

ANIMAL GENETICS AND BREEDING UNIT A joint unit of NSW DPI and UNE



Genetic parameters for lean tissue deposition, birth weight, weaning weight and age at puberty

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Aim

- 1. Estimate the heritability for the slope and intercept of lean tissue deposition.
- 2. Estimate genetic parameters for individual piglet birth and weaning weights and within litter variation of piglet birth weight. Obtain genetic correlations between these piglet weight traits and other traits of commercial importance.
- 3. Investigate the relationship between blood creatinine levels and protein deposition.

Background to research

A good knowledge of genetic parameters is essential to develop accurate selection indices and to optimally design breeding programs and performance recording systems for maximum economic gain or profit.

This project is the first attempt to obtain genetic parameters for parameters of a growth model widely used in pig production, the linear-plateau model, whose principles are being used in AUSPIG, for example. This will allow further fine-tuning of genetic improvement programs for growth, including fat and lean meat growth, feed intake and ultimately feed efficiency using combined knowledge of genetic principles and information obtained from projects with nutritional objectives.

A further aspect of this project is to investigate the genetic foundation of individual piglet birth and weaning weight. Previous research has shown that piglet survival depends on the size of individual piglets. In order to maximise the number of healthy piglets weaned it is important to have minimum variation in individual piglet weights within a litter.

Methodology

This project requires new approaches in performance recording as well as data analyses. In order to obtain genetic parameters for parameters of the growth model it is necessary to performance record different groups of pigs under different feeding levels. It was necessary to adapt electronic feeders at Bunge Meat Industries to allow different pigs to be fed a different feeding level within each group. Analyses of data at the Animal Genetics and Breeding Unit will then apply covariance functions which allow the estimation of heritabilities for parameters describing the shape of a curve, ie. a growth curve or a feed intake curve.

The second aspect of the project will include a survival analysis of piglet survival until weaning. Further analyses will obtain genetic parameters for individual piglet birth weight and weaning weight. These traits will be linked with further reproductive traits of the sow as well as performance, carcase and meat quality traits.

Conclusions obtained so far

Reduce the number of piglets weighing less than one kg at birth. It was shown that piglets weighing less than one kg accounted for half of all mortalities although these piglets only represented 15% of all piglets born. Optimise selection for litter size. Initial studies showed that larger litters with more than 13 piglets are not always desirable given the high mortality rates of these litters. Furthermore, the number of litters with less than 8 piglets born in total needs to be reduced since number of piglets weaned was reduced for these smaller litters.

Reduce the within litter variation in piglet weight at birth. Mortality rates were increased for litters with larger variation. In litters with the largest variation every 4th piglet died. In contrast, litters with the lowest variation had a mortality rate of 5% only. Reduction of within litter variation will reduce requirements for cross-fostering.

Investigate the effect of cross-fostering on piglet growth and survival. Cross-fostering is a valuable management tool to reduce within litter variation in piglet weight and is used extensively in this herd.

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