.6</td>
<td>0.5</td>
<td>-0.3</td>
</tr>
</tbody>
</table>

**Streak**

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Imf %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>-1.0</td>
<td>0.6</td>
</tr>
</tbody>
</table>

**Ham**

<table>
<thead>
<tr>
<th></th>
<th>Lean %</th>
<th>Scf %</th>
<th>Imf %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>-2.1</td>
<td>1.5</td>
<td>0.5</td>
</tr>
</tbody>
</table>
Analysis II - Heavy hog

The least squares analysis of variance for the heavy hog dissection characters is given in table 4.2.23.

Interaction effects

As at pork weight and in heavy hog analysis I, cross x protein level interaction was an unimportant source of variation. There were no statistically significant interactions and no trends were observed in the fat %, scf % or back scf % results to substantiate the cross x protein level interaction for loin, or in the joint % or tissue joint % results to substantiate the cross x protein level interaction for hindq, observed in the heavy hog analysis I.

There were significant cross x sex and protein x sex interactions and these will be described, but the replicate interactions will not be presented.

Consistent trends were observed within the protein x sex interactions, the means of which are presented in table 4.2.24. For fat percentages, castrates responded to high protein with decreased fat percentages for total, subcutaneous and back and had subcutaneous fat percentages, whereas gilts gave the reverse response, more fat on high protein than on low protein. The interactions for total bone and shoulder bone percentages arose because castrates had more bone and gilts less bone on high protein compared to low protein. The interactions gave no changes in rank.
Table 4.2.23. Heavy hog Analysis II. Mean Squares

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DCG</th>
<th>Cc.vr.</th>
<th>LTOF</th>
<th>PIHt</th>
<th>LTOF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>0.516***</td>
<td>0.262***</td>
<td>167.77***</td>
<td>0.014</td>
<td>0.110***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.0000</td>
<td>0.070*</td>
<td>74.28***</td>
<td>0.021*</td>
<td>0.024</td>
</tr>
<tr>
<td>C x R</td>
<td>34</td>
<td>0.094**</td>
<td>0.068**</td>
<td>17.47</td>
<td>0.013*</td>
<td>0.021</td>
</tr>
<tr>
<td>Litters</td>
<td>56</td>
<td>0.0042</td>
<td>0.051</td>
<td>15.84</td>
<td>0.007</td>
<td>0.015</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.002</td>
<td>0.004</td>
<td>0.23</td>
<td>0.001</td>
<td>0.000</td>
</tr>
<tr>
<td>Sex (S)</td>
<td>1</td>
<td>1.383***</td>
<td>1.153***</td>
<td>102.67***</td>
<td>0.052***</td>
<td>1.152***</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.014</td>
<td>0.004</td>
<td>16.43</td>
<td>0.005</td>
<td>0.002</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.028</td>
<td>0.014</td>
<td>5.29</td>
<td>0.005</td>
<td>0.006</td>
</tr>
<tr>
<td>C x S</td>
<td>5</td>
<td>0.014</td>
<td>0.016</td>
<td>10.04</td>
<td>0.008*</td>
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Table 4.2.23 contd. Heavy Hog Analysis II. Mean Squares.

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<th>Fat %</th>
<th>Subcut. fat%</th>
<th>Intermusc. fat%</th>
<th>Bone %</th>
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<th>Ham %</th>
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<td>------------</td>
<td>------------</td>
<td>------------</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lean %</td>
<td>Scf %</td>
<td>Imf %</td>
<td>Bone %</td>
</tr>
<tr>
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<tr>
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<td>Scf %</td>
<td>Imf %</td>
<td>Bone %</td>
</tr>
<tr>
<td>-------------------</td>
<td>----</td>
<td>--------</td>
<td>--------</td>
<td>-------</td>
<td>--------</td>
</tr>
<tr>
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<td>9.77</td>
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Table 4.2.24. Heavy Hog Analysis II  Protein level x Sex. Interactions.

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<tr>
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<th>Fat %</th>
<th>Scf %</th>
<th>Back Scf %</th>
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<tbody>
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<td>Castrate</td>
<td>Gilt</td>
<td>Castrate</td>
</tr>
<tr>
<td>High protein</td>
<td>34.2</td>
<td>30.3</td>
<td>28.0</td>
</tr>
<tr>
<td>Low protein</td>
<td>34.8</td>
<td>29.8</td>
<td>28.5</td>
</tr>
<tr>
<td>High-Low</td>
<td>-0.6</td>
<td>+0.5</td>
<td>-0.5</td>
</tr>
</tbody>
</table>

|                  | Ham scf %                  | Bone %                      | Sh. Bone %                  |
|                  | Castrate | Gilt | Castrate | Gilt | Castrate | Gilt |
| High protein     | 25.3     | 22.6 | 7.4      | 7.6  | 11.2     | 11.4 |
| Low protein      | 25.9     | 21.9 | 7.3      | 7.7  | 10.9     | 11.5 |
| High-Low         | -0.6     | +0.7 | +0.1     | -0.1 | +0.3     | -0.1 |

Lean % results showed a related trend but were not significant at the 5% level. The lean % means were:

<table>
<thead>
<tr>
<th></th>
<th>Castrate</th>
<th>Gilt</th>
</tr>
</thead>
<tbody>
<tr>
<td>High protein</td>
<td>40.4</td>
<td>44.0</td>
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<tr>
<td>Low protein</td>
<td>40.0</td>
<td>44.5</td>
</tr>
<tr>
<td>High-Low</td>
<td>+0.4</td>
<td>-0.5</td>
</tr>
</tbody>
</table>

The cross x sex interactions are presented in table 4.2.25. The LTGR interaction can be attributed to the larger sex differences for LWW and LW pigs. Rank changes resulted. The LWW result reiterates the earlier pork result. While less clear cut, the lean and scf percentage interactions follow the pattern of the LTGR performances, rank changes due to the larger sex differences of LWW and LW pigs. Pietrain crosses also showed large sex differences for the tissue and joint tissue percentages and an alternative view of the results may be taken in that the tissue and joint tissue interactions (excepting that for LTGR) occurred due to smaller sex differences for the W x LW and L x LW crosses.
<table>
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<th>Cross x Sex Interactions</th>
<th>Lean %</th>
<th>LTGR (lbs/day)</th>
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<tr>
<td>Pietrain x LW</td>
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<tr>
<td>Landrace x LW</td>
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<td>0.523</td>
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<tr>
<td>Essex x LW</td>
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<td>0.538</td>
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<tr>
<td>LW x Wessex</td>
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<td>0.533</td>
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<td>24.7</td>
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<td>25.8</td>
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<td>Pietrain x LW</td>
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<td>26.1</td>
<td>22.1</td>
<td>4.0</td>
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<tr>
<td>Landrace x LW</td>
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<td>24.9</td>
<td>2.6</td>
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<tr>
<td>Essex x LW</td>
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<td>25.3</td>
<td>3.9</td>
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<td>LW x Wessex</td>
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<table>
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<th>&lt;sup&gt;♂&lt;/sup&gt;-&lt;sup&gt;♀&lt;/sup&gt;</th>
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<tr>
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<td>39.9</td>
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<th>&lt;sup&gt;♂&lt;/sup&gt;-&lt;sup&gt;♀&lt;/sup&gt;</th>
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<td>45.4</td>
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<td>46.5</td>
<td>-7.6</td>
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<th>&lt;sup&gt;♀&lt;/sup&gt;</th>
<th>&lt;sup&gt;♂&lt;/sup&gt;-&lt;sup&gt;♀&lt;/sup&gt;</th>
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Protein level

In contrast to the general significant effect of protein level for the pork tissue characters, there were no significant protein level effects at the heavy hog slaughter weight for tissue characters and no consistent responses indicative of an advantageous or disadvantageous effect of the higher dietary protein level.

Cross

Table 4.2.26 presents the significant cross effects as deviations from the LW controls. LTGR was not influenced by genotype despite a cross effect at pork weight, and rankings generally corresponded to those at pork weight. The cross contrasts show that the Pietrains had the slowest live and carcass daily gain despite a slight advantage for LTGR. The difference is principally explained by the negative contrasts for FTDR and FFBGR. Again the Pietrain cross had a large advantage for carcass weight and advantages for lean, fat and bone percentages. Streak and ham proportions were larger than the controls, shoulder proportions equivalent and the back joint smaller. The advantages for shoulder and streak tissue percentages were the same as back tissues percentages exceeded and ham tissue percentages were smaller than the overall tissue advantages.

As at pork weight the Landrace cross grew faster than the controls, with a comparable FTDR and the fastest FFBGR. Landrace carcass weight was the same as the LW and the carcass had 0.9% more lean, 0.7% less fat and the same bone %. While the back and streak proportion contrasts were positive, the shoulder contrast was negative. Essex and the Wessex reciprocal
<table>
<thead>
<tr>
<th>Cross</th>
<th>DG (lbs/day)</th>
<th>CLG (lbs/day)</th>
<th>Crc.wt (lbs)</th>
<th>FTDR (lbs/day)</th>
<th>FFGR (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.09</td>
<td>0.07</td>
<td>-1.4</td>
<td>0.041</td>
<td>0.031</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.15</td>
<td>-0.10</td>
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<td>-0.067</td>
<td>-0.030</td>
</tr>
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<td>0.05</td>
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<td>0.05</td>
<td>-0.9</td>
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<table>
<thead>
<tr>
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<th>Fat %</th>
<th>Scf %</th>
<th>Inf %</th>
<th>Bone %</th>
<th>Sh %</th>
<th>Back %</th>
<th>Str %</th>
<th>Hm %</th>
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<tbody>
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<td>0.5</td>
<td>0.4</td>
<td>-0.0</td>
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<td>-0.7</td>
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<tr>
<td>Pietrain x LW</td>
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<td>2.6</td>
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<td>0.8</td>
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<tr>
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<td>0.7</td>
<td>0.5</td>
<td>0.2</td>
<td>-0.0</td>
<td>-0.9</td>
<td>0.5</td>
<td>0.8</td>
<td>0.1</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-0.1</td>
<td>1.0</td>
<td>0.6</td>
<td>0.4</td>
<td>-0.3</td>
<td>-0.5</td>
<td>0.2</td>
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<td>-0.3</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.3</td>
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<td>0.4</td>
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<td>-0.3</td>
<td>0.4</td>
<td>0.2</td>
<td>-0.5</td>
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<table>
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<tr>
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<th>Inf %</th>
<th>Bone %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Inf %</th>
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<tbody>
<tr>
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<td>0.6</td>
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<td>0.7</td>
<td>0.5</td>
</tr>
<tr>
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<td>0.2</td>
<td>0.4</td>
<td>-0.6</td>
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<td>0.1</td>
</tr>
<tr>
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<td>0.2</td>
<td>1.2</td>
<td>-1.5</td>
<td>-0.1</td>
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<tr>
<td>Essex x LW</td>
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<td>0.0</td>
<td>0.9</td>
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<td>-1.2</td>
<td>0.7</td>
<td>0.5</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.3</td>
<td>0.6</td>
<td>0.5</td>
<td>0.2</td>
<td>-1.8</td>
<td>1.0</td>
<td>0.6</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Inf %</th>
<th>Bone %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Inf %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>Inf %</th>
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<tr>
<td>Wessex x LW</td>
<td>-2.1</td>
<td>1.5</td>
<td>-1.7</td>
<td>1.0</td>
<td>0.3</td>
<td></td>
<td></td>
<td>-1.7</td>
<td>1.0</td>
<td>0.3</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.0</td>
<td>3.3</td>
<td>2.4</td>
<td>-1.8</td>
<td>0.1</td>
<td></td>
<td></td>
<td>2.4</td>
<td>-1.8</td>
<td>0.1</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>-0.4</td>
<td>0.7</td>
<td>0.1</td>
<td>-0.0</td>
<td>-0.6</td>
<td></td>
<td></td>
<td>0.1</td>
<td>-0.0</td>
<td>-0.6</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-1.5</td>
<td>1.2</td>
<td>-1.8</td>
<td>1.7</td>
<td>0.3</td>
<td></td>
<td></td>
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<td>1.7</td>
<td>0.3</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-1.8</td>
<td>1.2</td>
<td>-1.1</td>
<td>0.6</td>
<td>0.2</td>
<td></td>
<td></td>
<td>-1.1</td>
<td>0.6</td>
<td>0.2</td>
</tr>
</tbody>
</table>
crosses gave similar results. Growth characters (except LTGR) had large positive contrasts, carcass weight contrasts were about -1.0 lbs and lean percentages were lower, fat percentages higher and bone percentages equivalent to the control performance. Carcasses had smaller shoulder and ham and larger back and streak proportions. The shoulder tended to have more lean and the streak less fat than the overall carcass level.

The cross tissue and joint weights in table 4.2.27 indicate the absolute values of tissue production at a 257 lbs live slaughter weight. Pietrain cross pigs, compared to their nearest competitor, the Landrace cross, had a 6 lb advantage for lean meat production and compared to all crosses produced more lean in all carcass joints and, except in the shoulder, the least fat. The efficiency of food conversion to live weight and lean tissue is given in analysis III.

**Sex**

Significant sex effect contrasts are given in table 4.2.28. All characters except FFBGR, shoulder percentage, streak percentage and ham bone percentage were influenced by sex and generally reflected the trends observed at pork weight, faster castrate DG, CDG and FTDR and superior gilt carcass composition. However, contrary to the pork results in which no sex difference for LTGR was observed, at the heavier weight gilts had superior LTGRs. The combination of superior gilt LTGR and a faster castrate FTDR improved the gilt lean percentage advantage although in absolute terms the gilt lean advantage was marginally counterbalanced by the superior
Table 4.2.27. Heavy Hog Cross tissue and joint weights (lbs) at
257 lbs live weight.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean</th>
<th>Fat</th>
<th>Scf</th>
<th>Ifm</th>
<th>Bone</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW</td>
<td>204.6</td>
<td>86.1</td>
<td>66.1</td>
<td>54.6</td>
<td>11.5</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>203.2</td>
<td>82.5</td>
<td>67.5</td>
<td>55.3</td>
<td>12.2</td>
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<tr>
<td>Pietrain x LW</td>
<td>207.4</td>
<td>94.2</td>
<td>62.0</td>
<td>60.0</td>
<td>12.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>204.5</td>
<td>87.9</td>
<td>64.6</td>
<td>55.6</td>
<td>11.0</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>203.7</td>
<td>83.7</td>
<td>67.8</td>
<td>55.6</td>
<td>12.2</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>205.8</td>
<td>83.4</td>
<td>67.5</td>
<td>55.2</td>
<td>12.2</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Shoulder</th>
<th>Back</th>
<th>Streak</th>
<th>Ham</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW</td>
<td>51.8</td>
<td>56.5</td>
<td>29.5</td>
<td>36.8</td>
</tr>
<tr>
<td>Wessex x LW</td>
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<td>56.7</td>
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<td>35.4</td>
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<tr>
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<td>56.2</td>
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</tr>
<tr>
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<td>57.5</td>
<td>31.1</td>
<td>37.0</td>
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<tr>
<td>Essex x LW</td>
<td>50.5</td>
<td>56.6</td>
<td>30.4</td>
<td>36.1</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>51.0</td>
<td>57.1</td>
<td>29.8</td>
<td>35.7</td>
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<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean</th>
<th>Scf</th>
<th>Ifm</th>
<th>Bone</th>
<th>Lean</th>
<th>Scf</th>
<th>Ifm</th>
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<tr>
<td>LW</td>
<td>26.5</td>
<td>12.9</td>
<td>4.5</td>
<td>5.9</td>
<td>25.1</td>
<td>20.7</td>
<td>3.2</td>
</tr>
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<td>12.3</td>
<td>4.8</td>
<td>5.8</td>
<td>24.5</td>
<td>21.1</td>
<td>3.5</td>
</tr>
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<td>Pietrain x LW</td>
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<td>11.4</td>
<td>4.8</td>
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<td>27.6</td>
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<tr>
<td>LW x Wessex</td>
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<td>4.7</td>
<td>5.9</td>
<td>24.4</td>
<td>21.5</td>
<td>3.6</td>
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<table>
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<th>Cross</th>
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<th>Scf</th>
<th>Ifm</th>
<th>Lean</th>
<th>Scf</th>
<th>Ifm</th>
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<tr>
<td>Wessex x LW</td>
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<td>13.1</td>
<td>20.6</td>
<td>8.7</td>
<td>1.5</td>
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<tr>
<td>Pietrain x LW</td>
<td>14.0</td>
<td>11.8</td>
<td>24.3</td>
<td>8.5</td>
<td>1.6</td>
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<tr>
<td>Landrace x LW</td>
<td>13.0</td>
<td>13.2</td>
<td>22.2</td>
<td>8.8</td>
<td>1.4</td>
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<tr>
<td>Essex x LW</td>
<td>12.4</td>
<td>13.0</td>
<td>20.9</td>
<td>9.2</td>
<td>1.5</td>
<td></td>
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<tr>
<td>LW x Wessex</td>
<td>12.0</td>
<td>12.8</td>
<td>21.0</td>
<td>8.7</td>
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Table 4.2.28. Heavy Hog Analysis II. Sex effects. Castrate-Gilt contrasts.

<table>
<thead>
<tr>
<th></th>
<th>DG (lbs/day)</th>
<th>CEG (lbs/day)</th>
<th>Castr wt. (lbs)</th>
<th>LTGR (lbs/day)</th>
<th>FTDR (lbs/day)</th>
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<tbody>
<tr>
<td>Castrate-Gilt</td>
<td>0.12</td>
<td>0.11</td>
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<table>
<thead>
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<th>Scf %</th>
<th>IMF %</th>
<th>Bone %</th>
<th>Back %</th>
<th>Ham %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrate-Gilt</td>
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<td>4.4</td>
<td>3.7</td>
<td>0.8</td>
<td>-0.3</td>
<td>0.5</td>
<td>-0.5</td>
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<table>
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<tr>
<th></th>
<th>Lean %</th>
<th>Scf %</th>
<th>IMF %</th>
<th>Bone %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>IMF %</th>
<th>Bone %</th>
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<tbody>
<tr>
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<td>6.6</td>
<td>0.8</td>
<td>-0.7</td>
</tr>
<tr>
<td>Back</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Castrate-Gilt</td>
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<table>
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<th>Scf %</th>
<th>IMF %</th>
<th>Bone %</th>
<th>Lean %</th>
<th>Scf %</th>
<th>IMF %</th>
<th>Bone %</th>
</tr>
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<tbody>
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<td>1.3</td>
<td>-0.1</td>
<td>-5.7</td>
<td>3.5</td>
<td>0.4</td>
<td>0.2</td>
</tr>
<tr>
<td>Back</td>
<td></td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>Castrate-Gilt</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
castrate killing out percentage. Within the carcass, shoulder and streak percentages were similar for both sexes but castrates had a larger proportion of back and a smaller ham than gilts. The lighter castrate ham reiterates the pork result and, as at pork, the gilt tissue advantages were greatest in the back joint and least in the streak.

Analysis III - Pork

The least squares analysis of variance for the pork pen mean characters is given in table 4.2.29

Interaction effects

The cross x protein level mean squares were only statistically significant for FFBGR and in general were smaller than the residual mean squares. The LTGR and lean % mean squares were exceptions and the subclass means for these characters, for FFBGR and for the difference between FFBGR and LTGR are presented in table 4.2.30. The percentage changes in the characters due to increasing protein level are also given.

The FFBGR interaction means show rank changes with increasing dietary protein level and the percentage changes indicate that the significant differences in rank resulted from the small effect of protein increment on LW and MLW FFBGR, only -0.5 and 1.0% respectively. The other genotypes responded to the increased protein level with an improved FFBGR (5 to 0%).

Consideration of the LTGR and FFBGR-LTGR results shows that within the fat free carcass growth responses there were differential contributions of lean and accessory tissues, e.g. PLW and ELW have similar percentage changes for LTGR, 6.0 and 5.5% respectively but their responses for the remainder of the
### Table 4.2.29. Pork Analysis III. Mean Squares.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
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<th>Fat %</th>
<th>DG</th>
<th>FCE</th>
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<td>125.30***</td>
<td>69.48***</td>
<td>0.175***</td>
<td>0.155*</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>12.05</td>
<td>41.02***</td>
<td>0.054**</td>
<td>0.369***</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>6.56</td>
<td>9.01</td>
<td>0.021</td>
<td>0.074</td>
</tr>
<tr>
<td>Litters</td>
<td>62</td>
<td>8.25</td>
<td>8.80</td>
<td>0.016</td>
<td>0.052</td>
</tr>
<tr>
<td>Protein level (P)</td>
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<td>15.01**</td>
<td>26.48***</td>
<td>0.018</td>
<td>0.080*</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>1.99</td>
<td>1.85</td>
<td>0.006</td>
<td>0.015</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.94</td>
<td>0.90</td>
<td>0.006</td>
<td>0.069**</td>
</tr>
<tr>
<td>Residual</td>
<td>97</td>
<td>1.87</td>
<td>2.03</td>
<td>0.006</td>
<td>0.019</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DFI</th>
<th>CDG</th>
<th>LTGR</th>
<th>FTDR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
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<td>14.454***</td>
<td>0.076***</td>
<td>0.032***</td>
<td>0.036***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.729***</td>
<td>0.016</td>
<td>0.013</td>
<td>0.012**</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>0.130</td>
<td>0.014</td>
<td>0.004</td>
<td>0.004</td>
</tr>
<tr>
<td>Litters</td>
<td>62</td>
<td>0.134</td>
<td>0.010</td>
<td>0.006</td>
<td>0.004</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.007</td>
<td>0.026*</td>
<td>0.021***</td>
<td>0.004</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.015</td>
<td>0.003</td>
<td>0.002</td>
<td>0.000</td>
</tr>
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<td>R x P</td>
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<td>0.099</td>
<td>0.006</td>
<td>0.001</td>
<td>0.001</td>
</tr>
<tr>
<td>Residual</td>
<td>97</td>
<td>0.062</td>
<td>0.004</td>
<td>0.001</td>
<td>0.001</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>FFDR</th>
<th>LTPC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>0.056**</td>
<td>17.617***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.062***</td>
<td>5.668**</td>
</tr>
<tr>
<td>C x R</td>
<td>35</td>
<td>0.010</td>
<td>1.534</td>
</tr>
<tr>
<td>Litters</td>
<td>62</td>
<td>0.010</td>
<td>1.348</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.051***</td>
<td>4.284***</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.005*</td>
<td>0.276</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.005</td>
<td>0.286</td>
</tr>
<tr>
<td>Residual</td>
<td>97</td>
<td>0.002</td>
<td>0.340</td>
</tr>
</tbody>
</table>
### Table 4.2.30. Pork Analysis III. Cross x Protein level subclass means and percentage changes.

#### FFGR (lbs/day)

<table>
<thead>
<tr>
<th>Cross</th>
<th>HP</th>
<th>LP</th>
<th>HP/LP % change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>1.015</td>
<td>1.020</td>
<td>-0.5</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>1.033</td>
<td>1.023</td>
<td>1.0</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>1.057</td>
<td>1.005</td>
<td>5.2</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>1.113</td>
<td>1.072</td>
<td>3.8</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>1.060</td>
<td>1.000</td>
<td>6.0</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>1.096</td>
<td>0.977</td>
<td>3.0</td>
</tr>
</tbody>
</table>

#### LTGR (lbs/day)

<table>
<thead>
<tr>
<th>Cross</th>
<th>HP</th>
<th>LP</th>
<th>HP/LP % change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>0.585</td>
<td>0.587</td>
<td>-0.3</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>0.570</td>
<td>0.565</td>
<td>0.9</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>0.650</td>
<td>0.613</td>
<td>6.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.647</td>
<td>0.613</td>
<td>5.5</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.606</td>
<td>0.576</td>
<td>5.2</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.569</td>
<td>0.555</td>
<td>2.5</td>
</tr>
</tbody>
</table>

#### FFGR-LTGR (lbs/day)

<table>
<thead>
<tr>
<th>Cross</th>
<th>HP</th>
<th>LP</th>
<th>HP/LP % change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>0.430</td>
<td>0.433</td>
<td>-0.7</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>0.463</td>
<td>0.458</td>
<td>1.1</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>0.407</td>
<td>0.392</td>
<td>3.8</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.466</td>
<td>0.459</td>
<td>1.5</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.454</td>
<td>0.424</td>
<td>7.1</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.457</td>
<td>0.422</td>
<td>3.6</td>
</tr>
</tbody>
</table>

#### Lean %

<table>
<thead>
<tr>
<th>Cross</th>
<th>HP</th>
<th>LP</th>
<th>HP/LP % change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>48.6</td>
<td>48.7</td>
<td>-0.2</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>46.3</td>
<td>46.2</td>
<td>0.6</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>52.2</td>
<td>51.2</td>
<td>2.0</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>49.1</td>
<td>48.0</td>
<td>2.3</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>48.2</td>
<td>47.7</td>
<td>1.0</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>47.6</td>
<td>47.0</td>
<td>0.9</td>
</tr>
</tbody>
</table>
FFDGR differed, 3.6% and 7.1% respectively. The data therefore suggests that not only is it possible that genotypes respond differentially to protein level for lean tissue but that within carcass weight gain there may be differential lean and accessory tissue responses.

**Protein level**

Protein level effects as high-low contrasts are given in table 4.2.31 and demonstrate the improved performance given by the high protein diet, an effect also shown, but not significantly, by DG and FIDR. Both diets had similar daily feed intakes and therefore similar energy intakes.

**Table 4.2.31. Pork Analysis III. Protein level effects. High-Low contrasts.**

<table>
<thead>
<tr>
<th>Lean %</th>
<th>Fat %</th>
<th>FCE (lbs/lbs)</th>
<th>CDG (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>High-Low</td>
<td>0.5</td>
<td>0.7</td>
<td>-0.04</td>
</tr>
<tr>
<td><strong>LTGR (lbs/day)</strong></td>
<td><strong>FFDGR (lbs/day)</strong></td>
<td><strong>LTFC (lbs/lbs)</strong></td>
<td></td>
</tr>
<tr>
<td>High-Low</td>
<td>0.02</td>
<td>0.03</td>
<td>-0.28</td>
</tr>
</tbody>
</table>

**Cross**

For all characters the influence of genotype was greater than that of protein level and, as expected, there were large appetite differences with the WLW crosses eating the most and the PLW crosses the least (table 4.2.32).

The cross differences for FCE showed that the ELW and PLW crosses had efficiencies comparable with the controls, Wessex crosses had inferior efficiencies and LLW were more efficient. Consequently LLW had the fastest daily live weight gain and only the PLW cross grew more slowly than the controls.
Table 4.2.32. Pork Analysis III. Cross effects. Deviations from Large White controls.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Fat %</th>
<th>DG (lbs/day)</th>
<th>FCE (lbs/lbs)</th>
<th>DFI (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-2.3</td>
<td>1.8</td>
<td>0.11</td>
<td>0.04</td>
<td>0.43</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.1</td>
<td>1.9</td>
<td>-0.06</td>
<td>-0.06</td>
<td>-0.19</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>-0.1</td>
<td>0.5</td>
<td>0.13</td>
<td>-0.12</td>
<td>0.43</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-0.7</td>
<td>1.0</td>
<td>0.06</td>
<td>0.00</td>
<td>0.20</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-1.5</td>
<td>1.6</td>
<td>0.03</td>
<td>0.08</td>
<td>0.20</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>CIG (lbs/day)</th>
<th>LTRG (lbs/day)</th>
<th>FTDF (lbs/day)</th>
<th>FTDFG (lbs/day)</th>
<th>LTRF (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.06</td>
<td>-0.02</td>
<td>0.05</td>
<td>0.01</td>
<td>0.99</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.03</td>
<td>0.05</td>
<td>-0.04</td>
<td>0.01</td>
<td>-0.85</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.10</td>
<td>0.04</td>
<td>0.05</td>
<td>0.07</td>
<td>-0.27</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>0.04</td>
<td>0.01</td>
<td>0.03</td>
<td>0.01</td>
<td>0.31</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>0.00</td>
<td>-0.02</td>
<td>0.03</td>
<td>-0.03</td>
<td>0.83</td>
</tr>
</tbody>
</table>

However, in direct contrast, PLWs had the fastest LTGRs and the slowest FTDF and therefore produced carcasses with the most lean and the least fat. Of the other crosses, LLW, LTGR was comparable with that of PLW, but the Landrace also had a high FTDF and therefore produced carcasses more comparable with those of the controls than the Pietrains. ELW carcasses had less lean and more fat than the controls and the relatively fast DG reflected only a small advantage for LTGR and a much faster FTDF.

The Wessex reciprocal crosses had the same rate of lean tissue gain but otherwise performed differently. WLW compared to LWW ate more, converted the food more efficiently to liveweight and therefore grew more quickly and had a comparable LTGR but a more rapid deposition of fat tissue.
Despite the faster FTR of the WLW, the reciprocal crosses had similar carcass fat percentage, although the LW did have a 0.8% advantage for lean. In comparison with the other genotypes, the Wessex crosses had the slowest LTGRs, the faster FTRs, gave carcasses with the least lean and the most fat and were the least efficient converters of food to lean.

Genotype comparison based solely on LTFC gave PLW as the top ranking genotype followed by LLW.

**Analysis III - Heavy Hog**

The least squares analysis of variance for the heavy hog pen mean characters is given in table 4.2.55.

**Interaction effects**

As in all previous analyses, cross x protein level interaction was usually an unimportant source of variation and of the ten characters considered only the interaction for FCE was significant.

The FCE cross x protein level means (lbs feed/lbs gain) are given below:

<table>
<thead>
<tr>
<th>Cross</th>
<th>High Protein</th>
<th>Low Protein</th>
<th>High-Low</th>
<th>% change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>3.83</td>
<td>3.95</td>
<td>-0.12</td>
<td>-3.1</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>3.95</td>
<td>3.99</td>
<td>0.06</td>
<td>1.5</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>4.09</td>
<td>4.01</td>
<td>0.08</td>
<td>1.9</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>3.78</td>
<td>3.91</td>
<td>-0.13</td>
<td>-3.2</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>3.91</td>
<td>3.90</td>
<td>0.01</td>
<td>0.1</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>3.99</td>
<td>3.99</td>
<td>0.00</td>
<td>0.1</td>
</tr>
</tbody>
</table>

Rankings changed principally as a result of the improved performance of LW and LLW with increased protein level, a consistent trend also shown for LTGR, LTFC, Lean percentage.
<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Lean %</th>
<th>Fat %</th>
<th>DG</th>
<th>FCE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>127.96***</td>
<td>71.55**</td>
<td>0.249***</td>
<td>0.189*</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>18.53</td>
<td>24.40</td>
<td>0.032</td>
<td>0.434***</td>
</tr>
<tr>
<td>C x R</td>
<td>34</td>
<td>10.74</td>
<td>14.31</td>
<td>0.034*</td>
<td>0.091</td>
</tr>
<tr>
<td>Litters</td>
<td>57</td>
<td>12.06</td>
<td>15.71</td>
<td>0.019</td>
<td>0.091</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>1.96</td>
<td>1.19</td>
<td>0.005</td>
<td>0.016</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>2.28</td>
<td>3.85</td>
<td>0.005</td>
<td>0.064*</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>1.81</td>
<td>3.97</td>
<td>0.011*</td>
<td>0.052*</td>
</tr>
<tr>
<td>Residual</td>
<td>92</td>
<td>2.73</td>
<td>3.33</td>
<td>0.005</td>
<td>0.021</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DF1</th>
<th>CDG</th>
<th>LTGR</th>
<th>FTDR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>2.540***</td>
<td>0.129***</td>
<td>0.007</td>
<td>0.058***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.795*</td>
<td>0.030*</td>
<td>0.009*</td>
<td>0.010</td>
</tr>
<tr>
<td>C x R</td>
<td>34</td>
<td>0.285</td>
<td>0.024*</td>
<td>0.005</td>
<td>0.007</td>
</tr>
<tr>
<td>Litters</td>
<td>57</td>
<td>0.354</td>
<td>0.013</td>
<td>0.003</td>
<td>0.007</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.000</td>
<td>0.004</td>
<td>0.000</td>
<td>0.001</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.100</td>
<td>0.003</td>
<td>0.000</td>
<td>0.001</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.019</td>
<td>0.007</td>
<td>0.002</td>
<td>0.002</td>
</tr>
<tr>
<td>Residual</td>
<td>92</td>
<td>0.090</td>
<td>0.004</td>
<td>0.001</td>
<td>0.001</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>FFBRGR</th>
<th>LTFC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>5</td>
<td>0.021**</td>
<td>16.768***</td>
</tr>
<tr>
<td>Replicate (R)</td>
<td>7</td>
<td>0.020**</td>
<td>10.210**</td>
</tr>
<tr>
<td>C x R</td>
<td>34</td>
<td>0.012**</td>
<td>2.922</td>
</tr>
<tr>
<td>Litters</td>
<td>57</td>
<td>0.006</td>
<td>3.265</td>
</tr>
<tr>
<td>Protein level (P)</td>
<td>1</td>
<td>0.001</td>
<td>0.035</td>
</tr>
<tr>
<td>C x P</td>
<td>5</td>
<td>0.005</td>
<td>1.476</td>
</tr>
<tr>
<td>R x P</td>
<td>7</td>
<td>0.004</td>
<td>1.012</td>
</tr>
<tr>
<td>Residual</td>
<td>92</td>
<td>0.002</td>
<td>0.802</td>
</tr>
</tbody>
</table>
and Fat percentage. Other genotypes gave little, none or the reverse response to increased protein level. Rank changes in other characters failed to reach significance even at the 10% level.

The possibility of randomly significant cross x protein level interactions is obviously high when many characters are analysed. Analyses I, II and III have presented results for 62 characters at each slaughter weight with some duplication of characters between analyses. At least two significant cross x protein level interactions might therefore be expected by chance alone. For pork pigs two, and for heavy hogs three cross x protein level interactions were observed. It is therefore possible to attribute the statistically significant cross x protein level interactions, including the heavy hog FCS interaction, to chance alone.

Possible biological explanations for the interactions will be discussed in section 4.5.

Protein

In keeping with earlier results, there were no significant protein level effects for the heavy hog pen mean characters and there was no tendency for improved performance with the high protein level.

Cross

Table 4.2.34 presents contrasts for the significant cross effect characters, while the LTGR cross means and cross heavy hog LTGRs as a percentage of their pork LTGRs are given over.
Cross Pork  Heavy hog  Hog/Pork %
Large White 0.586  0.535  91.3
Wessex x LW 0.567  0.530  93.5
Fiestrain x LW 0.651  0.558  85.3
Landrace x LW 0.630  0.561  89.0
Essex x LW 0.591  0.526  89.0
LW x Wessex 0.562  0.516  91.8

LTGR for the liveweight gain 60 to 260 lbs (heavy hog) was slower than for 60 to 130 lbs (pork), although rankings were similar with PLW and LLW to ELW and the Wessex crosses. Comparison of the cross LTGRs to pork and heavy hog weights indicates differential LTGR reduction with PLW having a larger decrease than the other crosses. WLW gave the smallest reduction. These differences reduced the LTGR variation between crosses and, in contrast to pork weight, no statistically significant cross effect was found.

All other characters had significant cross effects and cross contrasts (deviation from the LW controls) for these characters are given in table 4.2.3. As at pork weight, PLW had the smallest appetite, but with the longer growing period it had the least efficient food conversion and therefore the slowest daily gain. It was the only genotype to grow more slowly than the LW controls. However, despite its poor growth performance, PLW carcasses had the most lean and least fat as a result of a faster LTGR and the slowest FTDR. The Fiestrain cross had the most efficient LTFC.

Wessex and Essex cross performances were similar with, compared to the controls, larger appetites, slightly inferior FCE and therefore faster live weight gain, faster FTDR, slower LTGR, less efficient LTFC and carcasses with less lean and more fat.
Table 4.2.34. Heavy Hog Analysis III. Cross effects.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lean %</th>
<th>Fat %</th>
<th>DG (lbs/day)</th>
<th>FCE (lbs/lbs)</th>
<th>DFI (lbs/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>-1.2</td>
<td>0.7</td>
<td>0.05</td>
<td>0.03</td>
<td>0.26</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>3.4</td>
<td>-2.5</td>
<td>-0.17</td>
<td>0.16</td>
<td>-0.43</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.9</td>
<td>-0.8</td>
<td>0.02</td>
<td>-0.05</td>
<td>0.03</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-1.3</td>
<td>1.2</td>
<td>0.04</td>
<td>0.01</td>
<td>0.19</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-1.7</td>
<td>1.1</td>
<td>0.02</td>
<td>0.10</td>
<td>0.28</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>CDG (lbs/day)</th>
<th>FTDR (lbs/day)</th>
<th>FFBGR (lbs/day)</th>
<th>LTFC (lbs/lbs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wessex x LW</td>
<td>0.06</td>
<td>0.03</td>
<td>0.01</td>
<td>0.56</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>-0.12</td>
<td>-0.08</td>
<td>-0.04</td>
<td>-0.82</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>0.03</td>
<td>-0.00</td>
<td>0.03</td>
<td>-0.56</td>
</tr>
<tr>
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<td>0.03</td>
<td>-0.00</td>
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</tr>
<tr>
<td>LW x Wessex</td>
<td>0.02</td>
<td>0.02</td>
<td>-0.01</td>
<td>0.96</td>
</tr>
</tbody>
</table>

By contrast, LLW had an appetite similar to the controls, a better FCE, some advantage for DG, the fastest LTGR and a LTFC next in efficiency to the PLW. Its FTDR was equivalent to the controls and its carcass therefore had more lean and less fat.

Comparison of the performance of the different crosses at heavy hog and pork weights shows that rankings were similar at the two slaughter weights. The percentage change in performance is tabulated over the page for the different genotypes.

Generally the crosses gave consistent changes in performance which suggests that comparative genotype performances can be described independent of a particular slaughter weight within the range in current commercial usage. A possible categorisation of
Percentage change in performance between heavy hog and pork
slaughter weights.

<table>
<thead>
<tr>
<th>Cross</th>
<th>DFI</th>
<th>FCE</th>
<th>DG</th>
<th>CPG</th>
<th>LTGR</th>
<th>FTDR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Large White</td>
<td>33.3</td>
<td>29.7</td>
<td>2.5</td>
<td>4.7</td>
<td>-8.7</td>
<td>65.0</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>28.0</td>
<td>28.9</td>
<td>-0.6</td>
<td>3.0</td>
<td>-6.5</td>
<td>47.5</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>29.2</td>
<td>35.5</td>
<td>-3.9</td>
<td>-2.4</td>
<td>-14.7</td>
<td>60.3</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>29.1</td>
<td>33.3</td>
<td>-3.5</td>
<td>-0.7</td>
<td>-11.0</td>
<td>48.2</td>
</tr>
<tr>
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</table>

<table>
<thead>
<tr>
<th>Cross</th>
<th>Access Tiss.</th>
<th>Lean %</th>
<th>Fat %</th>
<th>LTFC</th>
</tr>
</thead>
<tbody>
<tr>
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<td>-13.6</td>
<td>39.8</td>
<td>46.8</td>
</tr>
<tr>
<td>Wessex x LW</td>
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</tr>
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<td>34.6</td>
<td>44.7</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>-12.2</td>
<td>-14.8</td>
<td>39.0</td>
<td>48.2</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>-11.9</td>
<td>-14.4</td>
<td>35.6</td>
<td>43.8</td>
</tr>
</tbody>
</table>

* Accessory tissue: All liveweight gain other than carcass lean and fat.

The performances arise from the discussion in Chapter 2 which gave appetite and lean gain as the characters underlying efficiency. The results of Analysis III suggest that the performances of the six genotypes can broadly be classified by their relative appetites and LTGRs in the following way. The control herd Large Whites had average LTGR and appetite, while the Essex cross and the Wessex reciprocal crosses had a relatively slow LTGR and a large appetite. These contrasted with the
Landrace cross which had a large appetite and a fast LTGR while the Pietrain cross combined a comparatively small appetite with a fast LTGR.

4.3 Discussion

Interactions

Any expectation that the genotypic variation for appetite and LTGR and the feeding of contrasting protein levels would generate several important genotype x protein level interactions was not realised. Statistically significant cross x protein level interactions were found at pork weight only for pH and FFBGR and at heavy hog weight only for loin backfat thickness, hind quarter weight and FCE. Out of a possible 62 interactions at each slaughter weight there were, therefore, only 2 at pork weight and 3 at heavy hog weight which were statistically significant. If independence of all characters is assumed, the proportion of significant interactions at each slaughter weight was that probable by chance alone at the significance level used. That many characters were patently correlated, and therefore presence or absence of significance for one character would probably dictate a correlated result in several other characters, merely adds weight to a sampling rather than a biological explanation for the observed cross x protein level interaction. In the same way any tenable biological explanation for the observed interactions would be indicated by a trend or trends within the remaining characters.

For the pork population the only growth economy or carcass composition cross x protein level interaction was FFBGR,
and then only in the pen mean analysis (III) and not in
the dissected population analysis (II). Assuming the
validity of the postulated rationale of genotype x nutrition
interaction, and as there were no indications of cross x
protein level interaction or protein level effects for daily
feed intake (i.e. appetite), then any biological explanation
for the FFBGR interaction will be indicated by trends for the
pork tissue characters.

Fat free body growth rate has been defined here as the
average daily gain of fat free carcass weight on test and is
therefore the difference between carcass daily gain and FTDR.
The analyses have shown that the small responses to protein
increment for CDG were generally equivalent to the LTGR
responses while FTDR responses were generally smaller than, but
proportional to, those shown by LTGR. As illustrated in
table 4.2.30 advantageous responses to protein increment were
shown by the Pietrain, Landrace and Essex crosses with the
Pietrain and Landrace giving the greater increases in carcass
lean percentage. The Large White controls and the Wessex
crosses did not respond to increased protein level and the sum
of the small differential LTGRs, FTDRs and accessory tissue gains
(table 4.2.30) produced the FFBGR interaction. Within the
pork results a trend was therefore observed for differential
genotypic response to protein increment which, with purebred
progeny and a wider range of protein level, would possibly have
given interactions in other characters.

As expected the effect of appetite on performance was
accentuated at heavy hog weight and the protein increment
response was minimal. No consistent response trends were
found and the only heavy hog cross x protein level interactions observed were for loin backfat thickness, hind quarter weight and FCE. The hind quarter interaction was previously dismissed as a chance effect, an explanation suggested and supported by the inconsistent fore/hind quarter subpopulation and total population carcass weight results. This explanation is further supported by the analysis of the dissected population joint proportions for which no cross x protein level interactions were found.

In the same way no biological explanation is demonstrable for the loin backfat thickness interaction as there were no interactions at the adjacent fat depth sites, C and K, at any other fat depth site or for back fat percentages or for total carcass fat percentage. The interaction was all the more remarkable in that the extreme differential responses were for the Wessex reciprocal crosses. These responses gave rank changes among the fatter crosses (WLW, LW and ELW) while the crosses of least fat, and smaller appetite, gave small inconsistent fat thickness changes and no changes in rank. In the absence of other interactions it seems very likely that the loin interaction, as well as that for hind quarter, was a chance effect.

Superficially the FCE interaction may also be discounted in this way. The postulated explanation of FCE genotype x nutrition interactions is based on the fact that energy cost of depositing a unit weight of fat is greater than that of lean (Houseman and McDonald, 1973), so that any increase in lean content, and therefore reduction in fat content, is expected to reduce the energy cost of liveweight gain and hence improve food conversion efficiency. Yet, despite the
occurrence of the FCE interaction, there were no significant protein level effects for either growth economy or carcass composition characters and no cross x protein level interactions for tissue characters.

Of the observed food conversion responses to protein increment, those of the Landrace, Large White and Pietrain crosses follow the pattern suggested by their carcass tissue changes, Landrace having more lean, less fat and an improved FCE, Large White giving no tissue or food conversion changes and Pietrain having more fat, less lean and a poorer food conversion. On the other hand, the tissue changes do not account for the FCE responses in, e.g. WLW, which had marginally less lean, a similar fat content and a depressed FCE when fed the high protein diet. The depressed FCE may be explained to some extent by a slower liveweight gain and hence a higher total maintenance requirement. By contrast LW gave no change in FCE with dietary protein increment but a faster daily liveweight gain, more fat and less lean. The faster DG may have reduced the total energy cost of maintenance and compensated for the more costly fat tissue deposition.

ELW responses cannot be explained by relating tissue and maintenance costs as the high protein diet gave no change in FCE, less lean, more fat but a slower daily gain.

Some of these apparent anomalies could possibly be explained by differences in the growth curves of the high and low protein populations. Such variable curves, illustrated by Davey and Morgan (1969), would give different maintenance costs (Chamberlain and Cooke, 1970) and hence possible differences in FCE. Routine internal weighings and/or serial slaughter
information would be necessary to indicate any growth curve variation and a complete explanation of the observed FCE interaction would, in addition, need to consider the possibility of different costs of unit protein deposition at the contrasting protein levels and for the different genotypes, as well as the interactive factors of relative tissue energy and maintenance costs. This information was not provided by the present study and it cannot be concluded that any single rationale, biological or statistical, explains the FCE interaction. More probably the interaction resulted from several complementary factors, insufficient in themselves to generate cross x protein level interactions for individual characters, but collectively producing an interaction for the complex character liveweight food conversion efficiency. However all FCE and component responses were small and considering the study involves over 50 characters the possibility of chance significance cannot be ignored.

A cross x protein level interaction was also found at pork weight for the meat quality measurement, pH. Rank changes resulted from LW, LLW and LWW pHs being little affected by dietary protein level, WLW and ELW giving higher pHs on the low protein diet and PLW having a higher pH on the high protein diet. There were no apparent correlated trends for the other meat quality characters, no substantiating interactions for Escol and while EHcond results were not tested statistically the results did not suggest any important cross x protein level interaction. The pH interaction was not repeated at heavy hog weight and in the absence of cross
and protein level effects for pH and in view of the small variation found in the interaction data, the interaction is of doubtful repeatability and has no practical importance.

In summary it can therefore be said that any biological interpretation of the pork pH and the heavy hog loin and hind quarter interactions is problematic and those for the pork FFBQ and heavy hog FCE interactions tenuous. The absence of other interactions may, however, be a result of the dietary protein increment imposed and more differential variation might have resulted with a wider protein contrast. Certainly the small differential response trends noted for FFBQ were consistent with expected performances and would support this supposition.

As regards a statistical explanation, the proportion of significant interactions at each slaughter weight is that probable by chance alone only if independence of all characters is assumed. That is obviously not so. As discussed for the individual FFBQ and FCE interactions some substantiating evidence was shown by correlated characters and although this was no more than tenuous, its scale was perhaps, as previously noted, a result of the small effect produced by the dietary protein increment. However, even if real, the FFBQ interaction is of doubtful economic importance. FFBQ is not a measurable character of economic importance and the component character responses would only be detected by expensive techniques such as dissection and not by the carcass evaluation techniques used in commercial grading.

With other characters having no important cross x protein level interaction the ranking of aggregate genotypes
will only be dependent on protein level if the heavy hog FCE interaction significantly alters the aggregate value of the genotypes. This is improbable as the effect of small differential FCE responses are likely to be negligible when compared to the wide genotypic differences for the characters independent of protein level. Therefore, despite the statistical significance of isolated interactions, the relative performances of the crosses with the Large White breed of the British Wessex, Essex and Landrace breeds and the imported Pietrain breed were unaffected by dietary protein level and an assessment of their relative merits for pork and heavy hog production can be made without reference to the protein level fed.

Other interactions examined within the comparison of crossbred performances were the interactions of sex with protein level and genotype which were studied as further aspects of possible practical importance. For example, it has been said that for optimum performance castrates have a lower dietary protein requirement than gilts (Blair et al., 1969). Results for the protein increment studied here do not support that conclusion, for at pork weight most sex x protein level mean squares were smaller than their residual mean squares and only DG and mid back fat thickness interactions and the dissected population carcass weight interaction reached significance at the 5% level.

The mid back fat interaction gave no rank change but castrates had thicker fat with the low protein diet and gilts more fat with the high protein. Other back fat thicknesses had proportional sex responses as did the relevant fat percentages.
It is therefore unlikely that the mid back fat interaction has any overall importance.

The DG interaction was a scale effect with castrates growing faster than gilts on both diets but with a reduced advantage on the high protein ration. Young et al. (1968), with a wider protein range, observed a similar tendency and Bell (1965) found that castrates outgained gilts on a low protein (13%) diet but showed less advantage under high protein (16%) feeding. No DG sex x protein level interaction was observed in the studies of Blair et al. (1969) and Bowland and Berg (1939) and there were no component character interactions in the present study, sex responses to protein increment being generally proportional for CDG, LTGR and FTDSU. A further sex x protein level interaction at pork weight was that for carcass weight in analysis II, the dissected population. The means showed a reduced castrate and an increased gilt 'offal' gain with high protein feeding. The interaction was not found in the total population and no supporting evidence is reported in the literature, in fact Young et al. (1968) found the reverse response, castrates having heavier carcass weights on the lower protein diets and gilts increased carcass weights with higher protein.

No heavy hog growth economy or split carcass interactions were observed but there were consistent sex x protein level interactions for lean, fat and bone characters. The interactions reiterated the trend shown at pork weight, the absence of rank change but a consistently larger castrate/gilt difference on the low protein diet. There are few equivalent studies in the literature and although Blair et al. (1969) report a sex x protein level interaction for the middle joint,
they found no tissue character interactions.

In conclusion it can be said that to pork weight the effects of sex and protein level for most performance characters were independent. However a trend was noted for larger castrate/gilt differences on the low protein diet which was reiterated at heavy hog weight for the carcass tissue characters. Whether the effects were large enough to justify recommendation of separate protein levels for castrates and gilts is debatable and the likelihood of any such recommendation being applied in commerce is, in any case, improbable. Obviously further evidence is necessary preferably examining a wider range of dietary protein concentration and including entire males as an additional sex.

It is generally considered that genotype x sex interactions are unimportant sources of error in breed or breed cross comparisons. It was therefore contrary to expectations that genotype x sex interactions were consistent statistically significant sources of variation at both slaughter weights. Although interaction generally contributed only a small proportion of the total variation, there were consistent rank changes suggesting a common biological interpretation.

To pork weight castrates of all genotypes except LWM grew faster but gave fatter carcasses than gilts as a result of having only a small advantage for LTGR but a much higher FTDR. Accessory tissue growth was also faster for castrates. The fatter carcasses of the castrates were probably associated with a larger appetite and/or a lower maintenance requirement. Individual DFIs were not recorded but castrates generally have larger appetites (Houseman, 1973). The LWM performance gave
rank changes as a result of its castrates gaining lean tissue less quickly than its gilts and yet having equivalent growth rates of the other essential tissues, the reverse of the performance observed for other genotypes. Similar, although less consistent, sexual differentiation occurred for heavy hogs. Contrasting performances were therefore shown by the castrates and gilts of the Wessex reciprocal crosses, with \( W^\delta \times LW^\varphi \) progeny performance following the general rule and \( LW^\delta \times W^\varphi \) progeny performance deviating sufficiently to generate consistent rank change interactions. Judged on castrate performance, the LW\( \times \)cross generally ranked last of the six genotypes whereas it ranked third or fourth on gilt performance.

Finding a single biological explanation for the genotype \( x \) sex interactions is difficult. If the occasional correlated results for \( LW^\delta \times W^\varphi \) and \( LW^\delta \times LW^\varphi \), as e.g. in heavy hog LTGR, occurred more frequently, a sex linked effect associated with the LW sires might be plausible. However the few incidences of an apparent LW sire breed effect contrasts with the more numerous and consistent interactions arising from the 'normal' sex differences of the progeny of LW dams mated to sires of the LW, W, E, P and L breeds and the 'abnormal' sex differences of the \( LW^\delta \times W^\varphi \) progeny, i.e. the progeny of Wessex dams. It is therefore more probable that the genotype \( x \) sex interactions were a result of a dam breed effect, although whether the effect was associated with the dam genotype or the maternal environment is unknown. It was previously noted that the interactions were less consistent at the heavier slaughter weight in agreement with the finding of Baker, Hazel and Reinmiller (1945) that maternal effects decrease with slaughter
weight and age. However whether any physiological explanation for a differential maternal effect on castrate and gilt lean and non-lean essential tissue can be found is doubtful.

No evidence to support the interactions found between sex and the Wessex reciprocal crosses could be found principally because the Wessex breed is not common outside Britain. However two recent studies in the U.S.A. have either studied or had the opportunity to study genotype x sex interactions for post weaning performance in the progeny of reciprocal crosses in which maternal influences were found to be important. Unfortunately both studies (Bereskin, Shelby and Hazel, 1971; Johnson, Omtvedt and Walters, 1975) assumed the interaction of sex with sire and dam breeds to be negligible for carcass traits. Johnson et al. (1975) did however fit sex in their analysis of growth economy characters for reciprocal crosses of the Duroc, Hampshire and Yorkshire breeds. The authors report differences in the maternal influences of the three breeds and sire and dam breed x sex interactions for daily gain, but fail to present subclass means for the interactions or to clarify these findings. Despite the significance of the interactions, sex was not an effect examined in the analysis of the carcass traits and the assumption that the interaction of sex and genotype was unimportant was not questioned, even though it could be tested easily and economically. The inclusion of sex as an additional effect in breed and breed cross comparisons and in studies of genotype x environment interactions is therefore advocated and more evidence may verify and explain the consistent genotype x sex interactions found within the present body of data.

Notwithstanding the uncertainty of their biological origin, the practical consequences of the genotype x sex interactions in
the present experiment are that they gave consistent rank changes which would have underrated the performance of the LW × Wp progeny if the breed cross comparison had been restricted to a castrate population. The possibility that such genotype × sex interactions may be important is recognised in national test programmes by comparing entire male, castrate and gilt progeny (e.g. M.L.C. 1970). The necessity and validity of insuring against possible genotype × sex interaction has been shown here, although in this case it is unlikely that the interaction effects will have altered the choice of the more competitive genotypes. The Wessex crosses, whether the progeny of a Wessex sire or dam, did not have performances comparable to the progeny of the Landrace, Pietrain or Essex breeds and were less likely to contribute usefully to British pig production. Therefore, as with genotype × protein level interaction, the statistically significant genotype × sex interactions observed were unlikely to be important in the overall assessment of the crossbred comparisons.

Discussion so far has been confined to a rationalisation of the observed interactions. By considering the relative crossbred performances and the effects of the dietary protein concentrations, it may be possible to relate the results to other genotypes and protein concentrations and to gain some indication of general principles.

Genotypes

Appetite and lean gain variation between breeds were suggested as the major components contributing genotype × nutrition interaction (section 2.2). From the observed crossbred performances for appetite and LTGR, a qualitative comparison
has been given at the end of the results section of heavy hog analysis III where appetites were classified as small, average or large and LTGRs as slow, average or fast. The classification is presented below.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Appetite</th>
<th>LTGR</th>
</tr>
</thead>
<tbody>
<tr>
<td>'Control' Large White (LW)</td>
<td>Average</td>
<td>Average</td>
</tr>
<tr>
<td>Wessex x LW</td>
<td>Large</td>
<td>Slow</td>
</tr>
<tr>
<td>LW x Wessex</td>
<td>Large</td>
<td>Slow</td>
</tr>
<tr>
<td>Essex x LW</td>
<td>Large</td>
<td>Slow</td>
</tr>
<tr>
<td>Pietrain x LW</td>
<td>Small</td>
<td>Fast</td>
</tr>
<tr>
<td>Landrace x LW</td>
<td>Large</td>
<td>Fast</td>
</tr>
</tbody>
</table>

Because of possible differential heterosis with the Large White, the crossbred performances are not directly comparable with the purebred performances presented in table 2.1. If these possible heterotic effects are ignored and the crossbred performances are taken as the parental mean, then in general genotypes performed as previously characterized. An exception was the Landrace cross which had a faster LTGR than that suggested by the indirect measures in the literature. The Landrace result agrees with that reported by Lean et al. (1972) who found some advantage for the purebred Landrace compared to the purebred Pietrain.

In addition to the possible inaccuracy caused by heterosis, some bias in the Stockton LTGR estimates may have resulted from the assumption that all genotypes had a constant initial lean tissue weight. Extrapolation of genotype lean percentages at pork and heavy hog weight suggests that the genotypes of above average lean percentage, the Pietrain and Landrace crosses, had under-estimated initial lean weight and therefore over-estimated
LTGRs, and that the LTGRs of below average lean genotypes, the Wessex and Essex crosses, were under-estimated. It is likely therefore that the range of between cross LTGR differences at pork weight is over-estimated. For heavy hogs any bias will be smaller but again it is likely that LTGR variation was over-estimated.

In consequence, the classification of the LTGRs of the crossbreds as slow, average or fast, has probably over-emphasised the LTGR variation existing between the crosses and their parent breeds. Nevertheless, the combinations of large appetite and 'slow' LTGR of the Essex and Wessex crosses, and small appetite and 'fast' LTGR of the Pietrain cross, do suggest that there exists some variation between the crosses and their component breeds for the efficiency of protein conversion to lean tissue, even if absolute rates of lean deposition are not very different.

As stated in the review, genotype x protein level experiments which use differences of protein concentration and ad libitum feeding confound responses to protein concentration with protein intake. However, as there were no genotype x protein level interactions for daily feed intake, the increment in dietary protein concentration will also have resulted in changes in the absolute level of protein intake for each genotype. These intake changes occurred with ad libitum feeding and it is therefore unlikely that energy will have limited genotypic responses to dietary protein increment. Consequently the combination of variation between crosses for the efficiency of protein conversion to lean tissue and the change in absolute
protein intake should have provided adequate contrast for the observation of any important genotype x protein level interaction.

**Protein level**

The foregoing conclusion assumes that responses to the protein increment were sufficient to show real differences between the dietary protein concentrations and between any differential responses of the genotypes. However responses to the dietary protein increment were small. The increment gave slightly improved pork growth economy and carcass composition but no similar effects or discernible trends were observed at heavy hog weight. The pork carcasses had 0.8% more lean, 0.8% less subcutaneous fat, 0.2% less intermuscular fat and 0.1% more bone when fed the high protein diet (table 4.2.19), and although protein increment had no significant effect on liveweight gain, carcass gain was improved by 0.02 lbs/day, LTGR by 0.02 lbs/day, liveweight food conversion efficiency by 0.04 lbs/day and LTFC by 0.25 lbs/lb. High protein fed pork pigs also had 0.25 lb heavier carcasses and FTDR (as observed on the dissected population) was significantly reduced by about 0.02 lbs/day. These responses, although small, are in agreement with the review findings of the ARC (1967) and Chamberlain (1972).

The absence of protein level effects at heavy hog weight is supported by the study of Blair et al. (1969). As in this experiment, the Aberdeen group found no growth economy or carcass composition effects for protein levels in excess of 14%. The advantage gained with the high protein diet to pork weight was therefore not sustained to the heavier slaughter-
weight. The plateauing of the essential tissue growth curve, schematically presented in figure 2.2, may explain the lack of protein level response and possibly also the loss of earlier advantage. As each diet gave similar daily liveweight gains and carcass lean percentages at heavy hog weight, the initial LTGR responses to the high protein diet will be counterbalanced by a long period of plateaued growth whereas the low protein population has slower initial LTGR but a shorter growth plateau. Figure 2.2 indicates that lean growth is still occurring at pork weight and hence the lean tissue responses to protein increment are both real and apparent.

The results highlight one of the difficulties in studying genotype x protein level interactions. Factorial experiments can either, as in this experiment, study a small difference to see if interactions occur within the range of commercial dietary composition or study larger differences as a guide to general principles. The latter runs the risk of not being applicable to the particular and the former meets the difficulty of all experiments examining responses near the maximum. As the maximum response always appears to be approached asymptotically, the nearer the crude protein concentrations are to the maximum the more difficult it is to distinguish between the responses to different concentrations (A.R.C. 1967). Consequently many experiments may not detect real differences simply because they are not sufficiently sensitive or large enough to do so.

An additional factor reducing experimental accuracy could have been faulty compounding of the contrasting diets. This possibility was eliminated by routine proximate analysis of each
diet batch and the character responses were therefore those produced by the intended protein increment, a difference similar to the range used in commerce.

It has already been concluded that there was considerable variation between the crossbred performances. The dangers of real differential responses not being detected because of low experimental sensitivity was therefore less likely. The accuracy with which the responses were measured was also high, as more than half the experimental population was dissected. The tissue responses gave no indication of trends suggesting possible genotype x protein level interactions of practical importance and notwithstanding the limitations imposed by the small responses to the protein increment, it is possible to conclude that within the narrow range of commercially competitive genotypes and protein concentrations important interactions are improbable.

Further discussion of genotype x protein level interactions will be given in chapter 5.

4.4 Summary

To finalise the account of the genotype x protein level interaction experiment, the results will be summarised and presented as points (a) to (f).

(a) Genotype x protein level interaction was not an important source of variation. Therefore the relative performances of the progeny of the British Wessex, Essex and Landrace breeds and the imported Pietrain breed were unaffected by dietary protein level and an assessment of their relative merits for pork and heavy hog production can be made without reference to the protein
level fed. Similarly protein level effects can be assessed without reference to a particular genotype.

(b) Protein level

(i) The effects of dietary protein level on pork pigs were small but consistently advantageous (table 4.2.4, 4.2.19 and 4.2.31).

(ii) There were no protein level effects on heavy hog performance (table 4.2.11, 4.2.23 and 4.2.33). It is therefore suggested that the high and possibly the low protein regime exceeded the heavy hog requirement for protein and that the low protein level is adequate, and possibly generous, for heavy hog production.

(c) Genotypes

(i) The performances to pork weight for the different genotypes are shown in table 4.4.1.

The crossbred progeny of the Pietrain and Landrace breeds were consistently superior to those of the Wessex and Essex breeds. Pietrain crosses compared to Landrace crosses were superior for tissue growth economy and carcass composition but inferior for liveweight economy and Pietrain crosses had the highest killing out percentage and gave the greatest weight of lean and least weight of fat in each joint. Landrace cross carcasses were the longest and Pietrain crosses the shortest. Pietrain crosses had a considerable advantage for EMA but an inferior meat quality with 1 in 6 eye muscles having an abnormal condition. Landrace crosses also had an inferior meat quality. Nonetheless the superior performance of the Landrace cross compared to the Essex and Wessex crosses supports
Table 4.4.1. Summarised performances of the genotypes to pork weight.

<table>
<thead>
<tr>
<th>Character</th>
<th>LW</th>
<th>W x LW</th>
<th>P x LW</th>
<th>L x LW</th>
<th>E x LW</th>
<th>LW x W</th>
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<td>Tissue</td>
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<td>growth</td>
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<td>economy</td>
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<td>Carcass</td>
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<td>composition</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heat Quality</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

* percentage abnormal incidence.
the dominant role of the breed as the choice for crossing with the Large White. The competitive performance of the Pietrain cross supports the results of Smith and Howard (1971) and suggests that the breed may be a competitive sire of pigs for pork production, although any stress susceptibility associated with its poor meat quality will militate against its commercial acceptance.

(ii) The performances to heavy hog weight for the different genotypes are shown in table 4.4.2.

With the exception of the liveweight growth economy characters of the Pietrain crosses and the meat quality of both breed crosses, Landrace and Pietrain progeny outperformed the progeny of the Wessex and Essex breeds. Wessex and Essex crosses gained liveweight faster than either Pietrain or Landrace crosses but had an inferior FCE to Landrace crosses and produced fatter carcasses than either of the other breed crosses. The Pietrain cross had the slowest DG, the worst FCE but the best LTFC, an above average LTGR and the slowest FTDR. The Landrace cross had the fastest LTGR, while the Pietrain cross combined advantages for killing out percentage and carcass lean and fat percentages to produce the highest weight of lean and the least weight of fat. The Landrace cross ranked second for tissue weight production. Carcass joint proportions followed those observed at pork weight and joint tissue weights reflected overall rankings. Pietrain and Landrace crosses had twice as many abnormal eye muscle conditions as Wessex and Essex crosses. Economic penalties for poor liveweight growth economy and meat quality probably
### Table 4.2.2. Summarised performances of the genotypes to heavy hog weight.

<table>
<thead>
<tr>
<th>Character</th>
<th>LW</th>
<th>W x LW</th>
<th>P x LW</th>
<th>L x LW</th>
<th>E x LW</th>
<th>LW x W</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liveweight</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>economy</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Tissue</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>economy</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Carcass</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>composition</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Tissue</td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>economy</td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Carcass</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>dimensions</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Carcass</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Neat Quality</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*percentage abnormal incidence.*
eliminates the Pietrain as a competitive sire of heavy hog
slaughter progeny whereas the Landrace had outstanding performance
for all characters except meat quality. Therefore, as at pork
weight, the superior performance of the Landrace supports the
dominant role of the breed as the choice for crossing with the
Large White.

(d) In terms of LTGR and LTFC pork was a more efficient
slaughter weight than heavy hog. The heavier slaughter weight
also had a far higher incidence of poor meat quality.

(e) Generally the effects of sex and protein level were
independent and there were few indications that castrates
had a lower dietary protein requirement than gilts.

(f) The relative performances of LW $^\delta \times W^\phi$ castrates and
gilts generated consistent genotype x sex interactions.

Interactions between genotype and feeding level and
genotype and protein level have been studied in the experiments
reported in Chapters 3 and 4. The conclusions drawn from
these genotype < nutrition interaction experiments are
summarised in Chapter 5 and their implications discussed in
the light of the possible future requirements of British pig
production.
CHAPTER 5

CONCLUDING DISCUSSION

Despite the statistical significance of isolated genotype x feeding level and genotype x protein level interactions, it has been concluded that the ranking of the genotypes studied was unaffected by the nutritional treatments. It is therefore unlikely that any inaccurate rankings of breeds or breed crosses will have been made because of genotype x nutrition interaction. Moreover it has been suggested that the relative change in performance for one genotype caused by moderate feed restriction or dietary protein increment would be the same as the change in performance for other genotypes likely to be used for the production of lean meat. It is therefore unlikely that levels of performance beyond those expected from independent assessments of genotypes and nutrition will be given by specific genotype/nutrition combinations.

From crossbred population comparisons one can therefore safely choose the genotypes most suited for efficient production systems, although the comparisons here have shown that, especially for the growth efficiency character, the crossbred performance cannot be assumed to fall on the average of the purebred parent performances. Therefore, if the first choice of genotype is based on purebred comparisons and the intention is to use a crossbred slaughter generation, it is advisable to first rank the alternative crossbreds.

Further genetic improvement can be made by intra-population selection and although it has been concluded that genotype x nutrition interactions were unimportant in the cross-
bred comparisons, it is possible that in alternative selection environments small differential responses may accumulate during intra-bred selection. Results in the present study, which are supported by the results of Lodge et al. (1972), suggest that feeding level and not dietary protein concentration is the major determinant of growth efficiency and carcass composition and therefore differences in feeding regime are more likely to give important differential responses. For example, selection on an ad libitum feeding regime compared to a restricted feeding regime, may produce pigs adapted to ad libitum feeding which on restricted feeding perform less well than pigs selected on that regime. While the present experiments did not investigate this problem directly, they provided some information relevant to the choice of an intra-breed selection environment, as described subsequently.

Of the characters appetite, lean tissue growth rate and daily maintenance requirement suggested as instrumental in the occurrence of genotype x nutrition interaction, the experiments demonstrated that there were appetite and lean tissue growth rate differences between breeds and crosses. Despite these differences, neither protein level increment for lean tissue growth rate and appetite, nor feeding level restriction for appetite and those characters providing indirect measurements of lean tissue growth rate, gave interactions between genotype and nutritional treatment. When energy requirement is not satisfied, dietary protein concentration will give variation in lean tissue growth rate through genotypic differences in the efficiency of protein conversion to lean tissue. The evidence presented here suggested that those differences are insufficient to give inter-
action between genotypes at economic levels of protein concentration. Interactions are more likely to be important when disproportionate energy intakes give differential deposition of lean and fat to a fixed slaughter weight.

There are also known to be within breed differences in appetite and, by inference, in lean tissue growth rate. Consequently if, for example, selection is made in ad libitum and restricted feeding environments, then accumulated differential lean tissue gains and appetite responses may give dissimilar genotypes ill-adapted to the alternative regime. Estimates of the genetic correlation between daily feed intake and lean tissue growth rate are required to predict the changes brought about by selection in alternative test environments, so that predicted changes can be related to feeding regimes of possible future use in commercial pig production. Unfortunately the numbers required for the accurate estimation of such parameters are very high (MLC, 1970).

That test feeding regimes must be more accurately assessed for their effects on appetite is illustrated by the results of selection on to-appetite feeding in the MLC test programme. Index selection within the Large White breed has given an improvement in the efficiency of food conversion accompanied by little change in liveweight gain and consequently a trend towards a self-restricting type of pig (King, 1975). Such selection against appetite is pointless when the restriction of feed intake can be attained technically, and selection pressure could be more profitably directed towards improvement in other economic characters. If a selection
environment for example suppresses appetite variation by applying a time scale feeding regime, then although short term economic objectives may be achieved, ultimately appetite will limit the expression of lean tissue growth rate. The overall conclusion of the genotype x nutrition interaction study that interactions were unimportant therefore does not preclude the possibility of nutritional environments producing interaction through differential selection responses for appetite and lean tissue growth rate on different feeding levels. The monitoring of genetic correlation parameters is required despite the estimation problems involved.

The experiments provided no measure of maintenance requirement variation which is both experimentally and conceptually difficult to quantify. However some breed differences for maintenance requirement have been shown by Okwuosa (1971) and Sharma et al. (1971). If selection for lean tissue growth rate leads to a higher energy requirement for maintenance as Keapter (1974*) has suggested and as breed differences may indicate (Okwuosa, 1971; Sharma et al., 1971), it would lead to the production of genotypes liable to show interactions in the following way. On a restricted level of feeding where maintenance would represent a high proportion of the energy balance, a fatter-type genotype with its associated lower maintenance requirement, could be a more efficient convertor of food to liveweight gain, while on a higher level of feeding, lean tissue gain would be the more important proportion of total energy balance and therefore the leaner-type genotype would be more efficient due to its lower energy requirement per unit of liveweight gain.
Therefore, despite the absence of genotype x nutrition interaction in the crossbred comparisons described in this thesis, it is not possible to dismiss the likelihood of differential selection responses for appetite, lean tissue gain and daily maintenance requirement leading to important interactions. Further estimation of the parameters, both between and within breeds, are required for these characters. From these a clearer choice may emerge of a feeding regime for selection purposes that is consistent with both the short and long term requirements of lean pig meat production.
REFERENCES


APPENDIX I

Estimation of Daily Food Intake Heritability from the parameters of its components, Food conversion efficiency and Daily Gain.

There are few published estimates of pig daily food intake (DFI) heritability. However, Turner and Young (1969) and Smith (1967) discuss the phenotypic and genetic relationships of a product trait to its components and derive an estimate of the product heritability. Pease (1973) has derived a comparable method. These methods can be applied to calculate estimates of DFI heritability from published estimates of its components, food conversion efficiency (FCE) and daily liveweight gain (DG).

DFI heritabilities were calculated using the equation:

\[ h_3^2 = \frac{h_1^2(1 + k^2 h_2^2 + 2 k_h r_{G_{12}})}{1 + k^2 + 2 k_p r_{P_{12}}} \]

(Turner and Young, 1969)

where:
- \( h_3^2 \) = heritability estimate of DFI
- \( h_1^2 \) = heritability of FCE
- \( h_2^2 \) = heritability of DG
- \( k_h^2 = h_2^2/h_1^2 \)
- \( k^2 = (\text{Coeff. of variation of } x_2)^2/(\text{Coeff. of variation of } x_1)^2 \)
- \( r_{G_{12}} \) = genetic correlation between FCE and DG
- \( r_{P_{12}} \) = phenotypic correlation between FCE and DG.

The literature provides parameters for the component traits FCE and DG which are defined as:
FCE = total food eaten on test/total liveweight gain on test.
DG = the average daily liveweight increment over the test period.
DFI is the average weight of food eaten daily over the test period.

Component Parameters and the derived Heritability for Daily Food Intake.

British data refers to a test period of 60 to 200 lbs., Scandinavian data from 44 to 200 lbs.
If data for both sexes were available, the castrate data was used.
Boxed data are the derived estimates.


<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>S.D.</th>
<th>h²</th>
<th>r_G</th>
<th>r_P</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCE (lbs/lbs)</td>
<td>3.41</td>
<td>0.24</td>
<td>0.50</td>
<td>-0.69</td>
<td>-0.66</td>
</tr>
<tr>
<td>DG (lbs/day)</td>
<td>1.52</td>
<td>0.14</td>
<td>0.41</td>
<td>-0.60</td>
<td>-0.57</td>
</tr>
</tbody>
</table>

DFI

0.39

The paper contains estimates of h² for DFI at 50 lbs. liveweight of 0.26
h² for DFI at 125 lbs. liveweight of 0.66
h² for DFI at 200 lbs. liveweight of 0.34

Data was from British Large White pigs individually fed "to appetite".


<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>S.D.</th>
<th>h²</th>
<th>r_G</th>
<th>r_P</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCE (dead)</td>
<td>4.34</td>
<td>0.36</td>
<td>0.46</td>
<td>-0.71</td>
<td>-0.67</td>
</tr>
<tr>
<td>DG (lbs/day)</td>
<td>1.45</td>
<td>0.11</td>
<td>0.41</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

DFI

0.37

FCE (dead) is the efficiency of food conversion to carcass weight (lbs/lbs).
The paper contains estimates of:

- \( h^2 \) for DFI at 50 lbs. liveweight of 0.19
- \( h^2 \) for DFI at 125 lbs. liveweight of 0.15
- \( h^2 \) for DFI at 200 lbs. liveweight of 0.41

Data was from British Landrace pigs individually fed "to appetite".


<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>S.D.</th>
<th>( h^2 )</th>
<th>( r_G )</th>
<th>( r_P )</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCE (lbs/lbs)</td>
<td>3.08</td>
<td>0.145</td>
<td>0.48</td>
<td>-0.92</td>
<td>-0.94</td>
</tr>
<tr>
<td>DG (g/day)</td>
<td>668.1</td>
<td>30.9</td>
<td>0.45</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Data from Danish Landrace individually fed "to appetite".


<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>S.D.</th>
<th>( h^2 )</th>
<th>( r_G )</th>
<th>( r_P )</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCE (kgs/kg)</td>
<td>3.03</td>
<td>0.21</td>
<td>0.50</td>
<td>-0.98</td>
<td>-0.85</td>
</tr>
<tr>
<td>DG (g/day)</td>
<td>770</td>
<td>72.7</td>
<td>0.61</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Data from German pigs fed twice a day "to appetite" from 40 to 110 kgs.


Strang calculated heritability estimates for FCE, DG and DFI for British Large White and Landrace fed "to appetite".

<table>
<thead>
<tr>
<th>Character</th>
<th>Heritability estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Large White</td>
</tr>
<tr>
<td>FCE (lbs/lbs)</td>
<td>0.44</td>
</tr>
<tr>
<td>DG (lbs/day)</td>
<td>0.39</td>
</tr>
<tr>
<td>DFI (lbs/day)</td>
<td>0.38</td>
</tr>
</tbody>
</table>
Data from Polish Large White pigs fed to a time scale, irrespective of liveweight gain. Theoretically this feeding regime allows no expression of difference in DPI. The high $h^2$'s obtained are presumably the result of the test terminating at a common liveweight rather than after a standard time interval, thus allowing differences in DPI.

No suitable source of data was located for pigs individually fed 'ad libitum'.

<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>S.D.</th>
<th>$h^2$</th>
<th>$r_G$</th>
<th>$r_P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Castrates</td>
<td>FCE (lbs/lbs)</td>
<td>5.691</td>
<td>0.348</td>
<td>0.446</td>
<td>-0.96</td>
</tr>
<tr>
<td>DG (g/day)</td>
<td>615</td>
<td>52</td>
<td>0.402</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gilts</td>
<td>FCE (lbs/lbs)</td>
<td>5.547</td>
<td>0.332</td>
<td>0.662</td>
<td>-0.93</td>
</tr>
<tr>
<td>DG (g/day)</td>
<td>629</td>
<td>57</td>
<td>0.651</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Data from Polish Large White pigs fed to a time scale, irrespective of liveweight gain. Theoretically this feeding regime allows no expression of difference in DPI. The high $h^2$'s obtained are presumably the result of the test terminating at a common liveweight rather than after a standard time interval, thus allowing differences in DPI.

No suitable source of data was located for pigs individually fed 'ad libitum'.

APPENDIX II

Results of Experiment 3, Analysis of Variance (over page)
<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>DG</th>
<th>FCE</th>
<th>DFI</th>
<th>Croc. wt.</th>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>1</td>
<td>0.005</td>
<td>0.000</td>
<td>0.015</td>
<td>12.006</td>
<td>4071.2***</td>
</tr>
<tr>
<td>Litters</td>
<td>16</td>
<td>0.033</td>
<td>0.136</td>
<td>0.203</td>
<td>7.874</td>
<td>199.1</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>0.001</td>
<td>0.307</td>
<td>0.781</td>
<td>0.266</td>
<td>376.6*</td>
</tr>
<tr>
<td>C x F</td>
<td>2</td>
<td>0.026</td>
<td>0.016</td>
<td>0.079</td>
<td>3.285</td>
<td>236.3</td>
</tr>
<tr>
<td>E_s</td>
<td>14</td>
<td>0.007</td>
<td>0.099</td>
<td>0.283</td>
<td>7.701</td>
<td>73.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Max</th>
<th>Mid</th>
<th>Loin</th>
<th>C</th>
<th>K</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>1</td>
<td>55.036</td>
<td>52.829</td>
<td>128.894</td>
<td>193.821*</td>
<td>279.545*</td>
</tr>
<tr>
<td>Litters</td>
<td>16</td>
<td>32.448</td>
<td>21.485</td>
<td>31.304</td>
<td>31.206</td>
<td>42.837</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>19.981</td>
<td>45.956**</td>
<td>31.659</td>
<td>35.412</td>
<td>80.739*</td>
</tr>
<tr>
<td>C x F</td>
<td>2</td>
<td>32.538</td>
<td>1448</td>
<td>0.077</td>
<td>15.875</td>
<td>24.266</td>
</tr>
<tr>
<td>E_s</td>
<td>14</td>
<td>10.682</td>
<td>3.569</td>
<td>11.512</td>
<td>10.326</td>
<td>10.750</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>EMA</th>
<th>Streak</th>
<th>Fat score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross (C)</td>
<td>1</td>
<td>165.613***</td>
<td>28.617*</td>
<td>0.215</td>
</tr>
<tr>
<td>Litters</td>
<td>16</td>
<td>10.820</td>
<td>5.994</td>
<td>0.071</td>
</tr>
<tr>
<td>Feeding level (F)</td>
<td>1</td>
<td>8.016</td>
<td>3.363</td>
<td>0.096</td>
</tr>
<tr>
<td>C x F</td>
<td>2</td>
<td>4.580</td>
<td>0.020</td>
<td>0.036</td>
</tr>
<tr>
<td>E_s</td>
<td>14</td>
<td>9.028</td>
<td>6.696</td>
<td>0.092</td>
</tr>
</tbody>
</table>
Table 11.2. **Experiment 3.** Least squares means and standard errors for HP and LW sired progeny and for ad libitum and restricted feeding levels.

<table>
<thead>
<tr>
<th>Character</th>
<th>Hampshire/Pietrain Mean</th>
<th>S.E.</th>
<th>Large White Mean</th>
<th>S.E.</th>
<th>Restricted Mean</th>
<th>S.E.</th>
<th>Ad libitum Mean</th>
<th>S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DG 1 lbs/day</td>
<td>1.40</td>
<td>0.02</td>
<td>1.37</td>
<td>0.03</td>
<td>1.38</td>
<td>0.02</td>
<td>1.39</td>
<td>0.02</td>
</tr>
<tr>
<td>FCE 1 lb/lb</td>
<td>3.25</td>
<td>0.07</td>
<td>3.25</td>
<td>0.10</td>
<td>3.15</td>
<td>0.09</td>
<td>3.56</td>
<td>0.08</td>
</tr>
<tr>
<td>DFI 1 lbs/day</td>
<td>4.52</td>
<td>0.11</td>
<td>4.47</td>
<td>0.17</td>
<td>4.33</td>
<td>0.13</td>
<td>4.66</td>
<td>0.14</td>
</tr>
<tr>
<td>Cre. wt. 1 lb</td>
<td>144.0</td>
<td>0.59</td>
<td>142.6</td>
<td>0.88</td>
<td>145.4</td>
<td>0.78</td>
<td>145.2</td>
<td>0.71</td>
</tr>
<tr>
<td>Length mm</td>
<td>769.7</td>
<td>1.82</td>
<td>794.1</td>
<td>2.71</td>
<td>785.6</td>
<td>2.41</td>
<td>778.2</td>
<td>2.20</td>
</tr>
<tr>
<td>Max mm</td>
<td>43.8</td>
<td>0.70</td>
<td>46.6</td>
<td>1.03</td>
<td>44.4</td>
<td>0.92</td>
<td>46.1</td>
<td>0.84</td>
</tr>
<tr>
<td>Mid mm</td>
<td>23.4</td>
<td>0.40</td>
<td>26.1</td>
<td>0.60</td>
<td>23.5</td>
<td>0.53</td>
<td>26.1</td>
<td>0.49</td>
</tr>
<tr>
<td>Loin mm</td>
<td>19.2</td>
<td>0.72</td>
<td>23.6</td>
<td>1.07</td>
<td>20.3</td>
<td>0.95</td>
<td>22.3</td>
<td>0.87</td>
</tr>
<tr>
<td>C mm</td>
<td>19.7</td>
<td>0.69</td>
<td>25.0</td>
<td>1.02</td>
<td>21.2</td>
<td>0.90</td>
<td>23.5</td>
<td>0.83</td>
</tr>
<tr>
<td>K mm</td>
<td>24.4</td>
<td>0.70</td>
<td>30.8</td>
<td>1.04</td>
<td>25.9</td>
<td>0.92</td>
<td>29.3</td>
<td>0.84</td>
</tr>
<tr>
<td>EMA sq.cm</td>
<td>32.83</td>
<td>0.64</td>
<td>27.92</td>
<td>0.95</td>
<td>29.84</td>
<td>0.85</td>
<td>30.92</td>
<td>0.77</td>
</tr>
<tr>
<td>Streak mm</td>
<td>18.4</td>
<td>0.55</td>
<td>20.4</td>
<td>0.82</td>
<td>19.7</td>
<td>0.73</td>
<td>19.0</td>
<td>0.67</td>
</tr>
<tr>
<td>Fat score pts</td>
<td>2.4</td>
<td>0.06</td>
<td>2.6</td>
<td>0.10</td>
<td>2.5</td>
<td>0.09</td>
<td>2.6</td>
<td>0.08</td>
</tr>
</tbody>
</table>
APPENDIX III

Herd of origin of breed populations for the genotype x protein level experiment — Chapter 4.

**Landrace herds**

Wyndmore — E.W. Pepper Ltd., Wyndmore, Steeple Morden, Cambs.
Wych Cross — Wych Cross Estates, Birchgrove, Haywards Heath, Sussex.

**New Northdowns** — K.T. Kingston, South Ash Manor, Wrotham, Kent.

Ashtead — J.A.F. Wilson, Ringstead Farm, Ashwell, Herts.

**Essex herds**

Crossing — A. Cousins and Son, The Lodge, Crossing, Braintree, Essex.
Brightwell — J.W.F. Causton, Brightwell House, Brightwell, Ipswich, Suffolk.
Laver — F.J. Bosworth, Spains Hall, Willingale, Ongar, Essex.

**Wessex herds**

Merrywood — W.G. Williams and Sons, Home Farm, Coleshill, Swindon, Wilts.
Wrantage — W.J. Dobie and Son, Lyddons Farm, Curry Mallet, Taunton, Somerset.

Welwyn — G. Baron, Lockley Farm, Welwyn, Herts.

Hawsons — Warboys Farm Ltd., Poplar Farm, Bassingbourn, Royston, Herts.

APPENDIX IV

Prediction of Subplot Lean and Fat Percentages

All experimental animals gave observations for the traditional split carcass (analysis I) characters and, in addition, a random castrate/gilt pair from each subplot was dissected to provide the tissue (analysis II) character observations. Food consumption was measured on a pen basis, providing subplot observations for FCE and DFI. Any calculation of subplot tissue %s from the random castrate/gilt pair observations will be liable to sampling error, as will derived tissue food conversion ratios. Therefore a method was required which combined the concomitant and direct measurements of lean and fat tissue %s to give an unbiased estimate of mean subplot tissue characters.

The method of Conniffe and Moran (1972), a generalisation of double sampling techniques, is directly applicable. The method assumes that the prediction equation regressions are parallel, an assumption which was tested in the data. Multiple regression equations for lean and fat %s were derived in the dissected population using as concomitant variables: Max, Mid, Loin, C and K back fat thicknesses and EMA*, and initially overall regression equations for the main effects, cross, protein level and sex were compared. The analyses, presented in Table IV.1, were completed with a least squares programme (Harvey, 1968).
<table>
<thead>
<tr>
<th>Source</th>
<th>Deviation from hypothesis</th>
<th>Pooled regressions residual</th>
<th>Overall regression residual</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SS</td>
<td>MS</td>
<td>F</td>
</tr>
<tr>
<td>Pork;Cross</td>
<td>156.1</td>
<td>4.460</td>
<td>1.094</td>
</tr>
<tr>
<td>H;HogtCross</td>
<td>81.6</td>
<td>2.330</td>
<td>1.094</td>
</tr>
<tr>
<td>Pork;Protein</td>
<td>301</td>
<td>8.905</td>
<td>1.094</td>
</tr>
<tr>
<td>H;HogtProtein</td>
<td>7.4</td>
<td>1.050</td>
<td>1.094</td>
</tr>
<tr>
<td>Pork;Slice</td>
<td>31.0</td>
<td>4.150</td>
<td>1.094</td>
</tr>
<tr>
<td>H;HogtSlice</td>
<td>7.4</td>
<td>1.050</td>
<td>1.094</td>
</tr>
<tr>
<td>PAX</td>
<td>185.7</td>
<td>14.130.9</td>
<td>1.094</td>
</tr>
<tr>
<td>H;HogtPAX</td>
<td>31.0</td>
<td>8.905</td>
<td>1.094</td>
</tr>
<tr>
<td>S;Pork</td>
<td>70.2</td>
<td>12.960.9</td>
<td>1.094</td>
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</table>

Notes: NS indicates not significant.
Table IV.1. Tests for the Equality of Regression Equations  

<table>
<thead>
<tr>
<th>Source</th>
<th>LEAN</th>
<th>FAT</th>
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<tbody>
<tr>
<td>Deviation from hypothesis</td>
<td>df 7</td>
<td>df 7</td>
</tr>
<tr>
<td></td>
<td>SS 30.5</td>
<td>SS 68.3</td>
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<tr>
<td></td>
<td>NS 4.359</td>
<td>NS NS</td>
</tr>
<tr>
<td></td>
<td>F 2.010</td>
<td>F 3.711</td>
</tr>
<tr>
<td>Pooled regressions residual</td>
<td>df 409</td>
<td>df 1074.8</td>
</tr>
<tr>
<td></td>
<td>SS 887.0</td>
<td>SS 1074.8</td>
</tr>
<tr>
<td></td>
<td>NS 2.169</td>
<td>NS 2.618</td>
</tr>
<tr>
<td>Overall regression residual</td>
<td>df 416</td>
<td>df 1143.1</td>
</tr>
<tr>
<td></td>
<td>SS 893.0</td>
<td>SS 1143.1</td>
</tr>
</tbody>
</table>

NS = Not significant
Only the multiple regression equations for the prediction of lean and fat %s for crosses at pork weight and for the prediction of fat % for sexes at pork and heavy hog weights were significantly different from the overall prediction equations. The remaining equations therefore had parallel slopes and an overall prediction equation could be fitted. Tests for the equality of slope for the significantly different regression equations are given in Table IV.2. (over page).

The regression coefficients were not found to differ significantly except for the equations predicting fat %s of the sexes at pork weight. It was therefore decided that, while main effect constant terms differed, the slopes of all regression equations could, in practice, be regarded as parallel. The decision took into account the number of tests performed, and therefore the possibility of chance significance for the sex coefficients, the small number of subplots with disproportionate sex ratios and the likely improvement in fat % prediction given by separate equations.

Overall equations for lean and fat %s at each slaughter weight were therefore calculated using the same 6 concomitants fitted with a step-wise regression programme (Nelder, 1973). The regression coefficients derived and subsequently fitted, and the % total variance the equation explained, were:

<table>
<thead>
<tr>
<th></th>
<th>% Total Variance explained</th>
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<tbody>
<tr>
<td>Pork</td>
<td>73.0</td>
</tr>
<tr>
<td>(Lean (=0.312x_1) + (0.257x_5) + (0.490x_6))</td>
<td>69.0</td>
</tr>
<tr>
<td>(Fat (=0.398x_4) + (0.311x_5) + (0.232x_6))</td>
<td>85.8</td>
</tr>
<tr>
<td>Heavy Hog</td>
<td>85.6</td>
</tr>
<tr>
<td>(Lean (=0.207x_1) + (0.164x_5) + (0.373x_6))</td>
<td></td>
</tr>
<tr>
<td>(Fat (=0.142x_1) + (0.203x_4) + (0.208x_5) + (0.106x_6))</td>
<td></td>
</tr>
</tbody>
</table>

where \(x_1 = \text{Max, } x_4 = C, x_5 = K\) and \(x_6 = \text{EMA}\)
<table>
<thead>
<tr>
<th>Source</th>
<th>LEAN</th>
<th>FAT</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>df</td>
<td>SS</td>
</tr>
<tr>
<td>Deviation from hypothesis</td>
<td>5</td>
<td>29.8</td>
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<tr>
<td>Pooled regressions residual</td>
<td>435</td>
<td>1257.2</td>
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<tr>
<td>Overall regression residual</td>
<td>440</td>
<td>1287.0</td>
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</table>

**FAT Pork:Cross**

<table>
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<tr>
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<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deviation from hypothesis</td>
<td>1</td>
<td>17.4</td>
<td>17.430</td>
<td>4.838*</td>
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<tr>
<td>Pooled regressions residual</td>
<td>439</td>
<td>1581.7</td>
<td>3.603</td>
<td></td>
</tr>
<tr>
<td>Overall regression residual</td>
<td>440</td>
<td>1599.2</td>
<td></td>
<td></td>
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</table>

**FAT Pork:Sex**

<table>
<thead>
<tr>
<th>Source</th>
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<th>MS</th>
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</thead>
<tbody>
<tr>
<td>Deviation from hypothesis</td>
<td>1</td>
<td>2.7</td>
<td>2.740</td>
<td>0.997 NS</td>
</tr>
<tr>
<td>Pooled regressions residual</td>
<td>415</td>
<td>1140.4</td>
<td>2.748</td>
<td></td>
</tr>
<tr>
<td>Overall regression residual</td>
<td>416</td>
<td>1143.1</td>
<td></td>
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