

Selection for production and reproduction traits in pigs

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Selection for production and reproduction traits in pigs

Proefschrift

ter verkrijging van de graad van
doctor in de landbouwwetenschappen,
op gezag van de rector magnificus,
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Aan mijn ouders
Aan Marijke en Dian

VOORWOORD

Het in dit proefschrift beschreven onderzoek is uitgevoerd bij de vakgroep Veefokkerij van de Landbouwniversiteit te Wageningen. Het onderzoek werd mede gefinancierd door het Produktschap voor Vee en Vlees (P.V.V.) te Rijswijk. Voor het mogelijk maken van het onderzoek ben ik de Landbouwniversiteit en het P.V.V. zeer erkentelijk.

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STELLINGEN

1. In zeugenlijnen is selectie op vruchtbaarheid minstens zo belangrijk als selectie op mest- en slachteigenschappen.
Dit proefschrift.
2. Wanneer bij de fokwaardeschatting van varkens veel familie-informatie meegenomen wordt, moet er minder scherp geselecteerd worden.
Dit proefschrift.
3. Voor het beperken van inteelt is het inzetten van een groot aantal beren een beter alternatief dan binnen-familie selectie.
Dit proefschrift.
4. Van minstens de helft van de tomen in een zeugenlijn hoeven geen beren op produktiekenmerken getoetst te worden.
Dit proefschrift.
5. In de topfokkerij dienen voor zeugenlijnen tweemaal zoveel zeugenplaatsen aanwezig te zijn als voor berenlijnen.
Dit proefschrift.
6. Door de concurrentiepositie van een fokkerij-organisatie kan het optimale fokdoel voor de korte termijn afwijken van dat voor de lange termijn.
Dit proefschrift.
7. Bij het doorrekenen van fokprogramma's rekent men zich meestal te rijk.
8. Een hogere vruchtbaarheid leidt tot minder varkens.
9. Selectie van dieren is geen vorm van genetische manipulatie op dier-niveau, maar op populatie-niveau.
10. Het milieu mag niet achter blijven bij het genotype.
11. Fokken is simpel, selecteren is veel moeilijker.
12. Afschaffing van de militaire dienstplicht zou in Nederland ten koste gaan van het wetenschappelijk onderzoek.

*Proefschrift van Alfred G. de Vries,
Selection for production and reproduction traits in pigs.
Wageningen, 3 november 1989.*

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INTRODUCTION

Efficiency of pig meat production depends on the levels of a large number of traits. These traits can be divided into production and reproduction traits (Smith, 1964). Production traits (growth and carcass characteristics of slaughter pigs) are important for the performance of fattening herds, whereas reproduction traits (fertility and longevity of sows) are important for piglet production herds. Pig breeding organizations improve both groups of traits by selection. Animals with the highest breeding values in the nucleus populations are selected to produce the next generation. Optimization of the selection method in nucleus populations is important, because these populations determine the performance in all levels of the breeding pyramid, including the piglet production and fattening herds.

The method of selection is determined by a variety of factors (breeding goal, population size, testing capacity, etc.). Optimization of these factors requires a careful study, because in pig breeding many complicating aspects have to be dealt with (multi-trait and multi-stage selection, overlapping generations, inbreeding, reductions in selection intensity due to small numbers). In relation to the aspect of small numbers, it needs to be considered that selection in pigs is a continuous process, which means that animals of the same generation are not all available for selection at the same moment (Hill, 1976).

Production traits can be measured on young boars and gilts during a performance test. Reproduction traits (e.g. litter size) are sex-limited and can be measured only on sexually mature sows. Another difference between the two groups of traits is that for selection on production traits only one test record is available per animal, whereas for reproduction traits the number of records per sow increases with parity number. As a result, effects of many factors (e.g. generation interval, testing capacity) on selection response will be different for the two groups of traits. This forms an additional complication for the optimization of pig breeding programmes.

Most of the previous optimization studies for pig breeding were focussed on selection for only one group of traits, either production (e.g. De Roo, 1988) or reproduction traits (e.g. Avalos and Smith, 1987). However, an important question at the moment, for the majority of pig breeding

organizations, is how to improve both groups of traits simultaneously (Ollivier, 1988).

The objective of this thesis is to optimize pig breeding programmes with simultaneous selection for production and reproduction traits. Results are focussed on genetic response to selection and rate of inbreeding.

Current pig breeding programmes consist of a breeding pyramid with a closed nucleus. The nucleus consists of specialized sire and dam lines (Webb and Bampton, 1987; Knap, 1989). Sire lines provide the boars used by commercial herds for piglet production, whereas dam lines provide the sows of these herds. In sire lines, selection for production traits is important, but in dam lines selection is for production traits as well as for reproduction traits (Smith, 1964). Therefore, emphasis in this thesis is given to selection in dam lines.

Optimization of a pig breeding programme involves the definition of the breeding goal for each line and the choice of selection traits. Other factors that need to be studied are population size (i.e. number of sows), sow/boar ratio, test capacity, testing and selection system (number of animals tested and selected per family) and generation interval. These factors determine the balance of selection (between production and reproduction traits), intensity of selection and time of selection.

Breeding organizations want to maximize profitability of their breeding programme. Therefore, predicted response to selection and costs are the most important criteria for optimization of a breeding programme. However, not only short-term returns but also long-term prospects of selection are important. This means that rates of inbreeding should also be taken into account, as additive genetic variance within a population decreases with the level of inbreeding. Another aspect to be considered is the variability of selection response due to random drift (Hill, 1977). Rate of inbreeding and random drift are determined by effective population size of the nucleus lines.

One of the first steps in optimization of breeding programmes is definition of the breeding goal (Harris et al., 1984). To weigh traits in a breeding goal, their economic values need to be estimated. These economic values can be used for selection within a population and also for choices

among breeds or crosses, evaluation of gene effects, and for design of optimum breeding programmes (Danell, 1980; Ollivier, 1986). For some traits, no economic values were available in the literature, whereas for others no recent values could be found. A deterministic model was developed to derive economic values of traits at a commercial level. The construction of this model and its application for the Dutch pig industry are in Chapter 1.

Economic values derived at a commercial level can be used to define the breeding goal for a breeding organization; however, this is not always optimal. The value of improvement of a trait for a breeding organization is determined by its impact on saleability of the breeding stock. This impact is influenced by the competitive position of the breeding organization, i.e. the performance of its breeding stock compared to other breeding organizations. A generally applicable method to take these effects into account is given in Chapter 2.

After definition of the breeding goal, the other elements of a breeding programme should be optimized. Dam lines are selected for production as well as for reproduction traits. Family information in these lines is very important because of the low heritability of reproduction traits (Avalos and Smith, 1987). As a result, accuracy of selection in dam lines is influenced by population structure (family structure, age distribution). Family structure depends on population size and sow/boar ratio. Large families will give a high accuracy of selection, but efficient use of family information is only possible with a large number of families available at each time of selection. Effects of population size and sow/boar ratio on response to selection for production and reproduction traits and on inbreeding are studied with a stochastic simulation model. This study is described in Chapter 3.

Selection on production and reproduction traits reduces effective population size of dam lines, which results in high rates of inbreeding (ΔF). One of the alternatives to reduce ΔF is to put restrictions on the numbers of boars tested and selected per family. Another argument for restrictions on the number of boars tested per family is the reduction in testing costs. Effects of restrictions of family size in selection and testing on selection response and inbreeding are examined with stochastic simulation in Chapter 4.

Boars and sows can be selected at several stages. An important stage of selection is just after the performance test. However, part of the selection can be done before the test, which will reduce costs of the breeding programme. Another aspect of multi-stage selection is sequential culling, where an animal is culled as soon as a better replacement is available. Generation interval will then be optimized automatically. Selection of boars before the performance test and sequential culling of sows are studied for dam lines with stochastic simulation. This is reported in Chapter 5.

Most breeding organizations have a nucleus with sire as well as dam lines. In the short-term, total nucleus and testing capacity of a breeding organization are fixed, but the distribution over lines can be varied. Therefore, optimization of population size and testing capacity has to be done simultaneously for sire and dam lines. A deterministic model with parameters derived from stochastic simulation was used to optimize the distribution of nucleus and testing facilities over lines in various situations. This study is described in Chapter 6.

The first two chapters can be used by pig breeding organizations to derive the optimal breeding goal (for sire lines as well as for dam lines). Chapters 3, 4 and 5 show the effects of the most relevant factors of the breeding programme (population size, sow/boar ratio, testing and selection system, testing capacity and generation interval) on selection response and inbreeding in dam lines. Due to the stochastic simulation approach in these chapters, all direct and indirect effects of these factors were taken into account (De Vries et al., 1988). The conclusions from the simulation studies, together with the semi-deterministic method in Chapter 6, make it possible to derive optimum designs for the total breeding programme of a pig breeding organization.

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Chapter 1

A MODEL TO ESTIMATE ECONOMIC VALUES OF TRAITS IN PIG BREEDING

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ABSTRACT

A model was constructed to estimate economic values of traits in pig breeding. The model describes efficiency of meat production as a function of breeding goal traits. Traits in the breeding goal were: oestrus traits, mature weight and feed requirements of sows, longevity of sows, litter traits, growth rate and daily feed intake of young pigs and of fatteners, mortality rate of pigs, PSE incidence and carcass traits.

The model was applied to the Dutch situation. Economic values (Dfl. per slaughter pig) of most important traits were: -0.09 (per day) for age at first oestrus, -0.32 (per day) for interval weaning-oestrus, 8.90 (per pig litter⁻¹) for litter size born alive, -1.10 (per %) for mortality rate of piglets in suckling period, 2.30 (per farrowing) for longevity of sows, 0.26 (per g day⁻¹) for growth rate of fatteners, -0.06 (per g day⁻¹) for daily feed intake of fatteners and 3.10 (per %) for lean content.

Sensitivity analysis showed that relative values of traits might change in future and that a reduction of absolute values is more likely than an increase.

1. INTRODUCTION

In pig breeding, attention has to be given to a great number of traits (Schaaf et al., 1985). Not only traits directly selected on (measured traits), but also traits of economic importance that are genetically correlated with the selection criteria should be included in the breeding goal (Gjedrem, 1972; James, 1982). To weigh traits in the breeding goal, their economic values need to be estimated. Appropriate economic values are not only important for selection within a population, but also for choices among breeds or crosses, evaluation of gene effects, and for design of optimum breeding programmes (Danell, 1980; Ollivier, 1986).

The aim of the present study was to develop a model to estimate the economic values of fertility (oestrus and litter traits), longevity (culling rates of sows) and production traits (growth performance and carcass quality). The values are used to define a breeding goal for within population selection that is optimal for the pig industry. The model can be used in many situations. In this paper an application is given for the

situation in the Netherlands. The relative figures of the results of this application are probably not much different from the values of traits in other European countries. A study of effects of changes in economic parameters and in technical results on economic values is included.

2. METHOD

2.1. Conditions and strategy

Smith et al. (1986) imposed two conditions for derivation of economic values. The first is that extra profit resulting from extra output should be excluded. The second is that changes that correct previous inefficiency in the production enterprise should not be counted. A third condition for development of the present model has been that limitations of individual farms are not considered. If, for example, piglets reach their optimal weaning weight as a result of selection one day earlier, most farmers would not shorten the length of the suckling period, because they wean on a fixed day of the week. However, when a group of farms is considered, this limitation is not relevant, because there would also be some farmers who could now wean a week earlier. Therefore, average weaning age of the group of farms would be reduced.

For some traits (e.g. lean meat percentage), the economic value is not only influenced by the mean level but also by the variation between animals. This was taken into account in the model.

One of the methods to derive economic values is to use profit or efficiency equations (Danell, 1980; Brascamp, 1983). The economic value of a trait is calculated as the ratio of the change in profit (or efficiency) to a small change in genetic level of the trait. The equations can be based on individual efficiency, on dam-progeny efficiency or on herd efficiency (Elsen et al., 1986).

Danell (1980) gives a lot of examples of studies where economic values were calculated based on effects of traits on producer's profit. However, such a basis would give a violation of the first condition of Smith et al. (1986). An appropriate way to cope with the conditions of Smith et al. (1986) is to derive economic values based on efficiency of production (cost per unit of product), and to regard all costs as variable with the level

of output. This strategy was followed in the present study.

2.2. Model description

The model simulated the performance of a group of sows and their offspring. Efficiency of production was calculated as total net costs per kg offspring output (kg carcass weight) minus adjustment of price for carcass quality. Total net costs was defined as sow costs minus returns for culled sows plus costs for offspring:

$$\text{efficiency} = (\text{total net costs} / \text{offspring output}) - \text{adjustment of price}$$

$$\text{total net costs} = \text{sow costs} - \text{sow returns} + \text{offspring costs}$$

The traits studied with the model are in Table 6. For each trait, the effect of a small change in level of performance on efficiency of production (per kg carcass weight) was calculated. Change in efficiency was expressed on a per slaughter pig basis (change in efficiency per slaughter pig produced), to assist in a better interpretation of results. These values were derived by multiplication of change in efficiency with initial offspring output per slaughter pig. The economic value of a trait was calculated as:

$$(\text{change in efficiency per slaughter pig}) / (\text{change of trait})$$

The computer model is written in Fortran-77. Equations for calculation of sow costs and returns, offspring costs and output and adjustment of price are given in Appendix A.

2.2.1. Sow costs and returns for culled sows

The model started with 100 purchased gilts of 200 days old. Figure 1 illustrates how the course of life of these animals was simulated. A new cycle was initiated at the time of weaning of each litter. Within each cycle, three categories of culled sows were distinguished. Sows of the

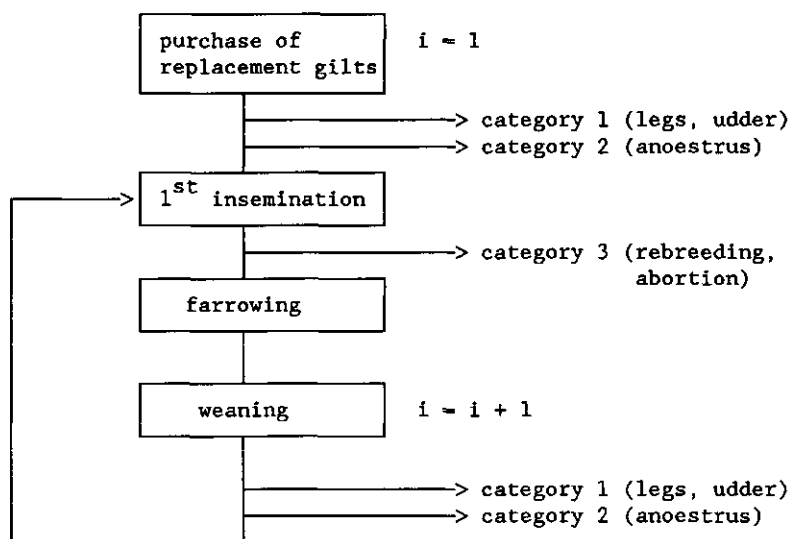


Figure 1. Course of life of sows (i = cycle number).

first category were culled shortly after purchase or shortly after weaning because of visually assessed defects (leg weakness, udder problems). The next category consisted of sows that did not show heat in time. In the third category, sows were culled after one or more unsuccessful inseminations. After cycle number 10, all remaining sows were sold shortly after weaning (category 1).

Sow costs were calculated from the following components:

- purchase costs per replacement gilt (representing all costs per gilt made by the breeder);
- basic non-feed costs per day (labour, management, housing, interest on livestock investment, water, electricity and miscellaneous);
- basic feed costs per day (requirements for growth and maintenance);
- extra non-feed costs per farrowing (labour, management, veterinary and heating costs; extra costs for housing before and after lactation);
- extra non-feed costs per lactation day (extra costs for housing);
- breeding costs per first insemination;
- feed costs for development of gestation products per pig born;
- feed costs for milk production per lactation day per pig weaned;

i. costs associated with selling of sows.

Basic costs per day (components b. and c.) were specified for three age categories:

- replacement gilts, from time of purchase to first insemination;
- gilts, from time of first insemination to first farrowing;
- sows, after first farrowing.

Extra costs for housing (components d. and e.) reflected the difference between costs per place in the farrowing house and costs per place in the breeding/gestation house.

Weight differences between culling categories were assumed to be only due to differences in maturity. (The effect of recovering from weight losses during lactation on live weight gain was excluded.) Carcass price per kg for culled sows was dependent on cycle number.

When age at first oestrus or interval weaning-oestrus changes, state of maturity of culled sows also changes. This needs to be included, when economic values of these traits are calculated. Therefore, live weight of sows in each cycle was adjusted by the value for growth rate in that cycle multiplied by the change in age:

$$\Delta w s_i = \Delta a f o e \times g r s_i + (i-1) \times \Delta i w o e \times g r s_i$$

where $\Delta w s_i$ = change in weight of sows;

$\Delta a f o e$ = change in age at first oestrus;

$\Delta i w o e$ = change in interval weaning-oestrus (all cycles);

$g r s_i$ = growth rate of sows in cycle no. i;

i = cycle number.

2.2.2. Offspring costs and output

Three growing stages were distinguished for the offspring of the sows:

- from birth to weaning (stage 1);
- from weaning to feeder pig weight (stage 2);
- from feeder pig weight to slaughter weight (stage 3).

Birth weight, weaning weight, feeder pig weight and slaughter weight were fixed.

Offspring costs were calculated from:

- a. feed costs per day in each of these stages;
- b. non-feed costs per day in stage 2 and 3 (labour, management, housing, interest on livestock investment, water, heating, electricity and miscellaneous);
- c. extra costs per pig weaned in stage 1 (iron injection, castration, tail cutting);
- d. extra costs in stage 3 per feeder pig (transportation of feeder pigs, veterinary costs; labour, management and housing costs during empty days between batches);
- e. costs associated with selling of slaughter pigs.

For animals that died during stage 2 or 3 half of the feed and the time-dependent non-feed costs in that particular stage were counted.

Total number of piglets weaned was reduced by mortality in stage 2 and 3 to give total number of slaughter pigs. Output (kg carcass weight) per PSE-free pig was fixed, but output per pig with PSE-syndrome indications was reduced by a specified percentage (transport death, weight loss).

2.2.3. Adjustment of price for carcass quality

The Dutch classification system for carcass quality is a dual grading system according to estimated lean meat percentage (ELMP) and according to type classes: C (negligible numbers), B, A and AA. Basic prices refer to 52% ELMP and type A, with reductions for lower and premiums for higher classes.

Average adjustment of price for ELMP is a function of the fraction of carcasses in group 1 (ELMP < 52%) and group 2 (ELMP ≥ 52%) and the average ELMP of each group.

The approach for calculation of change in price due to shifts in type classes was based on the strategy for derivation of economic values for categorical traits (Danell, 1980; Danell and Rønningen, 1981). The distribution for the underlying scale was defined with the truncation points that correspond with the frequencies of type B and AA in the basic situation. The change in frequency of type B was calculated as $-\Delta\text{type} \times z_B / (z_B + z_{AA})$, while change in frequency of type AA was calculated as $+\Delta\text{type}$

$x z_{AA}/(z_B + z_{AA})$, where $\Delta type$ is shift in type class and z_B and z_{AA} are the heights of the distribution ordinate for type B and type AA, respectively.

2.3. Levels of genetic traits and parameters (basic situation)

The model was applied to the situation in the Netherlands. Parameters originate from different Dutch sources and are close to the real situation in 1987.

Culling percentages of purchased gilts for category 1, 2 and 3 were 1%, 3% and 8%, respectively. Marginal culling rates after each farrowing for sows are given in Table 1. From these cullings 47%, 8% and 45% were classified in category 1, 2 and 3, respectively. Culling times of sows were specified as follows:

- category 1: 7 days after weaning (for replacement gilts: 7 days after purchase);
- category 2 and 3: 40 and 70 days, respectively, after first insemination of animals without oestrus problems.

Age at first oestrus was 200 days. Values for litter traits and interval weaning-oestrus are in Table 1.

Live weight of replacement gilts at time of purchase was 95 kg. Daily gain after this time was 300 gram. Daily gain after first insemination was 200 gram. Live weight and daily gain of sows dependent on age is in Table 2.

Table 1. Fertility traits and culling rates of sows per cycle number (base level).

	Cycle number									
	1	2	3	4	5	6	7	8	9	10
Int. wean.-oestr. (d)		12	9	8	8	7	7	7	7	7
Marginal culling (%)		14.7	16.1	17.5	18.9	20.3	22.4	24.5	26.6	30.1
No. born alive	9.4	10.1	10.6	10.9	11.0	10.9	10.8	10.7	10.6	10.5
Mortal. stage 1 (%)	14.9	13.9	15.1	14.7	16.4	15.6	15.7	16.8	17.0	17.1

Table 2. Weight and daily gain of sows one month after weaning (base level).

	Cycle number					
	2	3	4	5	6	≥7
Live weight (kg)	140	161	179	188	196	200
Daily gain (g day ⁻¹)	125	100	75	50	25	0

Replacement gilts needed 2.7 kg of sow feed per day. Gilts and sows needed 2.25 kg per day for growth and maintenance. During gestation 1.8 kg extra feed per pig born was required. During lactation sows needed 0.4 kg extra feed per pig per day.

Pigs were weaned at 7.8 kg, sold as feeder pig at 25 kg and slaughtered at 106 kg live weight. Performance in the three growing stages is given in Table 3.

Dressing percentage of slaughter pigs was 77%. For PSE incidence a value of 8% was assumed, i.e. 8% of the slaughter pigs had PSE-syndrome indications. Output (carcass weight) of these pigs was reduced by 3.33%.

Parameters for estimated lean meat percentage (ELMP) and type class dis-

Table 3. Offspring production traits (base level).

	Growing stage ¹⁾		
	1	2	3
Growth rate (g day ⁻¹)	200	400	679
Feed intake (g day ⁻¹)	30	720	2070
Mortality (%)		1.0	2.1

1) Stage 1: from birth to weaning;

Stage 2: from weaning to feeder pig weight;

Stage 3: from feeder pig weight to slaughter weight.

distribution were as follows:

- 29% in group 1 (ELMP < 52%) with an average of 48.6% lean meat;
- 71% in group 2 (ELMP \geq 52%) with an average of 54.9% lean meat;
- 17% type B, 70% type A and 13% type AA.

The values for the other parameters are given in the list of symbols in Appendix A.

3. RESULTS

3.1. Basic situation

Simulated performance of the sow herd is characterized in Table 4. The values given here can be used to verify the model. Simulated fertility performance and yearly culling rate are in agreement with average results of Dutch farms. Distribution of farrowings by cycle number is in Table 5. Efficiency (net costs minus price adjustment per kg carcass weight) in the basic situation was Dfl. 4.11/kg (sow costs, sow returns, offspring costs and premium were Dfl. 1.39, 0.15, 2.90 and 0.03 per kg, respectively; 56% of total net costs were feed costs). Output per slaughter pig sold was 81.4 kg.

Table 4. Simulated average performance of sows.

Trait	Average value
Litter size born (total)	11.2
Litter size born alive	10.4
Litter size weaned	8.8
Farrowings/sow/year ¹⁾	2.13
Total no. of farrowings/purch. gilt	4.24
Cullings/sow/year ¹⁾ (%)	48.3
Total costs/purch. gilt (Dfl.)	4091.--
Culling returns/purch. gilt (Dfl.)	429.--

1) Including gilts.

Table 5. Simulated distribution of farrowings.

	Cycle number									
	1	2	3	4	5	6	7	8	9	10
Distribut. (%)	20.8	17.7	14.9	12.3	9.9	7.9	6.1	4.6	3.4	2.4

Litter size may be used as an example of how the economic values (Table 6) were obtained. After calculation of the efficiency in the basic situation, variable $lsbl_1$ in the model (see Appendix A) was raised with $0.1 \text{ pig litter}^{-1}$, which resulted in higher sow costs, offspring costs and offspring output. The efficiency in this situation was Dfl. 0.011 per kg carcass weight higher than in the basic situation. Multiplied with output per slaughter pig and divided by $0.1 \text{ pig litter}^{-1}$, this gave an economic value of Dfl. 8.90 for litter size born alive.

The economic value for each trait in Table 6 was calculated under the condition that performance levels of all other traits in the table remained constant.

When gilts showed first oestrus 1 day earlier, sow costs were reduced and returns for culled gilts and sows were somewhat lower, because animals were a day younger when culled.

An increase of 1 kg in mature weight (base level = 200 kg) meant 0.5% more returns for culled sows, because weight and daily gain in each reproduction cycle were increased by 0.5%

When marginal culling rate in each reproduction cycle was lowered by 1%, there were four effects. The first one was a small change in average litter size weaned (+ 0.008 pigs/litter) due to an increase in average cycle number. Secondly, the difference between costs for ready-to-mate gilts and returns for cullings was spread over more litters (+ 0.20 litters/gilt). The other two effects were a higher farrowing index (farrowings/sow/year) and an increase of returns for cullings. These effects were different for each of the three culling categories due to the differences in culling time (see section 2.3).

With higher litter size or lower mortality rate in the suckling period,

Table 6. Economic values of traits (Dfl./slaughter pig) in basic situation.

Trait	Unit	Economic value
Age at first oestrus	day	-0.09
Mature weight of sows	kg	0.07
Feed requirements sows	g day ⁻¹	-0.011
Culling % category 1	%	-0.46
Culling % category 2	%	-0.65
Culling % category 3	%	-0.82
Litter size born alive	pig litter ⁻¹	8.90
Mortality % stage 1	%	-1.10
Interval weaning-oestrus	day	-0.32
Growth rate stage 1	g day ⁻¹	0.117
Growth rate stage 2	g day ⁻¹	0.086
Growth rate stage 3	g day ⁻¹	0.262
Feed intake stage 1	g day ⁻¹	-0.026
Feed intake stage 2	g day ⁻¹	-0.035
Feed intake stage 3	g day ⁻¹	-0.064
Mortality % stage 2	%	-1.22
Mortality % stage 3	%	-2.46
PSE incidence	%	-0.11
Estimated lean meat %	%	2.68

sow costs (excluding feed costs for development of gestation products and milk production) and returns for cullings were spread over more offspring. Average litter size weaned was raised by 0.085 pig per 0.1 pig extra born alive, while 1% lower mortality rate raised litter size weaned by 0.104 pig.

For 47% of the sows (culling category 1) interval weaning-oestrus was not important in their last reproduction cycle. As a result 0.9 sow days per reproduction cycle were saved for each day shorter interval, which reduced basic sow costs. Because of a lower age of culled sows, returns for cullings were slightly reduced.

A higher growth rate of piglets during suckling (stage 1) reduced the

length of this period. Basic sow costs, extra costs during lactation, sow feed costs for milk production and pig feed costs were reduced.

A higher growth rate in stage 2 (weaners) or stage 3 (fatteners) reduced time-dependent feed and non-feed costs.

Economic value of a 1% lower mortality rate for stage 2 and for stage 3 corresponded with 1% of the cumulated costs of the animals at death. The economic value of a 1% lower PSE incidence corresponded with 0.0333% (3.33% x 1%) of total costs per slaughter pig.

When average estimated lean meat percentage was improved by 1%, price adjustment per kg carcass weight was increased by 29% x (price reduction below 52%) + 71% x (price increase above 52%). An average shift of 0.01 type classes resulted in 0.54% decrease of frequency of type B and 0.46% increase of frequency of type AA.

3.2. Alternative situations

Four alternative situations were studied to test the sensitivity of economic values (expressed per kg carcass weight) to changes in price and production circumstances. Results are in Table 7.

When sow and pig feed prices were increased by 20%, economic values of feed requirements of sows and pigs also increased by 20%. Relative effects on other traits were smaller. Economic values of carcass traits did not have a feed component.

A 20% higher purchase price for gilts had an important effect on the economic values of longevity traits. Due to increased sow costs, importance of litter traits, viability traits and PSE incidence also changed. Other traits were not sensitive to changes in gilt price.

In future pig production systems, labour and management costs per unit of output will probably be reduced. When these costs decreased by 20%, importance of fertility and longevity traits decreased. Effects on the economic values for growth rate were relatively small, especially for growth rate in the fattening period.

Standards of performance of pig farms will probably continue to improve. Input for the model was modified based on the results of the group of farms (25%) with the highest profit per animal (see Appendix B). Table 7 shows that the economic values of almost all traits were reduced.

Table 7. Relative changes (%) of economic values (expressed per kg carcass weight) in alternative situations compared to the basic situation.

Trait	Feed prices + 20%	Gilt price + 20%	Labour and manag.costs - 20%	Better performance ¹⁾
Age at first oestrus	8.5	0	- 5.5	- 7.8
Mature weight of sows	0	0	0	- 7.4
Feed requirements sows	20.0	0	0	- 7.5
Culling % category 1	3.8	27.5	- 2.9	- 8.7
Culling % category 2	5.2	19.3	- 3.9	- 7.8
Culling % category 3	5.2	15.4	- 4.0	- 7.2
Litter size born alive	5.2	3.0	- 5.5	- 8.8
Mortality % stage 1	5.4	2.9	- 5.4	- 8.5
Interval weaning-oestrus	7.3	0	- 5.6	- 3.9
Growth rate stage 1	9.5	0	- 2.8	-10.3
Growth rate stage 2	14.2	0	- 3.3	- 8.0
Growth rate stage 3	14.7	0	- 1.6	-11.6
Feed intake stage 1	20.0	0	0	- 4.4
Feed intake stage 2	20.0	0	0	- 4.4
Feed intake stage 3	20.0	0	0	- 6.5
Mortality % stage 2	7.4	2.3	- 4.7	- 6.2
Mortality % stage 3	10.3	1.1	- 3.4	- 6.4
PSE incidence	11.3	0.8	- 2.8	- 5.7
Estimated lean meat %	0	0	0	0
Type class	0	0	0	0

1) See appendix B.

4. DISCUSSION

4.1. Model

The model used requires a lot of information, while not all the

information is needed for the economic values of a number of traits. For example, the economic value of estimated lean meat percentage is independent of basic levels of other traits. The equations given in Appendix A can be used to find partial derivatives of traits. This approach was followed by Karlsson (1977) and Knap (1986) and others. The advantage of this approach is that partial derivatives directly reveal the influence of parameters on the economic values.

Efficiency equations give the same results as when economic values are based on change in profit per unit of output, because with both methods, output is regarded as fixed. The advantage of the efficiency method is that estimation of the price per unit of output in the basic situation is not needed.

Only effects of traits on a commercial level (i.e. the level where slaughter pigs are produced) were considered. Reductions of costs at higher levels of the pig industry (nucleus, multiplier) were excluded.

A genetic change in fertility traits is expressed earlier than a genetic change in production traits. Differences in time lag have to be taken into account for the derivation of an optimal breeding goal. However, discounting for time lag has a small influence on the relative economic values.

In this study, economic values of all-or-none traits (PSE incidence, culling percentage, mortality percentage) were derived by calculation of the economic effect of 1% reduction in frequency. However, if such traits are used in the breeding goal, they need to be described by an underlying trait on a linear scale. The economic value of the underlying trait can be derived by multiplication of the economic value in Table 6 with the height of the distribution ordinate that corresponds with the frequency in the basic situation (Danell and Rønningen, 1981).

For pigs that died in stage 2 or 3, half of the feed and non-feed costs were counted. Perhaps this proportion is too high, because daily feed intake increases with age and death loss in the first half of these stages might be higher than in the second half.

4.2. Economic values of traits for within population selection

The economic values in Table 6 can be used for evaluation of breeds or gene effects and are important for optimization of selection within a

population. Absolute economic values always apply to specific production conditions, in this case in the Netherlands, but the relative figures are also useful for other European countries.

The most relevant traits for within population selection in Dutch pig breeding programmes are: age at first oestrus, interval weaning-oestrus, litter size born alive, mortality rate during suckling, growth rate and feed intake in the fattening period, lean content and longevity of sows related to leg and udder quality (Kanis, 1985; Knap et al., 1985; Knap, 1986). Other traits in Table 6 are probably correlated with these traits:

- culling percentage due to anoestrus is positively correlated with age at first oestrus and interval weaning-oestrus;
- growth rate of young piglets is negatively correlated with litter size (due to a lower milk consumption per pig) (Ritter et al., 1985; Van der Steen, 1986);
- mature weight and feed requirements of sows are positively correlated with growth rate of fatteners, which is unfavourable (assuming that 1 kg heavier sows need 10 g day^{-1} more feed, see Table 6);
- growth rates in stages 1 and 2 are positively correlated with growth rate in stage 3;
- viability traits and PSE incidence are positively correlated with lean content.

For an appropriate weighting of the traits in selection, more information about these correlations is needed.

Based on Averdunk et al. (1983), a 1% increase in lean content will give 0.7% improvement of estimated lean meat percentage. COV (1976) reported for the regression of type on lean content a value of 0.285 type classes per % lean content. In the current situation this regression is probably lower, because of a reduced variation in type. Therefore, a regression of 0.2 type classes per % lean content is expected (E. Kanis, personal communication). So when lean content is used as a trait in the breeding goal instead of ELMP and type, its economic value (per slaughter pig) is Dfl. 3.10 per % ($0.7 \times 2.68 + 0.2 \times 5.92$).

Usually longevity is expressed as number of farrowings per purchased gilt. A reduction of culling rate of 1% in each cycle corresponded with 0.2 extra farrowings per purchased gilt. This means that the economic value (expressed per slaughter pig) of longevity for category 1 is Dfl. 2.30 per

farrowing (0.46/0.2).

For fertility traits (litter size, mortality percentage in the suckling period and interval weaning-oestrus) Table 5 can be used to calculate the economic effects per cycle number separately. This can be useful particularly for the first cycle number, because the genetic correlation between size of the first litter and size of older litters is not equal to 1 (Knap, 1986; Vangen, 1986).

4.3. Future situation

Financial parameters will change in the future. Sensitivity analysis showed that relative values of traits might then change. The direction of these changes, however, is unpredictable. Parameters like feed prices and gilt price may go up or down.

For the design of optimum breeding programmes (e.g. choice of nucleus size, test capacity), absolute economic values of traits are needed. Expecting a reduction of labour and management costs and an improvement of technical results in the future, it can be stated that a reduction of absolute values of traits is more likely than an increase.

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APPENDICES

Appendix A. Essential equations in the model

A.1. Sow costs and returns for culled sows

for $i=2$ to $i=np+1$: $nrsows_i = nrsows_{i-1} * (1 - culpl_{i-1} - culp2_{i-1} - culp3_{i-1})$

$tins = \sum_{i=1}^{np} [nrsows_i * (1 - culpl_i - culp2_i)]$

```

      np+1
tfar = Σ nrsowsi
      i=2

      np+1
tnbl = Σ nrsowsi*lsbli
      i=2

      np+1
tnw  = Σ nrsowsi*lsbli*(1-mortppli)
      i=2

trgd = nrsowsi=1*[culpli=1*cult1
                  +culp2i=1*(afoe-arg+21*(nroe-1)+cult2)
                  +(1-culpli=1-culp2i=1)*(afoe+21*(nroe-1)-arg)]

tgtd = nrsowsi=1*culp3i=1*cult3+nrsowsi=2*(xdays+lgest)

      np
tsd  = Σ[nrsowsi*(pld+culpli*cult1+culp2i*(iwoei+cult2)+culp3i*(iwoei+cult3))
      i=2
      +nrsowsi+1*(iwoei+xdays+lgest)]
      +nrsowsi=np+1*(pld+cult1)

sow costs = nrsowsi=1*crg
            +(nfcrgd+frrgd*fps)*trgd+(nfcgtd+frgtd*fps)*tgtd
            +(nfcsd+frsd*fps)*tsd
            +tins*cins+tfar*(cfarfix+cfarvar*pld)
            +tnbl/(1-stillbp)*frpb*fps+tnw*frlact*pld*fps
            +nrsowsi=1*(1-mortps)*csls

sow returns = [prsi=1*drps*nrsowsi=1
               *(culpli=1*(wrg+cult1*grrg)
               +culp2i=1*(wrg+(afoe+21*(nroe-1)-arg+cult2)*grrg)
               +culp3i=1*(wrg+(afoe+21*(nroe-1)-arg)*grrg+cult3*grgt))
               +Σ prsi*drps*nrsowsi*(culpli*(wsi+(cult1-30.5)*grsi)
               +culp2i*(wsi+(iwoei+cult2-30.5)*grsi)

```


gilts and sows, respectively (Dfl. 2.02, 2.02, 2.02)

np - maximum no. of farrowings (10)
 nroe - oestrus no. at breeding of gilts (3)
 nrsows_i - no. of sows that start with cycle no. i (nrsows_{i=1} = 100)
 pld - length of the suckling period
 prs_i - carcass price (Dfl./kg) of culled sows in cycle no. i
 (for i=1 to i=11: 3.85, 3.45, 3.40, 3.35, 3.35, 3.35 3.35, 3.30,
 3.30, 3.30,3.30)
 stillbp - stillbirth % (7%)
 tfar - total no. of farrowings
 tgtd - total no. of gilt days
 tins - total no. of first inseminations
 tnbl - total no. of pigs born alive
 tnw - total no. of pigs weaned
 trgd - total no. of replacement gilt days
 tsd - total no. of sow days
 xdays - extra days open due to oestrus problems and rebreedings (8 days)
 wrg - weight of replacement gilts at moment of purchase
 ws_i - weight of sows in cycle no. i 30.5 days after weaning

A.2. Offspring costs, offspring output and adjustment of price per kg carcass weight

$$pld = (wn - birthw) / grl$$

$$p2d = (wfp - wnw) / gr2$$

$$p3d = (wsp - wfp) / gr3$$

$$tnfp = tnw * (1 - mortpp2)$$

$$tnsp = tnfp * (1 - mortpp3)$$

$$\begin{aligned}
 \text{offspring costs} = & \text{tnw} * (\text{cplfix} + \text{fip1} * \text{fppl} * \text{pld}) \\
 & + \text{tnw} * (1 - 0.5 * \text{mortpp2}) * (\text{nfc} * \text{p2d} + \text{fip2} * \text{fpp2}) * \text{p2d}
 \end{aligned}$$

$+tnfp*cp3fix$
 $+tnfp*(1-0.5*mortpp3)*(nfc3d+fip3*fpp3)*p3d$
 $+tnsp*cs1p$

offspring output = $tnsp*wsp*drpp*(1-rfpse*pse)$

adjustment of price = $freq1*(lm1-52)*prd1+freq2*(lm2-52)*prd2$
 $+freqAA*prdAA+freqB*prdB$

List of symbols in alphabetical order (values of parameters are given in brackets):

birthw = birth weight of pigs (1.4 kg)
 cplfix = fixed non-feed costs in stage 1 per pig weaned (Dfl. 3.00)
 cp3fix = fixed non-feed costs in stage 3 per feeder pig (Dfl. 11.26)
 cs1p = costs per slaughter pig sold (Dfl. 4.73)
 drpp = dressing % of slaughter pigs (77%)
 fip1, fip2, fip3 = daily feed intake in stage 1, 2 and 3, respectively
 fpp1, fpp2, fpp3 = feed price (Dfl./kg) for stage 1, 2 and 3, respectively
 (0.79, 0.79, 0.53)
 freq1, freq2 = frequency in group 1 (ELMP < 52%)
 and group 2 (ELMP ≥ 52%), respectively
 freqAA, freqB = frequency in type class AA and B, respectively
 gr1, gr2, gr3 = growth rate in stage 1, 2 and 3, respectively
 lm1, lm2 = average estimated lean meat % (ELMP) in group 1
 and group 2, respectively
 mortpp2, mortpp3 = mortality % in stage 2 and 3, respectively
 nfc2d, nfc3d = non-feed costs per day in stage 2 and 3, respectively
 (Dfl. 0.23, 0.40)
 p1d, p2d, p3d = length of stage 1, 2 and 3, respectively
 pse = incidence of PSE-syndrome indications
 rfpse = reduction factor for pigs with PSE indications (3.33%)
 tnfp = total no. of feeder pigs
 tnsp = total no. of slaughter pigs
 tnw = total no. weaned
 prd1, prd2 = price difference (Dfl./kg) per % of lean meat difference

	within group 1 and group 2, respectively (0.04, 0.03)
prdAA, prdB	- price difference (Dfl./kg) for type class AA and B, respectively (+0.10, -0.05)
wfp	- weight of feeder pigs (25 kg)
wsp	- slaughter weight of pigs (106 kg)
wnn	- weight of pigs at weaning (7.8 kg)

Appendix B. Modifications of input for a situation with better technical results

- extra days open due to oestrus problems and rebreedings: - 4 days
- culling % category 1 (excluding replacement gilts): - 0.5 %
- culling % category 2 (all cycles): - 0.5 %
- litter size born alive: + 0.2 pigs
- mortality % in suckling period: - 1.5 %
- growth rate in suckling period: + 8 g day⁻¹
- growth rate in nursery stage : + 16 g day⁻¹
- growth rate in fattening period: + 45 g day⁻¹
- feed intake in fattening period: + 20 g day⁻¹
- mortality % in fattening period: - 0.6 %

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Chapter 2

A METHOD TO INCORPORATE COMPETITIVE POSITION IN THE BREEDING GOAL

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ABSTRACT

The value of the improvement of a trait for a breeding organization is determined by its impact on the saleability of its breeding stock. This impact is influenced by the competitive position of the breeding organization, i.e. by the performance of its breeding stock relative to other breeding organizations. A method was developed to take effects of competitive position on the breeding goal into account in designing selection indexes. The main conclusions were as follows:

- (1) When the performance level of a trait is equal to the average performance level of other breeding organizations, its economic weight (i.e. its weighting factor in the breeding goal) is equal to its importance on a commercial level. With lower performance, the economic weight increases. With higher performance, it decreases.
- (2) The effect of competitive position on the economic weight of a trait depends on the degree of compensation between traits. When a weakness (negative monetary deviation compared with competitors) in one trait can be totally compensated by the strength (positive monetary deviation of the same order) in another trait, then competitive position has no influence on the economic weight.

INTRODUCTION

Breeding organizations are responsible for the genetic improvement of animals. A common way to weigh traits in a breeding goal for a breeding organization is to estimate the importance of each trait on a commercial level. This is the level where products are made with breeding animals bought from the breeding organizations. It is assumed then that the breeding goal that gives maximum profit for the clients of the breeding organizations, will also give maximum profit for the breeding organizations. This assumption is disputable (Flock, 1980; Knap and Molenaar, 1985; Schultz, 1986). The profit of a breeding organization depends on the number of breeding animals that can be sold, and on the selling price per breeding animal. Therefore, the value of improvement of a trait is determined by its impact on saleability of breeding stock. This impact is influenced by the competitive position of the breeding organization, i.e. the performance of

its breeding stock relative to other breeding organizations. Improvement of a trait with a low performance compared with competitors is very important, while improvement of a trait with an acceptable performance (i.e. the breeding stock is for this trait superior or equal to competitors) has a much smaller influence on sales volume (Schultz, 1986).

The attitude of potential buyers to a certain brand depends on the attributes of the brand. Lilien and Kotler (1983) distinguish two categories of marketing models to describe this relationship: compensatory and non-compensatory models. In a compensatory model, the weakness of a brand on one attribute can be compensated by the strength on another. In a conjunctive model, which is one of the non-compensatory models, a potential buyer will consider the purchase of a brand only if it meets certain minimum acceptable standards on important attributes. For breeding stock buyers, probably a model is valid that is partly compensatory.

Schultz (1986) proposes to define the desired selection response for each trait subjectively. This strategy is not optimal, because definition of such desired gains is influenced by personal and incidental factors. Other methods that allow for effects of competitive position on the breeding goal could not be found in literature.

In this paper a method (based on a conjunctive marketing model) is presented that can be used to take effects of competitive position on the breeding goal into account. The method is illustrated with an example.

DERIVATION OF THE METHOD

A breeding organization sells its breeding stock (brand) to commercial producers (clients). It is assumed that an organization has only one brand. A client buys a brand only if all traits (individual genetic traits, purchase price, service) reach an acceptable level. The acceptance level of a client for a certain trait is defined as the minimum performance level that he accepts for this trait, i.e. the level at which the brand is just good enough to be considered for purchase. The acceptance level for a trait is influenced by the performance of brands of competitors. It can also be influenced by the performance levels of other traits of the same brand. The acceptance level is not the same for each client. Some of them will buy the brand only if it is much better for the trait in question than the brands

of competitors, but there will be also clients that do not pay much attention to the trait. Classification of the total group of clients (actual customers of the breeding organization together with potential customers) according to their acceptance level for an individual trait is expected to reveal a normal distribution (see Figure 1). It is assumed that the standard deviation of this distribution (s) is equal for each trait, if it is expressed in monetary units based on profit on a commercial level. The value of s needs to be estimated with marketing research.

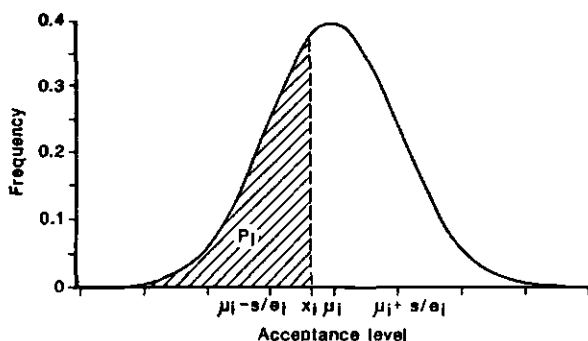


Figure 1. Distribution of clients according to their acceptance level for a trait (μ_i : mean acceptance level, s/e_i : standard deviation, p_i : proportion of clients that accept the level of the trait, x_i : level of the trait).

The proportion of clients that accept the performance level of trait i is equal to the probability that the acceptance level of a randomly chosen client is lower than or equal to the performance level of the brand.

$$p_i = \int_{-\infty}^{t_i} z_i dt_i \quad (1)$$

$$z_i = \exp(-0.5 t_i^2) / \sqrt{(2\pi)} \quad (2)$$

$$t_i = e_i * (x_i - \mu_i) / s \quad (3)$$

where p_i = proportion of clients that accept the performance level of trait i ;

x_i - performance level of the brand for trait i ;
 z_i - height of the distribution ordinate at point t_i ;
 t_i - difference between x_i and μ_i expressed in standard deviation units;
 s - standard deviation of the distribution function expressed in monetary units;
 e_i - value of trait i on a commercial level;
 μ_i - mean acceptance level of clients for trait i .

When saleability of the brand is determined by two traits, a client will only buy the brand if the level of both traits is acceptable. It is assumed that acceptance levels of traits are uncorrelated, i.e. a randomly chosen client with high requirements for trait 1 and a randomly chosen client with low requirements for this trait have the same probability of accepting the level of trait 2. The chance that both traits are acceptable for a randomly chosen client is then equal to the fraction of clients that accepts the level of the first trait (p_1) times the fraction that accepts the level of the second trait (p_2). Market share, i.e. the fraction of clients that buy the brand, is a function of this chance. For n traits we find:

$$ms = c * (p_1 * p_2 * \dots * p_n)$$

where ms = market share;

c = constant (dependent on number of competitors and number of traits).

Economic weights (i.e. weighting factors for the breeding goal) based on the marginal effects of traits on saleability (market share) can now be derived:

$$dms/dx_i = (e_i/s) * (z_i/p_i) * c * (p_1 * p_2 * \dots * p_n) \quad (4)$$

Although purchase price (PR) is not a genetic trait, it is assumed that it affects saleability in the same way as genetic traits do. This means that equation (4) also applies to PR. Each producer on a commercial level needs to buy breeding stock. Some of these producers buy expensive breeding stock, which means that their acceptance level for PR is high. Other producers only accept a brand with a low price. Assuming that the price of

the brand under study (x_{PR}) is equal to the mean acceptance level of clients (μ_{PR}), the effect of a change in price on market share can be derived:

$$dms/dx_{PR} = (e_{PR}/s) * \sqrt{(2/\pi)} * c * (p_1 * p_2 * \dots * p_n) \quad (5)$$

A higher purchase price of 1 monetary unit reduces profit per breeding animal on a commercial level by 1 unit, which means that $e_{PR} = -1$. We can now derive economic weights of the genetic traits relative to the effect of a price reduction of one monetary unit on saleability.

$$\begin{aligned} v_i &= [dms/dx_i] / [dms/-dx_{PR}] \\ &= [e_i * (z_i/p_i)] / [-e_{PR} * \sqrt{(2/\pi)}] \\ &= e_i * (z_i/p_i) * \sqrt{(\pi/2)} \end{aligned} \quad (6)$$

where v_i = economic weight of trait i in the breeding goal.

Mean acceptance level of trait i (μ_i) in equation (3) may be influenced by performance levels of other traits. It is expected that μ_i is close to the average performance level of competitors, when performance levels of other traits are equal to average performance levels of competitors. When performance levels of these traits are higher or lower than competitors, compensation between traits may play a role. To take this into account, a compensation factor (cf) is used that reflects the degree of compensation between traits. The value of cf needs to be estimated with marketing research. When $cf = 0$, the mean acceptance level of a trait is independent of the performance levels of other traits and will be close to the average performance level of competitors. When $cf > 0$, a lower performance level of a trait is acceptable, provided that the other traits have a high performance level. A value of $cf = 1$ means that there is 100% compensation between the traits, i.e. a weakness (negative monetary deviation compared with competitors) in one trait can be totally compensated by the strength (positive monetary deviation of the same order) in another trait.

$$\mu_i = ac_i - (cf/e_i) * \sum d_j \quad (j \neq i) \quad (7)$$

$$d_j = e_j * (x_j - ac_j) \quad (8)$$

where ac_i = average performance level of competitors for trait i ;
 cf = compensation factor reflecting the degree of compensation
between traits;
 d_j = difference between x_j and ac_j expressed in monetary units
based on profit on a commercial level.

Normally between competitive breeding stocks (brands) there are no large differences in total profitability on a commercial level. A brand with a high performance level of one of the traits may have a low performance level of another trait. When all traits have a high performance level, it is likely that clients have to pay a high price for the breeding animals. So regarding purchase price per breeding animal as a trait, and assuming no difference in total profitability between the brand and the average of competitors ($(d_i + \sum d_j) = 0$, thus $d_i = - \sum d_j$), the following derivation can be made:

From equation (7) and (8):

$$\begin{aligned} x_i - \mu_i &= x_i - ac_i - (cf/e_i) * d_i \\ &= x_i - ac_i - cf * (x_i - ac_i) \\ &= (x_i - ac_i) * (1 - cf) \end{aligned} \quad (9)$$

From equation (3) and (9):

$$t_i = e_i * (x_i - ac_i) * (1 - cf)/s \quad (10)$$

Under the assumptions made, only equations (1), (2), (6) and (10) are required for the calculation of the economic weights.

When the performance level of trait i is equal to the average performance level of competitors, $t_i = 0$ (equation 10) and thus $z_i/p_i = \sqrt{(2/\pi)}$ (equation 1 and 2), and $v_i = e_i$ (equation 6). This is also the case when there is 100% compensation between traits ($cf = 1$).

EXAMPLE

Consequences for the economic weights and genetic gains were studied using a breeding goal for pigs as an example.

For simplicity, only two traits were included in the breeding goal: litter size born alive (LSBL) and growth rate in the fattening period (GR).

Used parameters for LSBL (pig litter⁻¹) were $h^2 = 0.15$, $\sigma_p = 2.9$, and economic value on a commercial level (expressed in Dutch guilders per slaughter pig) = 8.9. Used parameters for GR (g day⁻¹) were $h^2 = 0.25$, $\sigma_p = 88$, and economic value on a commercial level = 0.13. Only single stage selection of boars was studied. The selection index of boars contained information on own performance and data on litter size of their mothers. Selection intensity was equal to 1.

Equations (1), (2), (6) and (10) were used to calculate effects of competitive position on economic weights of the two traits for four alternative values of parameter cf . Parameter s was assumed to be 2.5 Dutch guilders per slaughter pig. For LSBL, this meant that the standard deviation of the distribution of acceptance levels was equal to 0.28 pig litter⁻¹ ($2.5/8.9$), while for GR it was equal to 19 g day⁻¹ ($2.5/0.13$).

Results for LSBL are in Figure 2. A similar graph was obtained for GR. With $cf = 0.5$ (degree of compensation is 50%), the economic weight of LSBL doubled for a brand with 0.6 pig litter⁻¹ lower LSBL than competitive brands. For growth rate, this point was at 42 g day⁻¹ lower growth rate. With $cf = 1$, the economic weights of the two traits were constant.

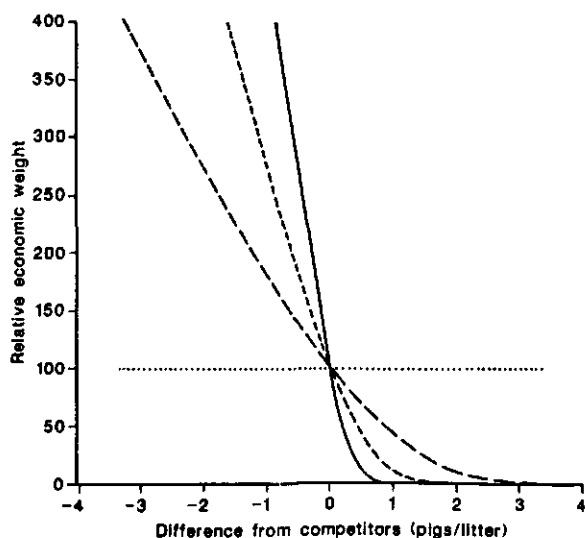


Figure 2. Relative economic weight of LSBL dependent on competitive position (— $cf=0$, - - - $cf=0.5$, - · - $cf=0.75$, $cf=1$).

- The following situation for the breeding stock in question was studied:
- level of LSBL 1 pig litter⁻¹ lower than the average level of competitors;
 - level of GR equal to the average level of competitors.

Economic weights of LSBL and GR for this competitive position were calculated for the four alternative values of cf (see Table 1). Genetic responses with optimal selection indices for these four sets of economic weights are given in Table 2. Comparing the responses in Table 2 for $r_g = 0$ with the last column of Table 1, it can be seen that the ratio of genetic gains changed in exactly the same way as the economic weight of LSBL. This is a specific property of a breeding goal with traits that are uncorrelated. Correlations between the four alternative indices are also in Table 2. Maximum loss in efficiency of selection was 22% (1-0.78) with $r_g = 0$. This occurred, when index 1 was used while index 4 was optimal or vice versa.

Table 2 also shows the effects of optimal indices when a genetic correlation of -0.1 or +0.1 between LSBL and GR was assumed. The ratio of genetic gains changed much more when the traits were negatively correlated. When the traits were positively correlated, the influence of economic weights on the ratio of gains was quite small. With $r_g = -0.1$, the maximum loss in efficiency was 34%. With $r_g = +0.1$, the maximum loss was 13%.

Table 1. Influence of degree of compensation (cf) on economic weight of LSBL (v_{LSBL}).

cf	Index	v_{LSBL}	v_{LSBL} ¹⁾
1	I1	8.9	1
0.75	I2	16.0	1.8
0.50	I3	24.3	2.7
0	I4	42.5	4.8

1) relative to the value of LSBL on a commercial level.

Table 2. Predicted correlated responses with alternative indices and correlations between alternative indices for three values of r_g .

Index	Responses of traits				Correlations between indices		
	LSBL	GR	LSBL/GR	LSBL/GR ¹⁾	I2	I3	I4
$r_g = 0$							
I1	0.122	18.2	0.0067	1	0.959	0.887	0.780
I2	0.168	14.0	0.0120	1.8		0.982	0.926
I3	0.191	10.5	0.0182	2.7			0.981
I4	0.208	6.5	0.0320	4.8			
$r_g = -0.1$							
I1	0.090	16.9	0.0053	1	0.928	0.810	0.656
I2	0.160	10.5	0.0152	2.9		0.970	0.890
I3	0.193	5.5	0.0351	6.6			0.974
I4	0.214	0.5	0.4280	80.4			
$r_g = +0.1$							
I1	0.160	19.2	0.0083	1	0.976	0.935	0.869
I2	0.190	16.4	0.0116	1.4		0.989	0.955
I3	0.205	14.1	0.0145	1.7			0.988
I4	0.217	11.4	0.0190	2.3			

1) relative to index I1.

DISCUSSION

The buying behaviour of breeding stock buyers was much simplified for the derivation of the method. For example, it was assumed that a client evaluates all brands that are available. In reality, an individual client may not be aware of all alternatives, and also some alternatives may not be feasible for him (Choffray and Lilien, 1978). For the prediction of market share, this needs to be considered. However, for the relative weights of traits, this is not relevant.

It was assumed that acceptance levels of traits are uncorrelated.

However, it is possible that clients with high requirements for trait 1 have (on average) low requirements for trait 2. With a numerical example, it was found that such a negative correlation results in a reduction of effects of competitive position on economic weights. Therefore, the influence of negative correlations between acceptance levels is comparable with the influence of the compensation factor in equation (7).

To derive equation (6), it was assumed that the price of the brand (x_{PR}) is equal to the mean acceptance level of clients (μ_{PR}). When x_{PR} is not equal to μ_{PR} , equation (5) and (6) have to be modified by using another value for z_{PR}/p_{PR} . However, such a modification will not affect the relative weights of genetic traits.

An important advantage of the described method is that correlations between traits are taken into account in an optimal way. With the desired gains method (Brascamp, 1984), it can happen that the desired combination of gains is difficult to realize because of a genetic correlation between the traits. An example with three different indexes may illustrate this. Suppose that the genetic correlation between LSBL and GR would be +0.5. When competitive position is neglected, use of an index results (for selection intensity = 1) in the following gains: 0.337 for LSBL and 21.5 for GR. When, because of competitive position (let $cf = 0$, see Table 1), the value of LSBL is multiplied by 4.8, selection responses with the resulting index are: 0.346 for LSBL and 20.4 for GR. For a desired gains index, the ratio of gains of LSBL and GR with the first index ($0.337/21.5$) is multiplied by 4.8 (to give the desired ratio of gains). The corresponding index gives a much lower selection response for both traits: 0.200 for LSBL and 2.6 for GR.

The parameters needed for the calculation of the economic weights with the presented method are e_i , cf , s , x_i and ac_i . The first three parameters are probably quite constant over time. Therefore, it is not necessary to estimate these parameters frequently. The opposite holds for x_i and ac_i . The difference between x_i and ac_i (competitive position) needs to be estimated frequently.

It was assumed that for each trait i the standard deviation of the distribution function of acceptance levels is equal to s/e_i . This assumption is justified as long as e_i is a good estimate of the value that clients give to the trait.

The compensation factor (cf) can be different between combinations of traits. For example, it is possible that a low GR can be easily compensated by a good feed conversion ratio (FCR), but very difficult by a high LSBL. In this situation, the economic weight of GR relative to FCR is not much influenced by the competitive position (i.e. v_{GR}/v_{FCR} almost equals e_{GR}/e_{FCR}), while the economic weights of GR and FCR relative to LSBL are much higher now than on a commercial level.

With the derivation of the method, it was assumed that differences between brands in performance levels of traits can be easily detected. However, for products like breeding stock, differences between brands may be underestimated. This can be taken into account by modification of equation (10).

$$t_i = e_i * (x_i - ac_i) * (1 - ue_i) * (1 - cf)/s$$

where ue_i = degree of underestimation of differences between brands for trait i.

When ue_i is equal for each trait, it affects the economic weights in the same way as the compensation factor (cf) does. When ue_i is different for each trait, equation (6) also needs to be modified.

$$v_i = e_i * (1 - ue_i) * (z_i/p_i) * \sqrt{(\pi/2)}$$

When competitive position for individual traits is taken into account, long-term selection response can be reduced. This is demonstrated in Figure 3. When short-term effects on saleability would be unimportant (e.g., one wants to maximize saleability after 10 years of selection), a good solution would be to ignore the competitive position and use a selection index based solely on the importance of traits on a commercial level (Figure 3, line 2). Competitors are expected to select also in this direction. However, short-term effects need to be considered, because a breeding organization also needs to have a saleable product in the short-term. Therefore, a compromise between the short-term and the long-term goal must be found.

For the total livestock industry, it would be optimal when clients, and thus also breeding organizations, would only look at total profitability of the stock. The compensation factor (cf) is then equal to 1, which means

that competitive position has no influence on the breeding goal. In this situation, long-term selection response would be highest (Figure 3).

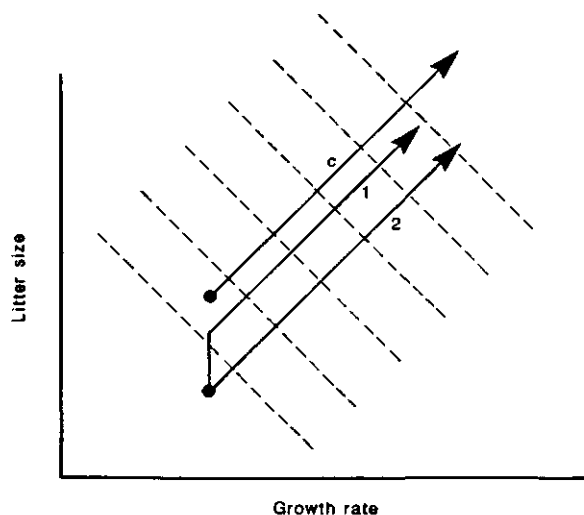


Figure 3. Long-term selection response with (line 1) and without (line 2) incorporation of competitive position in the breeding goal (dotted lines represent iso-profit contours on a commercial level; line c represents selection response of competitors).

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Chapter 3

OPTIMAL POPULATION SIZE AND SOW/BOAR RATIO IN A CLOSED DAM LINE OF PIGS

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ABSTRACT

The objective of this study was to optimize population size and sow/boar ratio in closed dam lines of pig breeding programmes. A stochastic simulation model was used to study changes in production and reproduction traits and inbreeding coefficient during 25 years of selection in lines with 50, 100, 200 and 400 sows combined with an annual number of 10, 15, 20, 25 and 40 boars. Number of boars used simultaneously was kept constant (3 or 6). Traits were assumed to be affected by many unlinked loci, each of small additive effect.

Selection of boars and gilts was on an overall index that combined estimated breeding values for reproduction and production traits. Breeding values for reproduction traits were estimated with a multi-trait animal model. To take all records and family relationships of at least three generations into account, all animals that were used for breeding during the previous 10 years were included in the mixed-model equations.

Increasing the number of sows had a large positive effect on selection response. An increase from 200 to 400 sows gave 11% more response. This might be high enough for most breeding organizations to offset the extra costs for sow and test places.

Variation in annual number of boars had a small influence on selection response, particularly in large populations. A high number of boars was needed to keep the rate of inbreeding acceptably low. Therefore, use of a high annual number of boars is recommended for dam lines.

1. INTRODUCTION

In most pig breeding programmes, a distinction is made between sire and dam lines. In sire lines, production traits are important. In dam lines, additional attention has to be given to reproduction traits. Although use of family information will increase response to selection for production traits (Belonsky and Kennedy, 1988), selection in sire lines can mainly be based on individual performance data. In dam lines, however, family information is very important, because of the low heritabilities of reproduction traits (Avalos and Smith, 1987).

Use of family information means that extra response can be achieved from

selection between families. The accuracy of selection between families depends on the size of the families. An increase in the number of sows (with a fixed number of boars) enlarges the size of paternal half-sib families, and thus increases the accuracy of selection for reproduction traits. Therefore, it is expected that the effect of an increased number of sows on response will be higher in dam lines than in sire lines.

Use of a small number of boars per year (with a fixed number of sows) means a high selection intensity and a high accuracy of selection (large families). However, use of family information can give a high correlation between indices of family members, which reduces selection intensity and response in situations with few paternal half-sib families (Hill, 1976, 1977a). Moreover, family information can contribute to an increased rate of inbreeding (Belonsky and Kennedy, 1988; Toro et al., 1988). Therefore, it is expected that in dam lines a higher annual number of boars is optimal than in sire lines.

De Roo (1987) developed a stochastic model to study breeding schemes in a closed pig population. He used the model to examine the effects of numbers of boars and sows on selection response and rate of inbreeding in a sire line (De Roo, 1988a).

The objective of this study is to optimize population size and sow/boar ratio in a closed dam line of pigs. In this paper adaptations of the model of De Roo (1987, 1988a) to a dam line are described. Effects of numbers of sows and boars on genetic response and inbreeding coefficient are studied with the adapted model. Results for a dam line are compared with the results for a sire line (De Roo, 1988a).

2. MATERIAL AND METHODS

2.1. General concepts

The model of De Roo (1987, 1988a) evaluated changes in production and reproduction traits and inbreeding coefficient over 25 years of selection in a closed swine herd. The model included overlapping generations, daily mating and farrowing and weekly selection of boars and sows. Week was the unit of time.

Breeding values were generated as

$$A_i = 0.5 \times A_j + 0.5 \times A_k + \sqrt{(0.5 \times CF) \times a \times \sigma_A} \quad (1)$$

$$\text{and } CF = 1 - 0.5 \times (F_j + F_k) \quad (2)$$

where A_i , A_j , A_k are breeding values of individual i , its sire j and its dam k ;

CF is a correction factor that accounts for the expected reduction in additive genetic variance when parents have inbreeding coefficients F_j and F_k (Thompson, 1977);

a is a random normal deviate; and

σ_A is the additive genetic standard deviation in the base population.

Inbreeding can have an effect on the additive genetic variance, and on the performance of traits subject to dominance (Falconer, 1981). De Roo (1988b) showed that a reduction in litter size due to inbreeding depression had a limited effect on selection intensity (and thus on additive genetic response), when number of boars tested per litter was restricted to two. Therefore, inbreeding depression was not included and a strictly additive model was assumed.

Phenotypes were simulated as

$$P_i = B + A_i + e \times \sigma_E \quad (3)$$

where P_i is the phenotypic value of individual i ;

B is the mean of the base population;

e is a random normal deviate; and

σ_E is the environmental standard deviation.

2.2. Reproduction traits

Litter size at birth (i.e. total number of piglets born per litter) was determined by ovulation rate (OR) and percentage of prenatal survival (PS) (De Roo, 1988a). PS depended on the phenotypic value of OR:

$$PS = 100\% \times OR_{50\%} / (OR + OR_{50\%}) \quad (4)$$

where $OR_{50\%}$ is the number of ovulations at which 50% of the embryo's survive. Mean values of OR for first to fifth parity were 14.0, 15.1, 16.3, 17.0 and 17.0.; values of $OR_{50\%}$ were 34.27, 36.97, 38.95, 40.63 and 40.63 (De Roo, 1988a). A minimum number of 4 ovulations was assumed necessary to establish pregnancy.

A value of 0.5 was used for the genetic correlation of ovulation rate (OR) in first parity with OR in later parities, corresponding to parameters for litter size (Knap, 1986).

De Roo (1988a) assumed no environmental correlations (r_E) between OR in different parities. However, a separate stochastic model, where 20,000 sows with three parities were simulated (De Vries, 1987, unpublished data), showed that the resulting repeatabilities for litter size at birth did not correspond to the literature values of Knap (1986). To obtain the proper repeatabilities, a value of 0.1 was required for r_E between OR in first parity and OR in later parities and a value of 0.2 for r_E between OR in later parities.

Mortality rate of piglets during the suckling period has a low heritability (Knap, 1986). Age at first oestrus and interval from weaning to oestrus have low economic values (Knap, 1986; De Vries, 1989). Therefore, only litter size at birth was included in the breeding goal for reproduction traits.

Litter size at birth was considered as two traits, size of the first litter (LSB1) and average size of later litters (LSB2); the genetic correlation between these two traits is less than one (Knap, 1986; Vangen, 1986). Relative weights of LSB1 and LSB2 in the breeding goal for reproduction traits (H_{repr}) were taken from De Vries (1989). For the derivation of these weights, it was assumed that first parity sows produce 20% of the litters at commercial farms.

$$H_{repr} = 1.8 \times A_{LSB1} + 7.1 \times A_{LSB2} \quad (5)$$

where A_i is the breeding values for trait i .

In principle, new breeding values should be estimated after each farrowing, because each recorded litter can increase the accuracy of selection for litter size. Under practical conditions this will not be

done, because the calculation procedure requires considerable computer time. In the simulation model breeding values for LSB1 and LSB2 were estimated every 4 weeks. Information of the last litter of a sow was therefore always included in the estimated breeding value when this sow had to be selected at time of weaning or when her progeny had to be selected to go on test.

Breeding values for litter size (LSB1 and LSB2) were estimated using a linear multi-trait animal model:

$$y_{ijk} = \mu_i + a_{ij} + p_j + e_{ijk} \quad (6)$$

where y_{ijk} is an observation of trait i on animal j in parity k ;

μ_i is the mean of trait i ;

a_{ij} is the breeding value of animal j for trait i ;

p_j is the permanent environmental effect for animal j ; and

e_{ijk} is the temporary environmental effect for trait i for animal j in parity k .

Herd-year-season effects were not included in the model, because in the simulation all animals belonged to one herd and it was assumed that year-season effects for litter size are of minor importance. Permanent and temporary environmental effects could be separated for LSB2, but were confounded for LSB1. Size of the second to the fifth litter were considered as repeated records of LSB2. Third to fifth litters were corrected to the level of the second litter according to the parity differences given by De Roo (1987) (third litter: +0.8 piglet; fourth and fifth litter: +1.3 piglet).

To estimate the breeding values (a_{ij}), the following equations were used (Henderson, 1975):

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'R^{-1}Y \\ Z'R^{-1}Y \end{bmatrix} \quad (7)$$

where Y is a vector with observations on litter size;

X is a design matrix for fixed effects;

Z is a design matrix for random effects;

R is a variance-covariance matrix for error terms;

D is a variance-covariance matrix for breeding values;

$\hat{\mu}$ is a vector with solutions for mean of LSB1 and mean of LSB2; and

\hat{a} is a vector with solutions for breeding values.

The D^{-1} matrix is equal to the direct product of the inverse of the relationship matrix (A^{-1} matrix) and the G^{-1} matrix. The G matrix is the additive genetic variance-covariance matrix for LSB1 and LSB2. The G and R matrices were set up with the parameters in Table 1. Permanent environmental effects were absorbed in the equations. The A^{-1} matrix was computed using the method of Henderson for inbred populations (1976).

Table 1. Parameters for estimation of breeding values for size of the first litter (LSB1) and size of 2nd and later litters (LSB2) (Knap, 1986; De Roo, 1987).

Phenotypic variance of LSB1 and LSB2	8.1
Heritability of LSB1 and LSB2	0.1
Phenotypic correlation between LSB1 and LSB2	0.1
Genetic correlation between LSB1 and LSB2	0.5
Repeatability of LSB2	0.2

Solutions for the mixed-model equations were derived by iteration on the data (Schaeffer and Kennedy, 1986). The method was modified to avoid the construction of pedigree files (Appendix). Successive overrelaxation together with block iteration was applied (Van Vleck and Dwyer, 1984; Misztal and Gianola, 1987). The iterative procedure was stopped, when the average quadratic change in animal solutions for the weighted sum of LSB1 and LSB2 was less than 10^{-4} . Weighting factors for LSB1 and LSB2 were equal to their relative economic values shown in equation (5) (LSB1: $1.8/(1.8+7.1)$; LSB2: $7.1/(1.8+7.1)$). With this criterion for convergence, the stop criterion relative to the variance in indexes (also including production traits) was less than 10^{-3} . Solutions from the previous iteration (4 weeks earlier) were taken as prior values for the first round of iteration. A relaxation factor of 1.4 was used.

Sows could have a maximum of five litters and boars were used for breeding from 8 to 12 months of age. Sows were three years old at birth of their fifth litter. To take all records and family relationships of at least three generations into account, all animals that were used in the breeding herd during the last 10 years were included in the breeding value analysis.

Reproduction indexes (I_{repr}) for selection candidates were calculated using the most recent estimated breeding values for litter size. Weighting factors for LSB1 and LSB2 were according to equation (5).

2.3. Production traits

Production traits in the breeding goal were daily growth rate, daily feed intake and lean percentage in the carcass. Differences in expression at a commercial level make improvement of reproduction traits in a dam line twice as important as improvement of production traits (Smith, 1964). Therefore, weights of production traits in the breeding goal, adopted from De Roo (1988a) for a sire line, were reduced by 50% relative to reproduction traits. Corresponding with this, the weighting factors for production traits in the index combining production and reproduction traits could also be reduced by 50%, as the genetic and phenotypic correlations between production and reproduction traits were assumed to be zero (Brien, 1986).

$$H_{prod} = 0.5 \times (0.178 \times A_{GR} - 0.05 \times A_{FI} + 3.0 \times A_{LEAN}) \quad (8)$$

$$I_{prod;boars} = 0.5 \times (0.0212 \times P_{GR} - 0.0004 \times P_{FI} + 1.5548 \times P_{LEAN}) \quad (9)$$

$$I_{prod;gilts} = 0.5 \times (0.0357 \times P_{GR} - 2.5965 \times P_{SF}) \quad (10)$$

where A_i and P_i are breeding values and phenotypic values for trait i ;

GR is the growth rate from 23 to 100 kg ($g \text{ day}^{-1}$);

FI is the feed intake ($g \text{ day}^{-1}$);

LEAN is the (estimated) lean percentage in carcass; and

SF is the side fat thickness (mm).

Potential breeding animals were performance tested. Boars were fed ad libitum, but gilts were kept on a restricted diet. To make comparisons

possible with the results for the sire line in the study of De Roo (1988a), only individual performance data were used in the production index. Variables in equation (9) and (10) were deviations from batch means (not corrected for genetic trend). Genetic and phenotypic parameters of production traits are in Table 2.

Lean percentage in boars was assumed to be estimated on live animals by means of modern equipment. Breeding values for lean percentage were assumed to be normally distributed. Phenotypes were expressed on a scale with a minimum of 35 and a maximum of 75 percent (De Roo, 1987).

Table 2. Genetic and phenotypic parameters of production traits in the base population.

Trait	Mean	h ²	σ _P	Correlations ¹⁾				
				Boars			Gilts	
				GR	FI	LEAN	GR	SF
Boars								
growth rate (GR, g day ⁻¹)	900	.25	88	1.00	.85	-.15	1.00	.00
feed intake (FI, g day ⁻¹)	2,400	.25	200	.65	1.00	-.35	.85	.40
lean percentage (LEAN)	52	.45	2.5	-.10	-.30	1.00	-.15	-.40
Gilts								
growth rate (GR, g day ⁻¹)	785	.20	42	n.r. ²⁾	n.r.	n.r.	1.00	.00
side fat thickness (SF, mm)	12.2	.30	0.9	n.r.	n.r.	n.r.	.10	1.00

1) Upper triangle: genetic correlations, lower triangle: phenotypic correlations.

2) Not relevant.

2.4. Selection

In dam lines, selection of young boars on pedigree index for litter size before the start of the performance test can reduce costs for testing. Testing of boars is expensive, because measurements of individual feed intake require individual housing. It was expected that 50% selection in the first stage (before the test) together with intensive selection on

production and reproduction traits in the second stage (after the test) would give almost the same response as selection among all animals after the test. To obtain about 50% first stage selection, only boars were tested that had a reproduction index higher than the average genetic level of the population. This genetic level was calculated every four weeks as the average reproduction index of sows that had a litter in the previous 16 weeks. Boars were two months old when first stage selection took place. Selection before the test (on pedigree index) was not considered for gilts, because testing of gilts in groups is not expensive. Moreover, a large number of tested gilts can be used for sub-nucleus purposes.

At sexual maturity, gilts entered the pool of replacement gilts. Each week a number of sows was selected for breeding. These sows came from the group of sows weaned in the previous week or from the pool of replacement gilts. The replacement gilts had to compete with the sows for a place in the breeding herd (sequential culling). An overall index was used as the selection criterion, combining the reproduction index (index weights according to equation 5) with the production index (equations 9 and 10):

$$I_{\text{overall}} = I_{\text{repr}} + I_{\text{prod}} \quad (11)$$

Selection of young breeding animals was considered as a multi-stage process. At the end of the test some animals were culled for conformation and a relatively mild selection on production index was performed (Table 3). At sexual maturity, another number of animals was culled for conformation. In addition, some boars were culled because of poor reproductive performance (semen quality). Culling chances for poor conformation or reproductive performance were independent of production and reproduction traits. For each sex, the animals with the highest overall indexes (equation 11) among the remaining boars or sows were ultimately selected for breeding.

2.5. Parameters

Most of the parameters were adopted from De Roo (1988a). Part of the characteristics of the line under study are in Table 3. It was assumed that 67 percent of sows that entered the breeding piggyery farrowed. Probabili-

ties that sows were culled at weaning for conformation or health problems were 10.0, 7.0, 7.5 and 10.0 percent for first, second, third, and fourth parity (De Roo, 1988a). This culling was independent of sow's performance for (re)production traits.

Table 3. General characteristics of nucleus breeding scheme.

General

maximum number of parities per sow	5
length of suckling period (weeks)	4.5
number of boars used simultaneously	3 ¹⁾
size of pool of replacement boars	4 ¹⁾
maximum relationship of partners at mating	0.125

Performance test

minimum start growth rate (0 - 23 kg, g day ⁻¹)	300
maximum number of boars tested per litter	2
maximum number of gilts tested per litter	6
total number of test places in a division	50 ²⁾
minimum production index at end of test, boars	-0.5 ³⁾
minimum production index at end of test, gilts	-1.0 ³⁾
percentage of boars culled for conformation	40
percentage of gilts culled for conformation	20

Sexual maturity

percentage of boars culled for reproduction	
(semen quality) or conformation	40
percentage of gilts culled for conformation	20

- 1) For alternatives with 40 boars per year, 6 boars were used simultaneously and the pool of replacement boars was enlarged to 8 boars.
- 2) For 200 and 400 sows, group size for gilts was enlarged to 80 and 160 places respectively. For 400 sows, group size for boars was enlarged to 80 places.
- 3) Expressed in standard deviations of production index.

Mating of close relatives was avoided; maximum inbreeding coefficient of potential offspring was 0.125. If no potential mates met this requirement, least related animals were mated.

2.6. Alternatives

De Roo (1988a) studied sire line populations of 25, 50, 100 and 150 sows combined with 5, 10, 15 and 20 boars per year. An annual number of 15 boars was optimal for populations of 100 or 150 sows. Selection response in a population of 150 sows (combined with 15 boars) was 13% higher than in a population of 100 sows.

Optimal number of sows and boars for dam lines was expected to be larger than for sire lines, so that combinations of 50, 100, 200 and 400 sows (referring to number of sow places available in the nucleus) with 10, 15, 20, 25 and 40 boars per year were examined. Three boars were used simultaneously for alternatives with 10 to 25 boars per year and six boars were used simultaneously for alternatives with 40 boars per year (Table 3). Five replicates were made for alternatives with 400 sows and 10 replicates for the other alternatives.

Founder population sizes were equal to nucleus population sizes. Founder animals were selected from a large base population. Production indices of founder sows were better than average in the population, and founder boars were at least one standard deviation better than average in production index.

3. RESULTS AND DISCUSSION

3.1. Selection response

Responses to selection for production and reproduction traits were expressed in Dfl. using the economic weights of equations (5) and (8). Values of the response in year 25, averaged over replicates, are given in Table 4. The alternative of 400 sows with an annual number of 40 boars might be used to illustrate the changes in individual traits. Accuracy of the reproduction index in this alternative (averaged over years 3 to 25) was equal to 0.25. After 25 years of selection, ORI (ovulation rate of

first parity sows) was raised from 14.0 to 22.9 ovulations, while OR2 was raised from 15.1 to 25.2 ovulations. This improved LSB1 by 3.9 pigs and LSB2 by 4.3 pigs. The response for production traits in this alternative corresponded to an improvement of 126 g day⁻¹ in growth rate and 10.7% in lean content, while change in feed intake was negligible.

Table 4. Cumulative responses up to year 25 for production (PROD) and reproduction traits (REPR) (response in Dfl.).

Alter- native ¹⁾	PROD	REPR	Alter- native ¹⁾	PROD	REPR
50/10	18.48 ±0.53 ²⁾	23.65 ±1.40	200/10	25.72 ±0.84	30.19 ±1.48
50/15	18.81 ±0.50	23.35 ±0.97	200/15	25.98 ±0.70	33.99 ±1.21
50/20	17.08 ±1.05	24.06 ±1.44	200/20	24.85 ±0.59	33.71 ±0.71
50/25	17.70 ±0.58	24.13 ±1.18	200/25	24.94 ±0.26	31.82 ±1.06
50/40	16.94 ±0.50	23.19 ±0.95	200/40	22.59 ±0.46	32.53 ±0.65
100/10	23.20 ±0.69	29.29 ±1.24	400/10	27.19 ±0.92	32.22 ±1.59
100/15	21.88 ±0.56	27.94 ±0.79	400/15	29.21 ±0.87	36.98 ±0.53
100/20	22.51 ±0.59	27.19 ±0.64	400/20	28.27 ±0.68	34.69 ±1.83
100/25	20.70 ±0.76	29.12 ±0.69	400/25	30.15 ±0.73	34.47 ±2.08
100/40	17.90 ±0.47	28.45 ±0.72	400/40	27.26 ±0.20	38.11 ±0.56

1) Number of sows/annual number of boars.

2) Standard error.

Overall response was calculated as the sum of response for production and reproduction traits. Curves of the overall response for each alternative are given in Figure 1. To quantify the characteristics of the response curves an exponential curve was fitted to the cumulative response (R_{cum}) for each replicate (De Roo, 1988a):

$$R_{cum} = R_{init} \times (YEAR - INTCP) \times \exp(-BEND \times (YEAR - INTCP)) \quad (12)$$

where R_{init} is the initial response per year, BEND represents the change

in response as time proceeds and $INTCPT$ is the intercept of the curve on the x-axis. $INTCPT$ was calculated from data of year 3 to year 10 by linear extrapolation. Replicate means of estimated parameters are in Table 5. The values for $BEND$ can be used to calculate relative deviations from a linear increase: $(1 - \exp(-BEND \times (YEAR - INTCPT)))$. For example, the relative deviation in the alternative with 50 sows and 10 boars was in year 25 equal to $(1 - \exp(-.0084 \times (25 - 0.29))) = 19\%$.

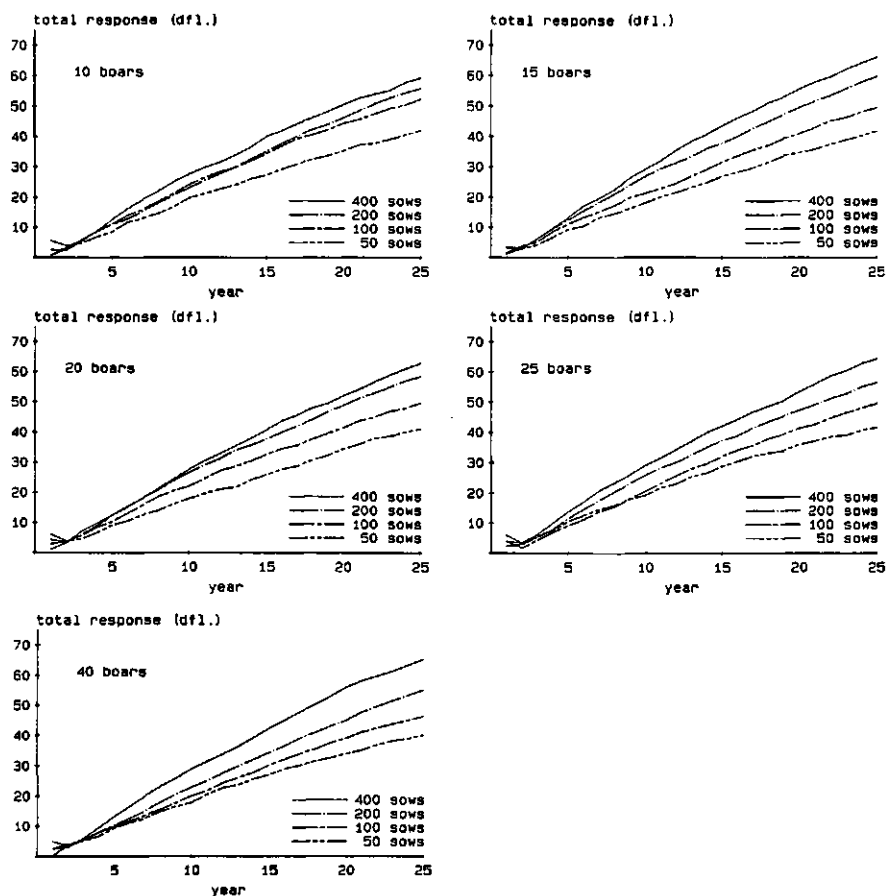


Figure 1. Effects of variation in size of the sow herd on progress of overall selection response over time for different numbers of boars used per year.

Table 5. Characteristics of overall response curves: intercepts of curves on x-axis (INTCPT), initial responses per year (R_{init}), deviations from linearity (BEND) and cumulative responses up to year 25 (R_{cum}) (response in Dfl.).

Alter-native ¹⁾	INTCPT	R_{init}	BEND	R_{cum}
50/10	0.29	2.11	.0084 \pm .0029 ²⁾	42.13 \pm 1.57
50/15	0.23	1.96	.0061 \pm .0043	42.17 \pm 0.96
50/20	0.12	1.87	.0056 \pm .0042	41.14 \pm 1.50
50/25	-0.59	2.03	.0086 \pm .0042	41.84 \pm 1.05
50/40	-0.02	2.00	.0081 \pm .0032	40.14 \pm 0.98
100/10	0.64	2.74	.0098 \pm .0017	52.48 \pm 1.46
100/15	0.03	2.30	.0059 \pm .0034	49.81 \pm 0.84
100/20	0.48	2.58	.0098 \pm .0013	49.70 \pm 0.98
100/25	0.90	2.36	.0046 \pm .0027	49.82 \pm 0.78
100/40	-0.18	2.01	.0025 \pm .0032	46.35 \pm 0.86
200/10	0.38	2.37	.0008 \pm .0037	55.92 \pm 1.45
200/15	0.75	3.14	.0101 \pm .0018	59.98 \pm 1.53
200/20	0.77	3.13	.0109 \pm .0028	58.56 \pm 0.71
200/25	1.13	3.20	.0127 \pm .0024	56.76 \pm 0.84
200/40	0.77	2.56	.0045 \pm .0023	55.12 \pm 0.69
400/10	0.96	3.41	.0137 \pm .0041	59.41 \pm 1.68
400/15	0.97	3.54	.0099 \pm .0025	66.19 \pm 1.14
400/20	0.63	3.05	.0063 \pm .0025	62.96 \pm 1.81
400/25	0.81	3.52	.0118 \pm .0021	64.62 \pm 1.61
400/40	0.95	3.49	.0101 \pm .0008	65.37 \pm 0.70

1) Number of sows/annual number of boars.

2) Standard error.

The differences in response between boar alternatives for production and reproduction traits were small (Table 4). The advantage of increased selection intensity with a low annual number of boars appeared to be offset by the disadvantage of a small number of half-sib families. With fewer boars, indices of selection candidates were more correlated, which reduced response to selection (Hill, 1976, 1977a). For populations with 50 and 100 sows, 10 boars per year gave a good overall response compared to the other boar alternatives (Table 5). For populations with 200 and 400 sows, a higher number of boars appeared to give a higher response.

Increasing the number of sows gave a large improvement in overall response, which was a result of increased selection intensity of males. It also raised the accuracy of the reproduction index (and thus its variance), due to the higher number of daughters per boar. When number of sows increased from 50 to 400 sows, the variance in reproduction index between boars at the end of test increased by 52% (averaged over year 3 to 25).

For reproduction traits, a larger increase in response with increased number of sows was expected than for production traits, because the production index only contained individual performance data, and thus its accuracy was not influenced by the number of daughters per boar. However, the increase in response in year 25 for both groups of traits was of the same order. This can be partly explained by the effects of correlations between indexes on selection intensity. With larger families, accuracy of selection is higher, but correlations between reproduction indexes of family members are also higher, which reduces selection intensity (Hill, 1976, 1977a). A second explanation for the reduced impact of population size on response for reproduction traits was the way litter size was modelled. With selection for this trait, ovulation rate (OR) is raised, while prenatal survival (PS) is reduced. At a higher level, further genetic improvement of OR has a smaller effect on litter size. Moreover, the variation in PS between litters is higher, which reduces the heritability of litter size because the variation in PS has no genetic component. Lean percentage also has a biological limit in the model, but growth rate can continue to improve. Therefore, the response for reproduction traits is more curvilinear than the response for production traits. This was confirmed when exponential response curves (equation 12) were fitted to cumulative responses of production and reproduction traits. Estimated

values of BEND are given in Table 6. Averaged over boar alternatives, BEND for production traits in lines with 400 sows was equal to 0.0029, which indicates a 7% deviation in year 25 from a linear increase. BEND for reproduction traits in lines with 400 sows was equal to 0.0156, corresponding to a 32% deviation from a linear increase.

Table 6. Deviations from linearity (BEND) for response of production traits (PROD) and for response of reproduction traits (REPR).

Alter- native ¹⁾	PROD	REPR	Alter- native ¹⁾	PROD	REPR
50/10	.0054 ± .0056	.0068 ± .0074	200/10	.0039 ± .0020	-.0056 ± .0079
50/15	.0004 ± .0047	.0078 ± .0060	200/15	.0070 ± .0020	.0113 ± .0035
50/20	-.0059 ± .0052	.0104 ± .0056	200/20	.0032 ± .0018	.0150 ± .0046
50/25	.0044 ± .0044	.0088 ± .0080	200/25	.0050 ± .0022	.0175 ± .0032
50/40	.0060 ± .0051	.0093 ± .0042	200/40	-.0043 ± .0040	.0091 ± .0030
100/10	.0005 ± .0034	.0154 ± .0026	400/10	.0054 ± .0028	.0202 ± .0059
100/15	-.0033 ± .0029	.0114 ± .0047	400/15	.0056 ± .0034	.0122 ± .0046
100/20	.0041 ± .0030	.0133 ± .0018	400/20	-.0003 ± .0019	.0111 ± .0038
100/25	-.0042 ± .0052	.0080 ± .0046	400/25	.0020 ± .0011	.0194 ± .0030
100/40	.0007 ± .0043	.0031 ± .0036	400/40	.0019 ± .0018	.0152 ± .0012

1) Number of sows/annual number of boars.

2) Standard error.

An increase from 50 to 400 sows gave 71% extra initial overall response (R_{init}) and 54% extra cumulative overall response in year 25 (R_{cum}), when averaged over boar alternatives (Table 5). Enlarging the sow herd is relatively more important for the short-term than for the long-term.

To describe cumulative overall response as a function of number of sows and annual number of boars, several statistical models were fitted to the values of R_{cum} in Table 5. Differences between alternatives in cumulative response are mainly a result of differences in selection intensity of males (i_m) and number of paternal half-sib families. Therefore, i_m and annual

number of boars (n) were used as covariables. Values of the proportion of males selected were calculated assuming 4 boars available for selection per sow per year and accounting for a 40% culling rate of boars after the test (conformation) and a 40% culling rate at sexual maturity (semen quality, conformation). Corresponding values of i_m were derived from tables for infinite populations (Becker, 1975). The population of 50 sows with 40 boars per year was not included in the analysis, because realized annual number of boars was lower than intended. The best fit was found with the following linear model ($\sigma_e^2 = 2.39$; $R^2 = 0.970$):

$$R_{cum} = b_0 + b_1 \times i_m + b_2 \times 1/\sqrt{n} \quad (13)$$

Parameter b_0 can be considered as the result of selection of females. The second term of the equation ($b_1 \times i_m$) represents the results of selection of males. The last term represents the reduction in selection response due to finite population size. This reduction is due to reduced selection intensity (small number of families) and to reduced genetic variance (inbreeding). Estimates for parameters b_0 , b_1 and b_2 were 33.63 ± 1.93 , 22.73 ± 1.00 and -86.76 ± 7.55 . Fitted responses with these parameters are in Figure 2 for populations with 10, 20 and 40 boars per year. The curves

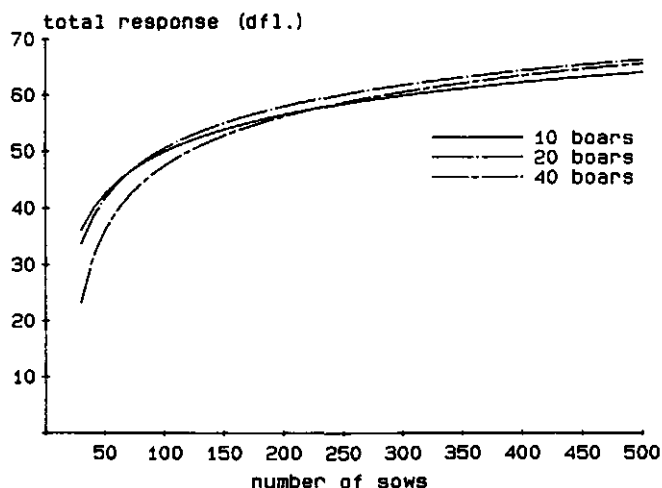


Figure 2. Cumulative overall response in year 25 as a function of number of sows and number of boars used per year.

show that with increasing numbers of sows, differences between boar alternatives decrease and annual number of boars giving maximum response increases.

3.2. Inbreeding coefficient

Changes in average inbreeding coefficient for each alternative is given in Figure 3. Rate of inbreeding depended mainly on annual number of boars.

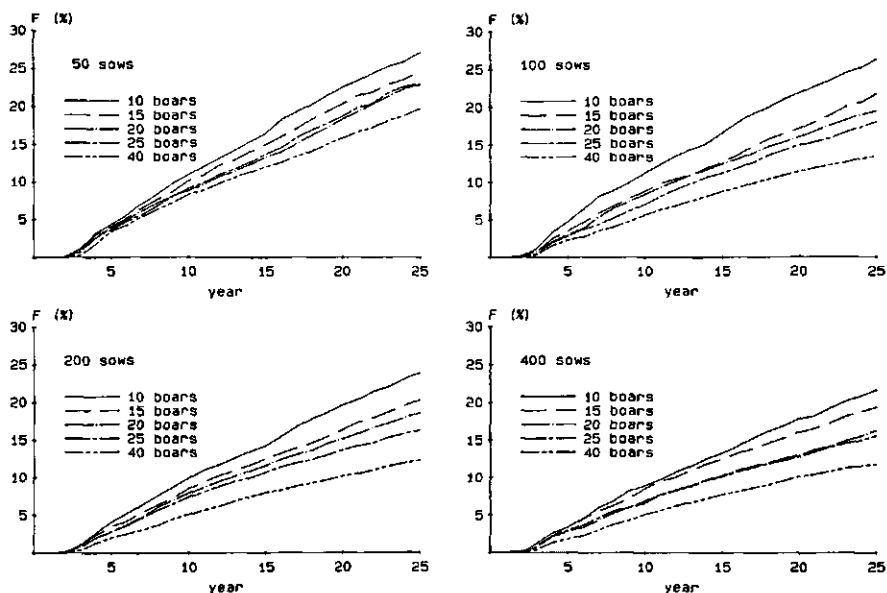


Figure 3. Change of inbreeding coefficient (F) over time as a function of number of sows and number of boars used per year.

Realized values of the yearly relative increase of F (ΔF_r) were calculated from Falconer (1981):

$$\Delta F_r = (F_t - F_{t-1}) / (1 - F_{t-1}) \quad (14)$$

where F_t is average inbreeding coefficient of pigs tested in year t.

Expected yearly relative increases of F were calculated according to Hill (1972):

$$\Delta F_e = (1/N_m + 1/N_f) / (8 \times L^2) \quad (15)$$

where N_m and N_f are numbers of males and females used for breeding during a year; and

L is the length of generation interval in years.

For each alternative, yearly increase in F was much higher than expected (Table 7). The relative differences were largest for alternatives with a high number of boars. The high increase of F is due to the use of the family information in the reproduction index. For selection of young boars and gilts, litter records of the mother and records of full-sibs and half-sibs of the parents were used, which led to unequal contributions of sires

Table 7. Inbreeding coefficients (F) in year 25, and expected (ΔF_e) and realized (ΔF_r) yearly relative increases in F.

Alter- native ¹⁾	F	ΔF_e	ΔF_r	Alter- native ¹⁾	F	ΔF_e	ΔF_r
50/10	27.3 ± 0.6 ²⁾	0.91	1.38	200/10	23.9 ± 0.5	0.80	1.18
50/15	24.8 ± 0.5	0.68	1.25	200/15	20.3 ± 0.6	0.57	0.98
50/20	23.0 ± 1.0	0.55	1.14	200/20	18.6 ± 0.4	0.45	0.89
50/25	23.1 ± 0.8	0.47	1.15	200/25	16.3 ± 0.4	0.37	0.76
50/40	19.8 ± 0.4	0.33	0.98	200/40	12.3 ± 0.2	0.24	0.58
100/10	26.1 ± 0.5	0.84	1.31	400/10	21.6 ± 0.7	0.77	1.05
100/15	21.5 ± 0.3	0.61	1.06	400/15	19.3 ± 0.5	0.54	0.93
100/20	19.3 ± 0.3	0.49	0.93	400/20	16.2 ± 0.3	0.43	0.77
100/25	17.9 ± 0.6	0.41	0.87	400/25	15.5 ± 0.7	0.35	0.73
100/40	13.3 ± 0.3	0.27	0.63	400/40	11.7 ± 0.3	0.22	0.55

1) Number of sows/annual number of boars.

2) Standard error.

and dams to subsequent generations. A large variation in family size reduces the effective population size (Robertson, 1961).

In alternatives with a small number of sows, a dam with a high reproduction index could have a large contribution to subsequent generations, because she was allowed to produce many litters, and because her progeny had a higher chance of being selected. Although not more than two boars per litter could be selected (Table 3), one dam could produce 10 selected boars, because she was allowed to have five litters.

3.3. Between line variance

The standard error of the response in year 25 (Table 5) can be multiplied by the square root of number of replicates to give the standard deviation of the response. For each alternative, drift variance was high because of the small effective population sizes. When number of observations included in the mean is large, error variance due to sampling can be ignored and expected variances of means can be calculated as (Hill, 1977b; Sorensen and Kennedy, 1983):

$$V_{P_t} = 2 \times F_{t+1} \times V_{A_0} \quad (16)$$

where V_{P_t} is the variance of means at year t ;

F_{t+1} is the average inbreeding coefficient at year $t+1$; and

V_{A_0} is the additive genetic variance in the base population.

Expected and realized standard deviations of means are in Table 8. Realized values were averaged over years 23 to 25. Realized drift variance was lower than expected, especially for reproduction traits. This can be explained by the biological limits for lean percentage and litter size.

3.4. General discussion

The results in Table 4 show that response for reproduction traits was higher than response for production traits. This can also be expected with a deterministic approach, when it is assumed that each female brings two litters and that the index consists of information on the dam, 2 full-sibs and 7 half-sibs of the dam, and 3 full-sibs and 7 half-sibs of the sire

Table 8. Expected (sd_e) and realized (sd_r) standard deviations of replicate means of response (averaged over years 23 to 25) for production traits (PROD), reproduction traits (REPR) and overall response (OVERALL).

Alter-native ¹⁾	PROD		REPR		OVERALL		Alter-native ¹⁾	PROD		REPR		OVERALL	
	sd_e	sd_r	sd_e	sd_r	sd_e	sd_r		sd_e	sd_r	sd_e	sd_r	sd_e	sd_r
50/10	2.6	2.0	5.4	4.7	6.0	4.8	200/10	2.5	2.7	5.1	4.7	5.6	4.5
50/15	2.5	1.3	5.2	2.9	5.8	2.9	200/15	2.3	2.1	4.7	3.6	5.2	4.6
50/20	2.4	3.1	5.0	4.4	5.5	5.0	200/20	2.2	1.8	4.5	2.3	5.0	2.1
50/25	2.4	2.0	5.0	3.8	5.6	3.6	200/25	2.0	0.8	4.2	3.3	4.7	2.8
50/40	2.2	1.6	4.6	3.1	5.1	3.1	200/40	1.8	1.4	3.6	2.0	4.1	2.1
100/10	2.6	2.3	5.3	4.0	5.9	5.1	400/10	2.3	2.2	4.8	3.5	5.4	3.8
100/15	2.3	1.7	4.8	2.4	5.4	2.5	400/15	2.2	1.9	4.6	1.4	5.1	2.4
100/20	2.2	1.6	4.6	2.2	5.1	3.2	400/20	2.0	1.6	4.2	4.3	4.6	4.1
100/25	2.1	2.2	4.4	2.3	4.9	2.3	400/25	2.0	1.6	4.1	4.6	4.5	3.7
100/40	1.8	1.4	3.8	2.4	4.2	2.6	400/40	1.7	0.8	3.6	1.8	4.0	2.3

1) Number of sows/annual number of boars.

(Avalos and Smith, 1987). From the parameters in Table 1 and 2 and the weighting factors in the breeding goal (equations 5 and 8) it can then be derived that the standard deviation of the reproduction index is Dfl. 2.06. This is about equal to the standard deviation of the production index for boars (Dfl. 2.07), but higher than the production index of gilts (Dfl. 1.33).

A comparison of the overall responses in year 25 (Table 5) with the results of the sire line of De Roo (1988a) demonstrates the high benefits of inclusion of reproduction traits in the breeding goal for dam lines. Selection on reproduction traits made first stage selection of young boars before the performance test possible (50% reduction of testing costs for boars), and it increased overall responses. For example, for the alternative of 100 sows with 15 boars, overall response was Dfl. 49.81. When

selection would have been only for production traits, response would have been $0.5 \times \text{Dfl. } 66.13 = \text{Dfl. } 33.07$ (De Roo, 1988a). It is important to realize that the relatively low response for production traits is partly due to the simplicity of the production index (e.g. no use of family information).

Effects of population size and sow/boar ratio on selection response probably depend on the proportion of first stage selection of boars (before test) and on the number of boars tested per litter. With a higher proportion of boars tested, effects of population size are expected to be somewhat smaller, because first stage selection (compared to selection of all animals after the test) gives a larger reduction in response in small populations where selection intensity after the test is low. This also holds for the number of boars tested per litter, because with a higher number tested per litter, effects of population size on selection intensity are smaller.

Averaged over boar alternatives, an increase from 50 to 100 sows gave 20% more response. The same increase in a sire line (De Roo, 1988a) gave 17% greater response. This means that the relative effect of population size on response is not much higher in dam lines than in sire lines. However, because of the possibilities of selection before the performance test, costs for increasing the sow herd are lower for dam lines. Therefore, optimal population size is larger for dam lines than for sire lines.

Optimal number of sows depends on the value of extra genetic improvement for the breeding organization relative to the costs for extra sow and test places. Averaged over boar alternatives, an increase from 200 to 400 sows gave 11% more response (Table 5). This might be high enough for most breeding organizations to offset the extra costs.

As expected (Belonsky and Kennedy, 1988; Toro et al., 1988) the use of family information for selection on reproduction traits resulted in a higher rate of inbreeding. For example, for 100 sows and 15 boars per year, average F was 21.5% in year 25. De Roo (1988a) found a value of 12.9% for this alternative for the sire line. To keep the rate of inbreeding at the same level, annual number of boars in a dam line should be much larger than in a sire line. Figure 2 showed that an increase from 20 to 40 boars resulted in a very small reduction in response, when population size was large. Therefore, use of a high annual number of boars can be recommended

for dam lines.

ACKNOWLEDGEMENT

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APPENDIX

Schaeffer and Kennedy (1986) described an efficient iterative procedure for solving mixed model equations of large order. Before the iteration could start, a coded pedigree file had to be created and sorted. For each animal the file had to contain a row to identify its pedigree (sire and dam in an animal model) and rows to identify its offspring and mates. With this information, the mixed model equation of an animal could be set up and solved with the newest solutions for its parents, offspring and mates.

The requirement of a sorted pedigree file has two disadvantages. The file will contain three rows for most animals, which can make it impossible to keep the file as an array in the working memory of the computer. This reduces speed of iteration considerably. Another disadvantage is that sorting of the pedigree file can take a lot of computer time.

For the simulation program described in the present paper, a small modification in the method of Schaeffer and Kennedy (1986) made it possible to avoid creation of the sorted pedigree file. The left hand side of the equation for a parent was kept in a working vector and was adjusted immediately after calculation of the new solution for an offspring. In this way, only sire and dam identification of each animal was needed, which could be done with two working vectors.

The modification of the method can be useful for breeding value estimations in current breeding programmes. In single trait situations, it reduces the required amount of computer memory by about 50%.

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Chapter 4

EFFECTS OF FAMILY SIZE IN SELECTION AND TESTING IN A CLOSED DAM LINE OF PIGS

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ABSTRACT

The objective of this study was to evaluate alternative selection and testing systems in closed dam lines of pig breeding programmes. A stochastic simulation model was used to study effects of alternative systems on variances in family size, rate of inbreeding and response to selection for production and reproduction traits. Traits were assumed to be affected by many unlinked loci, each of small additive effect.

Differences in selection response between alternative selection systems were small. A restriction on the number of boars selected per litter (within full-sib family selection) had little influence on rate of inbreeding and selection response. A restriction on the number of boars per sire (within paternal half-sib family selection) gave a small reduction in rate of inbreeding and response to selection. Increasing the number of boars was a better option for limiting the rate of inbreeding than within family selection.

Two alternative testing systems were compared. A system of one boar tested per litter gave about 10% lower response to selection than a system of two boars tested per litter.

1. INTRODUCTION

Important criteria for evaluation of alternative breeding schemes for closed pig populations are the response to selection and the rate of inbreeding. A high inbreeding coefficient is detrimental, because inbreeding reduces genetic variance available for further selection. Moreover, it gives a reduction in the mean for traits subject to dominance, known as inbreeding depression (Falconer, 1981).

In dam lines of pigs, attention has to be given to production and reproduction traits. Use of family information is important for selection response because of the low heritabilities of reproduction traits (Avalos and Smith, 1987). A disadvantage of use of family information is the reduced effective population size. This can lead to high rates of inbreeding in dam lines (Toro et al., 1988; De Vries et al., 1989).

Rate of inbreeding (ΔF) can be reduced by increasing the number of boars used per year as studied by De Vries et al. (1989). Another alternative to

reduce ΔF is selection of boars within paternal half-sib or full-sib families. This selection system is applied by some pig breeding organizations. In certain situations, selection within families can give a higher long-term selection response than mass selection (Dempfle, 1975).

Avalos and Smith (1987) gave three alternative systems for selection of boars: (a) a maximum of three boars per litter, (b) a maximum of one boar per litter, and (c) one boar per sire. Toro et al. (1988) found for systems b and c (compared to a) a lower ΔF , but also a lower response to selection, when selection was only for reproduction traits. However, for an appropriate comparison of selection systems, selection for production traits also has to be taken into account.

Alternative selection systems should be studied in combination with alternative testing systems, because of possible interactions. A restriction on the number of boars tested per litter reduces costs for testing facilities, but it also reduces response to selection. This reduction needs to be quantified.

The objective of this study is to evaluate alternative selection and testing systems for a dam line of pigs. Effects of alternative systems on variances in family size, response to selection and rate of inbreeding are studied with a stochastic simulation model. This model was developed for closed pig populations (De Roo, 1987 and 1988a) and adapted to a dam line (De Vries et al., 1989).

2. MATERIAL AND METHODS

2.1. General concepts

The model of De Roo (1987 and 1988a) evaluated changes in production and reproduction traits and inbreeding coefficient over 25 years of selection in a closed swine herd. The model included overlapping generations, daily mating and farrowing and weekly selection of boars and sows. Week was the unit of time.

Breeding values were generated as

$$A_i = 0.5 \times A_j + 0.5 \times A_k + \sqrt{(0.5 \text{ CF})} \times a \times \sigma_A \quad (1)$$

$$\text{and } CF = 1 - 0.5 \times (F_j + F_k) \quad (2)$$

where A_i , A_j , A_k are breeding values of individual i , its sire j and its dam k ;

CF is a correction factor that accounts for the expected reduction in additive genetic variance when parents have inbreeding coefficients F_j and F_k (Thompson, 1977);

a is a random normal deviate; and

σ_A is the additive genetic standard deviation in the base population.

Because a reduction in litter size due to inbreeding depression would have only a limited effect on selection intensity (and thus on additive genetic response (De Roo, 1988b)), inbreeding depression was not included and a strictly additive model was assumed.

Phenotypes were simulated as

$$P_i = B + A_i + e \times \sigma_E \quad (3)$$

where P_i is the phenotypic value of individual i ;

B is the mean of the base population;

e is a random normal deviate; and

σ_E is the environmental standard deviation.

2.2. Traits

Litter size at birth was determined by ovulation rate (OR) and percentage of prenatal survival (PS) (De Roo, 1988a). PS depended on the phenotypic value of OR:

$$PS = 100\% \times OR_{50\%} / (OR + OR_{50\%}) \quad (4)$$

where $OR_{50\%}$ is the number of ovulations at which 50 percent of the embryo's survive.

The genetic correlation (r_G) between OR in first parity and OR in later parities was 0.5, while environmental correlation (r_E) was 0.1. Between later parities r_G was 1, while r_E was 0.2. More details are given by De

Vries et al. (1989).

The overall breeding goal combined reproduction (H_{repr}) with production traits (H_{prod}). Reproduction traits were size of the first litter (LSB1) and average size of later litters (LSB2). Relative economic weights of LSB1 and LSB2 were taken from De Vries (1989):

$$H_{repr} = 1.8 \times A_{LSB1} + 7.1 \times A_{LSB2} \quad (5)$$

where A_i is the breeding value for trait i .

Breeding values for LSB1 and LSB2 were estimated every four weeks using a linear multi-trait animal model. Non-linearity of actual breeding values was not accounted for. All animals that were used in the breeding herd during the last ten years were included in the breeding value analysis. Parameters used to set up the equations are in Table 1. Further details of this procedure are given by De Vries et al. (1989).

Table 1. Parameters for estimation of breeding values for size of the first litter (LSB1) and size of 2nd and later litters (LSB2) (Knap, 1986; De Roo, 1987).

Phenotypic variance of LSB1 and LSB2	8.1
Heritability of LSB1 and LSB2	0.1
Phenotypic correlation between LSB1 and LSB2	0.1
Genetic correlation between LSB1 and LSB2	0.5
Repeatability of LSB2	0.2

Production traits in the breeding goal were daily growth rate, daily feed intake and lean percentage of the carcass. Differences in expression at a commercial level make improvement of reproduction traits in a dam line twice as important as improvement of production traits (Smith, 1964). Therefore, weights of production traits in the breeding goal, adopted from De Roo (1988a) for a sire line, were reduced by 50% relative to reproduction traits. Corresponding with this, the weighting factors for production traits in the index combining production and reproduction traits could also be reduced by 50%, as the genetic and phenotypic correlations between

production and reproduction traits were assumed to be zero (Brien, 1986):

$$H_{\text{prod}} = 0.5 \times (0.178 \times A_{\text{GR}} - 0.05 \times A_{\text{FI}} + 3.0 \times A_{\text{LEAN}}) \quad (6)$$

$$I_{\text{prod;boars}} = 0.5 \times (0.0212 \times P_{\text{GR}} - 0.0004 \times P_{\text{FI}} + 1.5548 \times P_{\text{LEAN}}) \quad (7)$$

$$I_{\text{prod;gilts}} = 0.5 \times (0.0357 \times P_{\text{GR}} - 2.5965 \times P_{\text{SF}}) \quad (8)$$

where A_i and P_i are breeding values and phenotypic values for trait i ;

GR is the growth rate from 23 to 100 kg (g day^{-1});

FI is the feed intake (g day^{-1});

LEAN is the (estimated) lean percentage in carcass; and

SF is the side fat thickness (mm).

Potential breeding animals were performance tested. Boars were fed ad libitum, but gilts were kept on a restricted diet. Only individual performance data were used in the index for production traits. Variables in equation (7) and (8) were deviations from batch means (not corrected for genetic trend). Genetic and phenotypic parameters of production traits are in Table 2.

Lean percentage in boars was assumed to be estimated on live animals by means of modern equipment. Breeding values for lean percentage were assumed to be normally distributed. Phenotypes were expressed on a scale with a minimum of 35 and a maximum of 75 percent (De Roo, 1987).

2.3. Selection

To reduce costs for testing facilities, only boars with a reproduction index higher than the average genetic level of the population were tested. This genetic level was calculated every four weeks as the average reproduction index of sows that had a litter in the previous 16 weeks. Boars were two months old when first stage selection took place. Selection of gilts before the test (on pedigree index) was not considered, because testing of gilts in groups is not expensive. Moreover, a large number of tested gilts can be used for subnucleus purposes.

Selection of young breeding animals was considered as a multi-stage process. At the end of the test some animals were culled for conformation

Table 2. Genetic and phenotypic parameters of production traits in the base population.

Trait	Mean	h ²	σ _p	Correlations ¹⁾				
				Boars			Gilts	
				GR	FI	LEAN	GR	SF
Boars								
growth rate (GR, g day ⁻¹)	900	.25	88	1.00	.85	-.15	1.00	.00
feed intake (FI, g day ⁻¹)	2,400	.25	200	.65	1.00	-.35	.85	.40
lean percentage (LEAN)	52	.45	2.5	-.10	-.30	1.00	-.15	-.40
Gilts								
growth rate (GR, g day ⁻¹)	785	.20	42	n.r. ²⁾	n.r.	n.r.	1.00	.00
side fat thickness (SF, mm)	12.2	.30	0.9	n.r.	n.r.	n.r.	.10	1.00

1) Upper triangle: genetic correlations, lower triangle: phenotypic correlations.

2) Not relevant.

and a relatively mild selection on production index was performed (Table 3). At sexual maturity, another number of animals was culled for conformation. In addition, some boars were culled because of poor reproductive performance (semen quality). Culling chances for poor conformation or reproductive performance were independent of production and reproduction traits.

Remaining boars could enter the young-boar pool from which new breeding boars were selected. Selection was on an overall index, combining the production index (equations 7 and 8) with the reproduction index (index weights according to equation 5):

$$I_{\text{overall}} = I_{\text{repr}} + I_{\text{prod}} \quad (9)$$

At sexual maturity, gilts entered the pool of replacement gilts. Every week, a number of sows was selected for breeding. These sows came from the group of sows weaned in the previous week or from the pool of replacement

Table 3. General characteristics of nucleus breeding scheme.

<u>General</u>	
maximum number of parities per sow	5
length of suckling period (weeks)	4.5
number of boars used simultaneously	3
size of pool of replacement boars	8
maximum relationship of partners at mating	0.125
<u>Performance test</u>	
minimum start growth rate (0 - 23 kg, g day ⁻¹)	300
maximum number of gilts tested per litter	6
total number of test places in a division	50 ¹⁾
minimum production index at end of test, boars	-0.5 ²⁾
minimum production index at end of test, gilts	-1.0 ²⁾
percentage of boars culled for conformation	40
percentage of gilts culled for conformation	20
<u>Sexual maturity</u>	
percentage of boars culled for reproduction (semen quality) or conformation	40
percentage of gilts culled for conformation	20

1) For 200 sows, group size for gilts was enlarged to 80 places.

2) Expressed in standard deviations of production index.

gilts. The replacement gilts had to compete with the sows for a place in the breeding herd (sequential culling). Selection was on an overall index (equation 9).

The model of De Roo (1987) was modified to make within family selection after the test possible. The strategy for selection of young boars is illustrated in Figure 1. For within full-sib family selection (i.e. a maximum of one boar selected per litter), a young boar could only enter the young-boar pool, when it could replace an inferior full-sib, or when it had no full-sib in the pool. In the latter situation, it could fill an

Boar has FS in YBP ?

Yes ----> Superior to FS in YBP ?

Yes -----> Replace FS with boar

No -----> Cull boar

No ----> Empty place in YBP ?

Yes -----> Select boar

No ----> Superior to a YBP-member ?

Yes ----> Replace YBP-member with boar

No ----> Cull boar

Figure 1. Decision process for selection of boars to the young-boar pool (YBP) for within full-sib family selection after the test (FS: full-sib).

empty place or it could replace an inferior pool member, as pool size was restricted.

Another modification for selection within full-sib families was the time of selection of boars for the breeding boar pool. To get the best member of each family, a boar with a better full-sib had to stay in the young-boar pool until this full-sib was sexually mature. Then, if the full-sib was not culled for conformation or reproduction reasons (semen quality), it replaced the boar (Appendix).

For within half-sib family selection, essentially the same procedure was followed as for within full-sib family selection. However, a strict system of one boar per sire appeared to be difficult to achieve. A concession had to be made to ensure a regular supply of new breeding boars. The maximum number of sons per sire in the young-boar pool was restricted to two instead of one. If possible, a son of a new sire (sire without a son as breeding boar) was selected as breeding boar. Otherwise, a boar of a sire with already one son as breeding boar was selected (Appendix).

2.4. Parameters

Most of the parameters were adopted from De Roo (1988a) and De Vries et al. (1989). Part of the characteristics of the line under study are in

Table 3. It was assumed that 67 percent of sows that entered the breeding piggery farrowed. Probabilities that sows were culled at weaning for conformation or health problems were 10.0, 7.0, 7.5 and 10.0 percent for first, second, third, and fourth parity (De Roo, 1988a). This culling was independent of sow's performance for (re)production traits.

Mating of close relatives was avoided; maximum inbreeding coefficient of potential offspring was 0.125. If no potential mates met this requirement, least related animals were mated.

2.5. Alternatives

Two alternative testing systems for boars were studied: a maximum of two boars tested per litter (TL2), and a maximum of one boar tested per litter (TL1).

Testing systems TL2 and TL1 were combined with two alternative selection systems: a maximum of one boar selected per litter (WFS1), and selection of boars within paternal half-sib families (WHS). Results for testing system TL2 combined with WFS2 (a maximum of two boars selected per litter) were taken from De Vries et al. (1989). The combination of testing system TL2 and selection system WFS1 implies within full-sib family selection after the test, while TL1/WFS1 and TL2/WFS2 imply mass selection after the test.

Differences between alternative selection and testing systems depend on population size and selection intensity (Dempfle, 1975). Therefore, the alternative systems were evaluated for three populations: 100 sows with 10 boars (per year), 200 sows with 10 boars, and 200 sows with 20 boars. Ten replicates were made for each alternative.

Founder population sizes were equal to nucleus population sizes. Founder animals were selected from a large base population. Production indices of founder sows were better than average in the population, and founder boars were at least one standard deviation better than average in production index.

2.6. Evaluation of variances in family size and rate of inbreeding

For each alternative, the pedigree data of the simulated breeding animals

(boars selected to the breeding boar pool, gilts selected to the breeding piggery) were analyzed to calculate the realized variances in family size. This information was used to check how strictly within family selection could be performed and to explain differences in rate of inbreeding between alternative selection systems.

Expected yearly relative increases of F (ΔF_e) were calculated according to Hill (1972), using the realized variances and covariances in family size and realized generation interval:

$$\Delta F_e = \left[(2 + \sigma_{mm}^2 + 2(N_m/N_f)\text{cov}(mm, mf) + (N_m/N_f)^2 \sigma_{mf}^2) / N_m + (2 + \sigma_{ff}^2 + 2(N_f/N_m)\text{cov}(fm, ff) + (N_f/N_m)^2 \sigma_{fm}^2) / N_f \right] / 32L^2 \quad (10)$$

where N_m and N_f are the numbers of selected males and females per year;
 σ_{mm}^2 , σ_{mf}^2 , σ_{fm}^2 and σ_{ff}^2 are the variances in number of selected
 male progeny from males, female progeny from males,
 male progeny from females, and female progeny from females;
 $\text{cov}(mm, mf)$ and $\text{cov}(fm, ff)$ are the covariances between number of
 selected male and female progeny from males, and between
 number of selected male and female progeny from females; and
 L is the length of generation interval in years.

Realized values of the yearly relative increase of F (ΔF_r) were calculated from Falconer (1981):

$$\Delta F_r = (F_t - F_{t-1}) / (1 - F_{t-1}) \quad (11)$$

where F_t is average inbreeding coefficient of pigs tested in year t .

3. RESULTS AND DISCUSSION

3.1. Variance in family size

For the populations of 100 sows with 10 boars (per year) and 200 sows with 20 boars, the average number of selected females per male (N_f/N_m) was equal to 21. For the population of 200 sows with 10 boars, N_f/N_m ranged between 41 and 42. Realized variances in family size are given in Table 4.

It is useful to compare the realized variances with the expected variances in family size for unselected populations, and for populations with strict within family selection. In a large population without selection on a heritable trait, family sizes are Poisson distributed. In

Table 4. Variances in family size for males to males (σ_{mm}^2), males to females (σ_{mf}^2), females to males (σ_{fm}^2) and females to females (σ_{ff}^2).

Popula- tion ¹⁾	Test- ing ²⁾	Selec- tion ³⁾	σ_{mm}^2	σ_{mf}^2	σ_{fm}^2	σ_{ff}^2
100/10	TL2	WFS2	0.98 ± 0.03 ⁴⁾	97.5 ± 4.7	0.0605 ± 0.0011	3.72 ± 0.05
	TL2	WFS1	0.94 ± 0.03	90.0 ± 4.2	0.0566 ± 0.0009	3.61 ± 0.03
	TL2	WHS	0.40 ± 0.01	83.2 ± 2.0	0.0560 ± 0.0007	3.68 ± 0.05
	TL1	WFS1	0.95 ± 0.02	91.4 ± 3.9	0.0539 ± 0.0010	3.75 ± 0.04
	TL1	WHS	0.50 ± 0.01	87.5 ± 4.3	0.0528 ± 0.0011	3.71 ± 0.03
200/10	TL2	WFS2	1.01 ± 0.03	241.4 ± 10.0	0.0289 ± 0.0004	3.86 ± 0.03
	TL2	WFS1	0.93 ± 0.02	227.2 ± 11.7	0.0287 ± 0.0004	3.93 ± 0.04
	TL2	WHS	0.36 ± 0.01	223.2 ± 9.1	0.0278 ± 0.0004	4.07 ± 0.03
	TL1	WFS1	0.94 ± 0.02	225.2 ± 11.3	0.0275 ± 0.0003	3.96 ± 0.05
	TL1	WHS	0.39 ± 0.01	209.5 ± 9.2	0.0271 ± 0.0004	3.93 ± 0.05
200/20	TL2	WFS2	1.10 ± 0.04	80.1 ± 2.7	0.0608 ± 0.0007	3.82 ± 0.03
	TL2	WFS1	1.09 ± 0.02	77.2 ± 2.9	0.0575 ± 0.0010	3.88 ± 0.03
	TL2	WHS	0.33 ± 0.01	69.9 ± 3.6	0.0583 ± 0.0006	3.89 ± 0.02
	TL1	WFS1	1.06 ± 0.03	80.2 ± 4.7	0.0556 ± 0.0007	3.91 ± 0.05
	TL1	WHS	0.46 ± 0.01	65.6 ± 1.5	0.0557 ± 0.0007	3.94 ± 0.04

1) Number of sows/annual number of boars.

2) TL2: two boars per litter; TL1: one boar per litter.

3) WFS2: maximum of two boars per litter; WFS1: maximum of one boar per litter; WHS: within half-sib family selection.

4) Standard error.

such a situation, variance in family size for males to males (σ_{mm}^2) and females to females (σ_{ff}^2) is equal to 1, while σ_{mf}^2 and $1/\sigma_{fm}^2$ are equal to the ratio of females to males (N_f/N_m). A strict within family selection system (each male has one son and N_f/N_m daughters, each female has one daughter and a probability of N_m/N_f of having one son) gives $\sigma_{mm}^2 = \sigma_{ff}^2 = \sigma_{mf}^2 = 0$, and $\sigma_{fm}^2 = (N_m/N_f)(1 - N_m/N_f)$ (Hill, 1972).

Without restrictions on family size, selected populations will have higher variances in family size than unselected populations. However, Table 4 (WFS1 and WFS2) shows that selection had no large influence on σ_{mm}^2 . Only in the population of 200 sows with 20 boars was σ_{mm}^2 significantly higher than 1. The small influence of selection on σ_{mm}^2 can be explained by the small number of paternal half-sib families available when a young boar had to be chosen as breeding boar, and by the relatively small contribution of the sire (reproduction records of female relatives of the sire) in the overall index of a young boar.

A strict system of one boar per sire (within half-sib family selection) was not possible. In the population of 100 sows with 10 boars and two boars tested per litter (TL2) σ_{mm}^2 could be reduced to 0.40. This means that 20% of the boars had two selected sons, 60% had one selected son, and 20% had no selected male progeny. When only one boar per litter was tested, σ_{mm}^2 remained higher. The highest reduction in σ_{mm}^2 was possible in the population of 200 sows with 20 boars.

A restriction of (a maximum of) one boar selected per litter (WFS1) reduced σ_{mm}^2 and σ_{fm}^2 . However, the reductions were very small. The small reduction in σ_{fm}^2 can be explained by the fact that excellent sows were allowed to have five litters. When a sow had two selected sons, these sons often came from different litters. As a result, a restriction of one boar per litter was not very effective.

In the population of 200 sows with 20 boars, the highest value of σ_{fm}^2 was equal to 0.0608 (TL2/WFS2). When females with more than two selected sons are neglected, this value means that 96.1% of the females had no selected male progeny, 3.1% of the females had one selected son and 0.8% had two selected sons. In a population without selection σ_{fm}^2 was expected to be equal to 0.0469 ($= N_m/N_f$). This means that selection increased σ_{fm}^2 by 30%.

Selection had a large influence on σ_{mf}^2 and σ_{ff}^2 . The high variances can

be explained by the high number of gilts available for selection per female, and by the large contribution of the reproduction index in the overall index for gilts. The small contribution of the production index (equation 8) is due to the low accuracy of the performance test for gilts.

3.2. Selection response

Responses to selection for production and reproduction traits were expressed in Dfl. using the economic weights of equations (5) and (6). Values of cumulative responses to year 25, averaged over replicates, are given in Table 5.

Overall response was calculated as the sum of response for production and reproduction traits. Curves of the overall response for each alternative are given in Figure 2. Values of the overall response in year 25 are in Table 6. The standard errors of the response can be multiplied by the square root of the number of replicates ($\sqrt{10}$) to give the standard deviation of the response.

Differences in response between alternative selection systems were small (Table 6, Figure 2). When only one boar per litter could be chosen as breeding boar (TL2/WFS1) instead of two (TL2/WFS2), average reduction in response was 2%.

Compared to mass selection (TL2/WFS2 and TL1/WFS1), selection of boars within half-sib families (WHS) gave an average reduction in response of 5%. In the population of 200 sows with 10 boars, reductions were small. This can be explained by the high number of sows per boar. Selection within families is expected to be more successful in populations with large families (Dempfle, 1975). When one boar per litter was tested (TL1), WHS and mass selection gave about the same response in the population of 100 sows with 10 boars. This was not expected from theory. Also for the other populations larger differences were expected. An explanation was found in the small number of families available at the time of selection of a new breeding boar. In the populations with 10 boars per year and 3 boars used simultaneously, very few half-sib families were available at the time of selection and many selection candidates had the same paternal grand-sire. As a result, between family selection could not contribute much to the response. Increasing the number of boars per year gave more possibilities

Table 5. Cumulative responses up to year 25 for production (PROD) and reproduction traits (REPR) (response in Dfl.).

Popula- tion ¹⁾	Tes- ting ²⁾	Selec- tion ³⁾	PROD	REPR
100/10	TL2	WFS2	23.20 ± 0.69 ⁴⁾	29.29 ± 1.24
	TL2	WFS1	23.00 ± 0.97	28.84 ± 1.33
	TL2	WHS	22.67 ± 0.92	26.72 ± 1.26
	TL1	WFS1	18.11 ± 0.65	26.07 ± 0.72
	TL1	WHS	18.87 ± 0.68	25.97 ± 1.45
200/10	TL2	WFS2	25.72 ± 0.84	30.19 ± 1.48
	TL2	WFS1	26.34 ± 0.71	31.48 ± 1.18
	TL2	WHS	23.37 ± 0.57	32.07 ± 1.00
	TL1	WFS1	22.79 ± 0.76	30.61 ± 1.03
	TL1	WHS	21.14 ± 0.85	29.54 ± 1.26
200/20	TL2	WFS2	24.85 ± 0.59	33.71 ± 0.71
	TL2	WFS1	25.27 ± 0.67	31.77 ± 0.82
	TL2	WHS	22.71 ± 0.75	31.76 ± 1.11
	TL1	WFS1	21.33 ± 0.47	31.60 ± 0.95
	TL1	WHS	19.22 ± 0.64	29.29 ± 1.09

1) Number of sows/annual number of boars.

2) TL2: two boars per litter; TL1: one boar per litter.

3) WFS2: maximum of two boars per litter; WFS1: maximum of one boar per litter; WHS: within half-sib family selection.

4) Standard error.

for selection between families, which explains the larger differences between selection systems in the populations of 200 sows with 20 boars (per year) compared to 100 sows with 10 boars.

As could be expected, response was reduced when only one boar per litter was tested (TL1) instead of two (TL2). The reduction (on average 10%) was mainly due to a reduced response for production traits (Table 5).

Table 6. Cumulative overall responses up to year 25 (R_{cum}) (response in Dfl.), inbreeding coefficient (F) in year 25, and expected (ΔF_e) and realized (ΔF_r) yearly relative increases in F.

Popula- tion ¹⁾	Tes- ting ²⁾	Selec- tion ³⁾	R_{cum}	F	ΔF_e	ΔF_r
100/10	TL2	WFS2	52.48 \pm 1.46 ⁴⁾	26.1 \pm 0.5	1.00	1.31
	TL2	WFS1	51.84 \pm 1.11	24.6 \pm 0.5	0.97	1.22
	TL2	WHS	49.39 \pm 1.51	21.8 \pm 0.4	0.82	1.06
	TL1	WFS1	44.18 \pm 0.92	24.2 \pm 0.4	0.96	1.21
	TL1	WHS	44.83 \pm 1.42	22.0 \pm 0.3	0.85	1.07
200/10	TL2	WFS2	55.92 \pm 1.45	23.9 \pm 0.5	0.90	1.18
	TL2	WFS1	57.82 \pm 1.45	24.1 \pm 0.7	0.87	1.18
	TL2	WHS	55.44 \pm 1.29	20.8 \pm 0.3	0.71	1.00
	TL1	WFS1	53.40 \pm 1.16	23.4 \pm 0.7	0.86	1.15
	TL1	WHS	50.68 \pm 1.74	20.1 \pm 0.4	0.72	0.96
200/20	TL2	WFS2	58.56 \pm 0.71	18.6 \pm 0.4	0.55	0.89
	TL2	WFS1	57.04 \pm 1.15	17.5 \pm 0.5	0.49	0.83
	TL2	WHS	54.47 \pm 1.00	14.9 \pm 0.4	0.40	0.70
	TL1	WFS1	52.93 \pm 1.04	17.0 \pm 0.6	0.53	0.81
	TL1	WHS	49.14 \pm 1.26	14.1 \pm 0.2	0.44	0.67

1) Number of sows/annual number of boars.

2) TL2: two boars per litter; TL1: one boar per litter

3) WFS2: maximum of two boars per litter; WFS1: maximum of one boar per litter; WHS: within half-sib family selection.

4) Standard error.

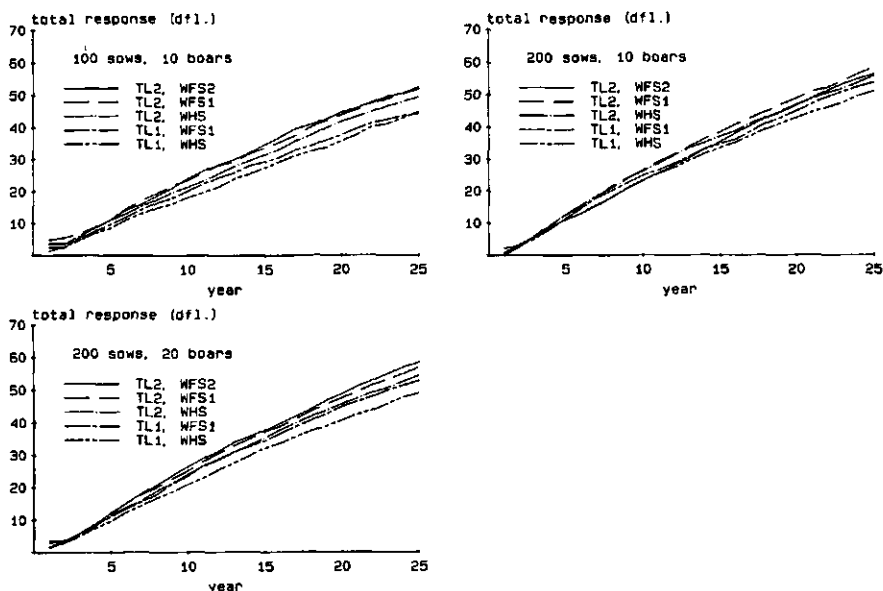


Figure 2. Effects of selection and testing system on progress of overall response over time for different populations (TL2: two boars tested per litter; TL1: one boar tested per litter; WFS2: maximum of two boars selected per litter; WFS1: maximum of one boar selected per litter; WHS: within half-sib family selection).

3.2. Inbreeding coefficient

Changes in average inbreeding coefficient for each alternative are given in Figure 3. Inbreeding coefficients (F) in year 25 and realized (ΔF_r ; equation 11) and expected (ΔF_e ; equation 10) yearly relative increases in F are in Table 6. It can be seen that ΔF_r and ΔF_e followed the same pattern, but ΔF_r was always much higher than ΔF_e . Although equation (10) accounted for the increased variances in family size of offspring from parents due to selection, it still underestimated the influence of selection on rate of inbreeding.

A restriction of one boar per litter (WFS1) gave only a small reduction of rate of inbreeding. As expected, selection of boars within half-sib families (WHS) gave a larger reduction, but rate of inbreeding still

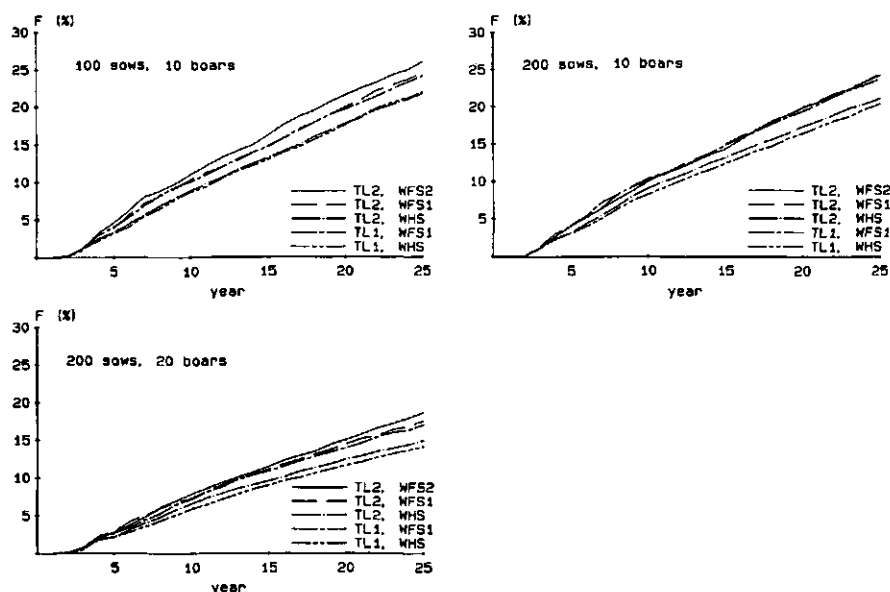


Figure 3. Effects of selection and testing system on change of inbreeding coefficient (F) over time for different populations (TL2: two boars tested per litter; TL1: one boar tested per litter; WFS2: maximum of two boars selected per litter; WFS1: maximum of one boar selected per litter; WHS: within half-sib family selection).

remained quite high. The standard error of F was also reduced (Table 6), which means that WHS reduced the variation between replicates in rate of inbreeding. This can be explained by the reduced variation between replicates in σ^2_{mm} (see standard error of σ^2_{mm} in Table 4).

3.3. General discussion

Selection of gilts within dams or within sires was not examined in this study. It is expected that this would not be a good option to reduce rate of inbreeding. From equation (10) it can be derived that restrictions on the number of daughters per parent in populations with a high number of sows can only give a small reduction in ΔF .

Selection for production traits was based only on individual performance

data. As a result, accuracy of the production index was not affected by the number of boars tested per litter. In a situation with family information in the production index, differences in response between one boar tested and two boars tested per litter will be somewhat higher. The same holds for the differences between alternative selection systems. Half-sib information in the production index improves response under mass selection, but it has no value when a strict system of selection within half-sib families is applied.

For selection on reproduction traits, all animals that were used in the herd during the previous ten years were included in the breeding value analysis. As a result, all records and family relationships of at least three generations were taken into account (De Vries et al., 1989). Data from earlier generations would have had very little influence on estimated breeding values. However, a problem of this method is that the base population changes in the statistical analysis. The resulting changes in base population parameters were not taken into account. Consequences of this simplification were expected to be negligible.

Table 6 showed that expected rate of inbreeding (ΔF_e ; equation 10) was always much lower than realized rate of inbreeding (ΔF_r ; equation 11). Averaged over alternatives $\Delta F_e/\Delta F_r$ was equal to 0.72. This means that unequal contributions of breeding animals to subsequent generations were not accounted for well enough. This is mainly due to the use of family information in the reproduction index. Not only were records of the dams of young boars and gilts included in the index, but also records of sibs of the parents. The records of these sibs lead to extra variance in the contributions of breeding animals of generation t to generation $t+2$. In an extreme example, it would be possible that all breeding boars in a generation have a different sire and dam, while they all have the same maternal grand-sire. Equation (10) only accounts for variances in family size of parents to offspring. A formula that also accounts for variances in family size of grand-parents to grand-offspring was derived by Wray (1989). This formula gave better predictions for ΔF than equation (10), but it still underestimated ΔF (averaged over alternatives $\Delta F_e/\Delta F_r$ was equal to 0.83).

Toro et al. (1988) evaluated with stochastic simulation three selection systems for boars. Relative to the results of selection system WFS3

(maximum of three boars per litter), they found for WFS1 13% and for WHS 21% lower response for reproduction traits. Rate of inbreeding was 15% lower for WFS1 and 45% lower for WHS. In the present study, effects of selection system on response and inbreeding were much smaller. This can be explained mainly by inclusion of production traits in the breeding goal (next to reproduction traits), which reduced the correlation between overall indices of sibs. This is particularly true for full-sibs, as pigs from the same litter have identical reproduction indices but different production indices.

Lower rates of inbreeding can also be achieved by increasing the number of boars. A disadvantage of this option is the higher costs to raise boars. However, within half-sib family selection will also give higher costs. This is due to the practical problem that the members of a half-sib family are not all available at one moment. As a result, many times a decision about the use of a boar for breeding has to be delayed, which means that the boar stays longer in the young-boar pool.

Selection within half-sib families reduced rate of inbreeding, but also response to selection. De Vries et al. (1989) showed that variation in number of boars per year had a small effect on response to selection, especially in herds with a large number of sows. A comparison of the results of De Vries et al. (1989) (TL2/WFS2) with the results for within half-sib family selection in Table 6 (TL2/WHS) shows that a higher number of boars (100/15 vs. 100/10, 200/15 vs. 200/10 and 200/40 vs. 200/20) gave higher overall responses (49.81 vs. 49.39, 59.98 vs. 55.44 and 55.12 vs. 54.47) and lower inbreeding coefficients in year 25 (21.5 vs. 21.8, 20.3 vs. 20.8 and 12.3 vs. 14.9). Therefore, it can be concluded that increasing the number of boars is a better option to limit ΔF than selection within half-sib families. In practice, a compromise between mass selection and within half-sib family selection might be optimal. Mass selection could be combined with certain restrictions on number of progeny per sire or per grand-sire.

Restrictions on the number of boars tested and selected per litter are not effective to reduce rate of inbreeding. The only important advantage of a restriction on the number of boars tested per litter is a reduction in costs for testing. This needs to be compared to the reduction in response to selection (on average 10%).

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APPENDIX

Selection from the young-boar pool to the breeding-boar pool.

For selection within full-sib families, two categories of boars were distinguished in the young-boar pool:

1. animals superior to their (sexually immature) full-sib;
2. animals inferior to their (sexually immature) full-sib.

Each time a new breeding boar was needed, the best of category 1 was chosen. If there were no category 1 animals, the best category 2 animal was chosen. When a boar was selected as breeding boar, its full-sib was culled.

For selection within half-sib families, four categories of boars were distinguished in the young-boar pool:

1. animals superior to their (sexually immature) half-sibs,
no half-sibs as breeding boar;
2. animals superior to their (sexually immature) half-sibs,
one half-sib as breeding boar;
3. animals inferior to one or more (sexually immature) half-sibs,
no half-sibs as breeding boar;
4. animals inferior to one or more (sexually immature) half-sibs,
one half-sib as breeding boar.

Each time a new breeding boar was needed, the best of category 1 was chosen. If there were no category 1 animals, the best of category 2 was chosen. If there were no category 2 animals, the best of category 3 was chosen, etc.. When a boar was selected as breeding boar, its full-sib was culled. When a boar of category 2 or 4 (one half-sib as breeding boar) was selected as breeding boar, all its half-sibs were culled.

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Chapter 5

MULTI-STAGE SELECTION IN A CLOSED DAM LINE OF PIGS

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ABSTRACT

The objective of this study was to optimize multi-stage selection in closed dam lines of pig breeding programmes. A stochastic simulation model was used to study effects of time of selection on accuracy of selection for production and reproduction traits, response to selection and rate of inbreeding. Traits were assumed to be affected by many unlinked loci, each of small additive effect.

First stage selection of boars was before the performance test. The proportion of boars selected in the first stage (p_1) was varied between 100% and 25%. From $p_1=100\%$ to $p_1=50\%$ the reduction in overall response was on average 3.5%, while from $p_1=50\%$ to $p_1=25\%$ the reduction was an additional 6%. The optimum of p_1 depends on the costs for testing, and on the size of the nucleus population relative to the total breeding pyramid. With a relatively large nucleus breeding herd, a low proportion of boars tested can be justified.

Breeding schemes with sequential culling of sows (weaned sows competing with replacement gilts) were compared to schemes without sequential culling (no genetic culling after weaning). Sequential culling gave on average 2-3% extra response.

1. INTRODUCTION

In modern pig breeding schemes, dam lines are selected for production (growth and carcass traits) and reproduction traits (litter size). This selection may be done at several stages. Before the start of the performance test for production traits, young pigs can be selected on an overall pedigree index for production and reproduction traits. After the performance test, the second stage of selection may take place. At this stage, pigs can be selected on an overall index, combining the pedigree indexes for production and reproduction traits with the just obtained test results for production traits.

Selection response will be highest, when all animals are performance tested. In this situation, time of selection for each animal is after the test. However, testing is expensive, especially for boars when they are individually housed. This means that selection before the test can give a

large reduction in costs. To optimize the proportion selected before the test the influence of this variable on selection response for production and reproduction traits has to be examined.

Young sows are selected shortly after the test. Additional genetic selection is possible after weaning a litter. In a sequential culling system a sow with a low index is replaced by a gilt with a higher index. Sequential culling is expected to increase selection response (Belonsky and Kennedy, 1988), but it will also increase costs because of a higher replacement rate. The impact on response is difficult to predict, because the index of sows changes after each litter as a result of extra available information on litter size.

Time of selection can also affect rate of inbreeding. Strong selection before the test is expected to increase variation in family size due to the higher relative importance of family information at this stage. As a result, rate of inbreeding will be higher. Sequential culling of sows is also expected to increase rate of inbreeding, because it reduces generation interval.

The objective of this study is to optimize multi-stage selection in a dam line of pigs. Effects of selection of boars before the performance test and of sequential culling of sows on accuracy of selection, genetic response as well as inbreeding are studied with a stochastic model. This model was developed for closed pig populations, in particular a sire line (De Roo, 1987 and 1988), and adapted to a sow line (De Vries et al., 1989).

2. MATERIAL AND METHODS

2.1. General concepts

The model of De Roo (1987 and 1988) evaluated changes in production and reproduction traits and inbreeding coefficient over 25 years of selection in a closed swine herd. The model included overlapping generations, daily mating and farrowing and weekly selection of boars and sows. Week was the unit of time.

Breeding values were generated as

$$A_i = 0.5 \times A_j + 0.5 \times A_k + \sqrt{(0.5 \times CF)} \times a \times \sigma_A \quad (1)$$

$$\text{and CF} = 1 - 0.5 \times (F_j + F_k) \quad (2)$$

where A_i , A_j , A_k are breeding values of individual i , its sire j and its dam k ;

CF is a correction factor that accounts for the expected reduction in additive genetic variance when parents have inbreeding coefficients F_j and F_k (Thompson, 1977);

a is a random normal deviate; and

σ_A is the additive genetic standard deviation in the base population.

Phenotypes were simulated as

$$P_i = B + A_i + e \times \sigma_E \quad (3)$$

where P_i is the phenotypic value;

B is the mean of the base population;

e is a random normal deviate; and

σ_E is the environmental standard deviation.

2.2. Traits

Litter size at birth (i.e. total number of pigs born) was determined by ovulation rate (OR) and percentage of prenatal survival (PS) (De Roo, 1988). PS depended on the phenotypic value of OR:

$$PS = 100\% \times OR_{50\%} / (OR + OR_{50\%}) \quad (4)$$

where $OR_{50\%}$ is the number of ovulations at which 50% of the embryo's survive. Parameters for OR are given by De Vries et al. (1989).

The overall breeding goal combined reproduction (H_{repr}) with production traits (H_{prod}). Reproduction traits were size of the first litter (LSB1) and average size of later litters (LSB2). Relative economic weights of LSB1 and LSB2 were taken from De Vries (1989):

$$H_{repr} = 1.8 \times A_{LSB1} + 7.1 \times A_{LSB2} \quad (5)$$

where A_i is the breeding value for trait i .

Breeding values for LSB1 and LSB2 were estimated every four weeks using a linear multi-trait animal model. All animals that were used in the breeding herd during the last ten years were included in the estimation of breeding values. Parameters used to set up the equations are given in Table 1. Further details of this procedure are given by De Vries et al. (1989).

Table 1. Parameters for estimation of breeding values for size of the first litter (LSB1) and size of 2nd and later litters (LSB2) (Knap, 1986; De Roo, 1987).

Phenotypic variance of LSB1 and LSB2	8.1
Heritability of LSB1 and LSB2	0.1
Phenotypic correlation between LSB1 and LSB2	0.1
Genetic correlation between LSB1 and LSB2	0.5
Repeatability of LSB2	0.2

Production traits in the breeding goal were daily gain, daily feed intake and lean percentage of the carcass. Differences in expression at a commercial level make improvement of reproduction traits in a dam line twice as important as improvement of production traits (Smith, 1964). Therefore, weights of production traits in the breeding goal, adopted from De Roo (1988) for a sire line, were reduced by 50% relative to reproduction traits. Corresponding to this, the weighting factors for production traits in the index combining production and reproduction traits could also be reduced by 50%, as the genetic and phenotypic correlations between production and reproduction traits were assumed to be zero (Brien, 1986):

$$H_{prod} = 0.5 \times (0.178 \times A_{GR} - 0.05 \times A_{FI} + 3.0 \times A_{LEAN}) \quad (6)$$

$$I_{prod;boars} = 0.5 \times (0.0212 \times P_{GR} - 0.0004 \times P_{FI} + 1.5548 \times P_{LEAN}) \quad (7)$$

$$I_{prod;gilts} = 0.5 \times (0.0357 \times P_{GR} - 2.5965 \times P_{SF}) \quad (8)$$

where A_i and P_i are breeding values and phenotypic individual performance values for trait i ;

GR is the growth rate from 23 to 100 kg (g day^{-1});

FI is the feed intake (g day^{-1});

LEAN is the (estimated) lean percentage in the carcass; and

SF is the side fat thickness (mm).

Potential breeding animals were performance tested. Boars were fed ad libitum, but gilts were kept on a restricted diet. Variables in equation (7) and (8) were deviations from batch means (not corrected for genetic trend). Genetic and phenotypic parameters of production traits are in Table 2.

Lean percentage in boars was assumed to be estimated on live animals by means of modern equipment. Breeding values for lean percentage were assumed to be normally distributed. Phenotypes were expressed on a scale with a minimum of 35 and a maximum of 75 percent (De Roo, 1987).

Table 2. Genetic and phenotypic parameters of production traits in the base population.

Trait	Mean	h ²	σ _p	Correlations ¹⁾				
				Boars			Gilts	
				GR	FI	LEAN	GR	SF
<hr/>								
Boars								
growth rate (GR, g day ⁻¹)	900	.25	88	1.00	.85	-.15	1.00	.00
feed intake (FI, g day ⁻¹)	2,400	.25	200	.65	1.00	-.35	.85	.40
lean percentage (LEAN)	52	.45	2.5	-.10	-.30	1.00	-.15	-.40
Gilts								
growth rate (GR, g day ⁻¹)	785	.20	42	n.r. ²⁾	n.r.	n.r.	1.00	.00
side fat thickness (SF, mm)	12.2	.30	0.9	n.r.	n.r.	n.r.	.10	1.00

1) Upper triangle: genetic correlations, lower triangle: phenotypic correlations.

2) Not relevant.

2.3. Selection

First stage selection of males was before the test. Each two weeks a fixed proportion of the available young boars (of about two months old) was selected (i.e. within-batch selection). Selection was on an overall index for males in first stage ($I_{ov,m1}$), combining for each animal its reproduction index based on family information (index weights according to equation 5) with the production indexes of its sire and dam (equations 7 and 8):

$$I_{ov,m1} = 0.5 \times (I_{prod,sire} + I_{prod,dam}) + I_{repr,m1} \quad (9)$$

Selection of gilts before the test was not considered, because testing of gilts in groups is not expensive. Moreover, a large number of tested gilts can be used for subnucleus purposes.

At the end of test, some males and females were culled for conformation and a relatively mild selection on own performance index for production traits was performed (Table 3). At sexual maturity, another number of animals was culled for conformation. In addition, some males were culled because of poor reproductive performance (semen quality). Culling chances for poor conformation or reproductive performance were independent of production and reproduction traits.

Selection between the remaining males at sexual maturity (second stage of selection) was on an overall index ($I_{ov,m2}$), combining for each animal its reproduction index based on family information with the production indexes of parents and the own performance index. The derivation of weighting factors for the production indexes is given in the Appendix.

$$I_{ov,m2} = I_{prod,m2} + I_{repr,m2} \quad (10)$$

$$I_{prod,m2} = 0.6907 \times 0.5 \times (I_{prod,sire} + I_{prod,dam}) + 0.9180 \times I_{prod,own} \quad (11)$$

At sexual maturity, gilts entered the pool of replacement gilts. Every week a number of sows was selected for breeding. These sows could come from the group of sows weaned in the previous week or from the pool of replacement gilts. An overall index ($I_{ov,f}$) was used as the selection

criterion:

$$I_{ov,f} = I_{prod,f} + I_{repr,f} \quad (12)$$

$$I_{prod,f} = 0.8763 \times 0.5 \times (I_{prod,sire} + I_{prod,dam}) + 0.8959 \times I_{prod,own} \quad (13)$$

2.4. Parameters

Most of the parameters were adopted from De Roo (1988) and De Vries et al. (1989). Part of the characteristics of the line under study are in Table 3. Total number of test places in a division (80) did not put an

Table 3. General characteristics of nucleus breeding scheme.

General

maximum number of parities per sow	5
length of suckling period (weeks)	4.5
size of pool of replacement boars	8
maximum relationship of partners at mating	0.125

Performance test

minimum start growth rate (0 - 23 kg, g day ⁻¹)	300
maximum number of boars tested per litter	2
maximum number of gilts tested per litter	6
total number of test places in a division	80
minimum own performance index at end of test, boars	-1.0 ¹⁾
minimum own performance index at end of test, gilts	-1.0 ¹⁾
percentage of boars culled for conformation	40
percentage of gilts culled for conformation	20

Sexual maturity

percentage of boars culled for reproduction	
(semen quality) or conformation	40
percentage of gilts culled for conformation	20

1) Expressed in standard deviations of own performance index.

additional restriction on number of boars or gilts tested per litter. It was assumed that 67 percent of sows that entered the breeding piggery farrowed. Probabilities that sows were culled at weaning for conformation or health problems were 10.0, 7.0, 7.5 and 10.0 percent for first, second, third, and fourth parity (De Roo, 1988). This culling was independent of sow's performance for (re)production traits.

Mating of close relatives was avoided; maximum inbreeding coefficient of potential offspring was 0.125. If no potential mates met this requirement, least related animals were mated.

2.5. Alternatives

For selection of boars before the test, four alternatives were examined. In the first alternative, proportion of boars selected in the first stage (p_1) was equal to 100%, i.e. all available animals were tested. Other alternatives were: $p_1 = 50, 33$ and 25%.

Two alternative selection systems for females were examined. In the first alternative, sows with one or more litters were not culled for genetic reasons (no sequential culling). In the second alternative, weaned sows had to compete with the available replacement gilts for a place in the breeding herd (sequential culling).

From theory it can be expected that the influence of time of selection on response will depend on sow/boar ratio. Therefore, two alternative nucleus populations were considered: 200 sows with 20 boars (per year) and 200 sows with 40 boars. In the first population, three boars were used simultaneously, while six boars were used simultaneously in the second population. Founder population sizes were equal to nucleus population sizes. Ten replicates were made for each alternative.

2.6. Theoretical predictions of selection response

Realized values (from simulated populations) of variances of aggregate genotype, accuracies of overall indexes (e.g. correlations between indexes and true breeding values) at both stages of selection, correlations between first and second stage indexes, proportions selected and generation interval were calculated to explain the influence of first stage selection

on selection response. Theoretical predictions of overall selection response were based on these calculated parameters. Predictions were only done for alternatives without sequential culling, as theoretical predictions under sequential culling were very complex.

A comparison of the theoretical predictions with the realized reductions of response due to first stage selection is very useful, as it gives information on the validity of predictions with a deterministic model. The advantage of such a model would be the low computational costs, which makes it possible to evaluate a lot of alternative situations.

The predictions of response were complicated by the mild independent culling on the own performance production index at the end of test (Table 3). This reduced the estimates for accuracy of selection. Therefore, two extra alternatives were simulated without independent culling on own performance index.

Predicted cumulative overall response (R_p) in year 25 was calculated from expected selection differentials for males (S_m) and females (S_f), and assuming 23 years of selection. To take two-stage selection into account S_m was calculated using the method of Cochran (1951).

$$R_p = 23 \times (S_m + S_f) / (2 \times L) \quad (14)$$

$$S_m = \sigma_H \times (r_{11H,m} \times z_1 \times p_2' + r_{12H,m} \times z_2 \times p_1') / (p_1 \times p_2) \quad (15)$$

$$S_f = i_f \times r_{1H,f} \times \sigma_H \quad (16)$$

where L is the generation interval (based on progeny born);
 σ_H is the standard deviation of overall aggregate genotype;
 $r_{11H,m}$ and $r_{12H,m}$ are the accuracies of first and second stage overall selection indexes of boars;
 $r_{1H,f}$ is the accuracy of the overall selection index for gilts;
 p_1 and p_2 are proportions of boars selected in first and second stage; and
 i_f is the selection intensity for females.

Variables z_1 and z_2 are the ordinates of a univariate normal curve corresponding to truncation points (k_1 and k_2) for first and second stage of selection. Values for k_1 and k_2 were derived with a bivariate normal

distribution function with correlation r_{II12} , while p_1' and p_2' are the integrals of a univariate normal curve corresponding to truncation points k_1' and k_2' :

$$k_1' = (k_1 - r_{II12} \times k_2) / \sqrt{(1-r_{II12}^2)}$$

$$k_2' = (k_2 - r_{II12} \times k_1) / \sqrt{(1-r_{II12}^2)}$$

3. RESULTS

3.1. Herd characteristics

When sows were culled only for non-genetic reasons (i.e. no sequential culling), 44% of the litters came from first parity sows. Sequential culling increased this frequency to 63-64%. Average parity number decreased from 2.1 to 1.6.

First stage selection was within groups of boars that were available within a time period of two weeks. Average number of boars available per time period of two weeks was 32. The number of boars was quite variable over time periods. Averaged over alternatives, a standard deviation of 5 boars was found.

Annual number of boars tested without first stage selection (i.e. $p_1=100\%$) was equal to 832 (32×26). Accounting for 40% non-genetic culling of boars at the end of test and 40% culling at sexual maturity, proportion of males selected was equal to 0.067 with 20 boars used per year, and 0.134 with 40 boars used per year.

Averaged over alternatives, 66 gilts were tested per time period of two weeks, which means an annual number of 1716 (66×26). Without sequential culling, on average 296 replacement gilts were needed per year. Accounting for 20% non-genetic culling at the end of test and 20% culling at sexual maturity (Table 3), proportion of females selected was equal to 0.267.

3.2. Characteristics of selection indices

Variances of aggregate genotype (equations 5 and 6) and accuracies of selection for production and reproduction traits (e.g. correlations between

indexes and true breeding values) were studied to explain effects of time of selection on genetic responses for both groups of traits.

Data of the simulated boars just before testing (two months of age) were used to estimate accuracy of first stage selection of boars. Data of tested boars and gilts (minus cullings at the end of test (Table 3)) at time of their sexual maturity (eight months of age) were used for the other parameters. Results are in Table 4 and 5. Variances of selection indexes were approximately equal to $r_{IH}^2 \times \sigma_H^2$.

Accuracy of selection of boars on production traits after the test was increased (r_{I2H} vs. r_{I1H} in Table 4) due to inclusion of own performance data in the production index. This increase was high because of the high accuracy of these data compared to pedigree data. Sequential culling of sows and first stage selection of boars had little influence on the accuracies of the production indexes.

Comparison of Table 4 and 5 shows that the variance of the first stage index of boars for production traits ($r_{I1H}^2 \times \sigma_{Hprod}^2$) was much smaller than the variance of the first stage index for reproduction traits ($r_{I1H}^2 \times \sigma_{Hrepr}^2$). This means that the reproduction index dominated the overall index for first stage selection.

The alternatives with $p_1=100\%$ in Table 5 show that accuracy of the reproduction indexes increased after the test (r_{I2H} vs. r_{I1H}), because more litter records of relatives (dam, female sibs of parents) became available. Averaged over alternatives with $p_1=100\%$, a small increase from 0.244 to 0.272 was observed. This means that the additional information (extra litter records of relatives) was limited. As a result, correlations between first and second stage reproduction indexes were high.

Sequential culling of sows reduced accuracy of selection on reproduction traits (Table 5). The reduction can be explained by the higher proportion of animals out of first litters (63-64% vs. 44%), which reduced the accuracy of information from the dams.

Due to the high contribution of the reproduction index in first stage selection, the remaining boars after this stage (i.e. the tested boars) showed reduced variances of aggregate genotype and accuracies of 2nd stage indexes for reproduction traits (Table 5). Comparison of the values from boars with the values from gilts reveals the effects of first stage selection, as selection before the test was not applied for gilts.

Table 4. Accuracies of 1st stage production indexes of boars (r_{11H}), 2nd stage production indexes of boars and gilts (r_{12H}), correlations between 1st and 2nd stage production indexes of boars (r_{11I2}) and variances of aggregate genotype for production traits (σ^2_{Hprod}) (averaged over years 3 to 25).

Popula- tion ¹⁾	Sel. syst. ²⁾	p_1 ³⁾	boars				gilts	
			r_{11H}	r_{12H}	r_{11I2}	σ^2_{Hprod}	r_{12H}	σ^2_{Hprod}
200/20	NSC	100%	0.232	0.471	0.444	9.73	0.326	10.40
		50%	0.222	0.464	0.440	9.63	0.325	10.35
		33%	0.231	0.470	0.451	9.55	0.326	10.42
		25%	0.225	0.479	0.442	9.69	0.328	10.41
	SC	100%	0.232	0.475	0.447	9.98	0.331	10.60
		50%	0.233	0.474	0.448	9.71	0.332	10.42
		33%	0.222	0.465	0.447	9.48	0.323	10.18
		25%	0.222	0.456	0.445	9.29	0.321	10.09
200/40	NSC	100%	0.246	0.493	0.471	10.04	0.351	10.74
		50%	0.246	0.490	0.467	10.06	0.347	10.84
		33%	0.248	0.485	0.474	9.80	0.351	10.63
		25%	0.245	0.497	0.480	9.93	0.348	10.65
	SC	100%	0.234	0.487	0.462	10.06	0.336	10.81
		50%	0.249	0.490	0.470	10.11	0.348	10.79
		33%	0.244	0.483	0.466	9.92	0.342	10.57
		25%	0.245	0.488	0.487	9.86	0.345	10.58

1) Number of sows/annual number of boars.

2) NSC: no sequential culling; SC: sequential culling of sows.

3) Proportion of boars selected in first stage.

4) Range of standard errors on replicate means: 0.004-0.010 for r_{11H} ;
0.003-0.009 for r_{12H} ; 0.003-0.009 for r_{11I2} ; 0.06-0.24 for σ^2_{Hprod} .

Table 5. Accuracies of 1st stage reproduction indexes of boars (r_{I1H}), 2nd stage reproduction indexes of boars and gilts (r_{I2H}), correlations between 1st and 2nd stage reproduction indexes of boars (r_{I1I2}) and variances of aggregate genotype for reproduction traits (σ^2_{Hrepr}) (averaged over years 3 to 25).

Popula- tion ¹⁾	Sel. syst. ²⁾	$p_1^{3)}$	boars				gilts	
			r_{I1H}	r_{I2H}	r_{I1I2}	σ^2_{Hrepr}	r_{I2H}	σ^2_{Hrepr}
200/20	NSC	100%	0.263	0.296	0.865	41.28	0.294	40.79
		50%	0.254	0.235	0.782	38.70	0.282	40.45
		33%	0.249	0.219	0.772	38.27	0.281	40.73
		25%	0.251	0.218	0.756	37.74	0.279	40.56
	SC	100%	0.230	0.253	0.852	39.16	0.254	39.33
		50%	0.224	0.230	0.791	38.89	0.250	39.44
		33%	0.224	0.218	0.772	38.23	0.253	39.90
		25%	0.214	0.213	0.762	36.17	0.247	38.56
200/40	NSC	100%	0.255	0.283	0.879	42.98	0.279	42.75
		50%	0.261	0.239	0.806	41.27	0.287	43.12
		33%	0.255	0.240	0.801	39.46	0.287	42.07
		25%	0.255	0.222	0.778	38.99	0.279	41.65
	SC	100%	0.228	0.256	0.875	43.09	0.252	42.79
		50%	0.231	0.224	0.811	40.26	0.246	41.39
		33%	0.224	0.217	0.802	40.26	0.249	41.75
		25%	0.219	0.219	0.783	38.55	0.245	40.50

1) Number of sows/annual number of boars.

2) NSC: no sequential culling; SC: sequential culling of sows.

3) Proportion of boars selected in first stage.

4) Range of standard errors on replicate means: 0.005-0.011 for r_{I1H} ; 0.005-0.015 for r_{I2H} ; 0.003-0.009 for r_{I1I2} ; 0.29-0.82 for σ^2_{Hrepr} .

In the base population, production and reproduction traits were uncorrelated. However, reproduction and production indexes of the tested animals in the simulated populations were negatively correlated. The correlations between first stage indexes ranged from -0.2 to -0.3, while the correlations between second stage indexes ranged from -0.1 to -0.2. The negative correlations between production and reproduction indexes of boars and gilts were a result of selection of their parents.

Accuracies of the production indexes in Table 4 were reduced due to the mild independent culling on own performance production index (Table 3). The two extra simulated alternatives without independent culling at the end of test (no sequential culling of sows, $p_1=100\%$) can be used to quantify this effect. Results are in Table 6. Comparison of these values

Table 6. Accuracies of 1st stage production indexes (PROD), reproduction indexes (REPR) and overall indexes (OVERALL= PROD + REPR) of boars (r_{11H}), 2nd stage indexes of boars and gilts (r_{12H}), correlations between 1st and 2nd stage indexes of boars (r_{11I2}) and variances of aggregate genotype (σ^2_H) (averaged over years 3 to 25) in the alternatives without independent culling on own performance production index (no sequential culling of sows and $p_1^{1)}=100\%$).

Popula- tion ²⁾	boars				gilts	
	r_{11H}	r_{12H}	r_{11I2}	σ^2_H	r_{12H}	σ^2_H
PROD						
200/20	0.238	0.551	0.424	10.92	0.388	10.94
200/40	0.255	0.571	0.445	11.29	0.406	11.33
REPR						
200/20	0.261	0.287	0.870	40.19	0.288	39.96
200/40	0.267	0.295	0.885	42.22	0.295	42.18
OVERALL						
200/20	0.227	0.346	0.617	50.41	0.288	50.30
200/40	0.223	0.348	0.621	52.15	0.289	52.20

1) Proportion of boars selected in first stage.

2) Number of sows/annual number of boars.

with the values in Table 4 (NSC, $p_1=100\%$) shows (on average) a reduction of 14% for accuracy of 2nd stage production indexes of boars. Effects of independent culling on accuracy of 1st stage production indexes were limited. The same holds for the reproduction indexes (Table 5). Due to the lower accuracies of the production indexes, accuracies of 2nd stage overall indexes of boars were reduced by 9%. Accuracies of overall indexes of gilts were reduced by 6%.

3.3. Selection response

Realized responses to selection for production and reproduction traits were expressed in Dfl. using the economic weights of equations (5) and (6). Values of the response in year 25, averaged over replicates, are given in Table 7. Overall response was calculated as the sum of response for production and reproduction traits. The standard errors of the responses can be multiplied by the square root of the number of replicates ($\sqrt{10}$) to give the standard deviations of the response.

Sequential culling gave a small improvement in overall response (on average 2.4%). Under this system the limited number of sow places in the nucleus were used in an optimal way. Averaged over alternatives, an improvement of 1% was found for production traits and 4% for reproduction traits. The higher improvement for reproduction traits compared to production traits can be explained by the extra stages of selection of females at older age (after one or more litters) and the reduced selection intensity at young age (at sexual maturity). Accuracy of the reproduction index increases with parity number, which is not the case for production traits.

Reduction of the proportion of males tested (p_1) gave small reductions in overall response. As was shown in Tables 4 and 5, selection on reproduction traits was already very effective before the test, while possibilities of selection on production traits were limited. Therefore, the reductions in overall response were due to lower responses for production traits. From $p_1=100\%$ to $p_1=50\%$, reductions in overall response were small (on average 3.5%). With $p_1=25\%$, on average a reduction of 9.4% was found. The relation between p_1 and overall response was not influenced

much by the selection system of sows (NSC or SC), and was also not very sensitive to annual number of boars (20 or 40).

Table 7. Cumulative realized responses (in Dfl.) up to year 25 for production (PROD) and reproduction traits (REPR), realized overall response (OVERALL= REPR + PROD), predicted overall response (R_p) (in Dfl.), and realized inbreeding coefficient in year 25 (F)

Popula- tion ¹⁾	Sel. syst.	$p_1^{3)}$	PROD	REPR	OVERALL	R_p	F
200/20	NSC	100%	26.90 $\pm 0.82^{4)}$	31.98 ± 0.79	58.88 ± 1.32	63.86	16.5 ± 0.4
		50%	26.23 ± 0.77	31.34 ± 0.77	57.57 ± 0.80	63.56	16.2 ± 0.3
		33%	24.29 ± 0.61	30.74 ± 0.78	55.03 ± 1.03	62.84	16.4 ± 0.5
		25%	22.94 ± 0.67	29.85 ± 0.90	52.79 ± 0.85	61.99	16.6 ± 0.4
	SC	100%	28.74 ± 0.74	32.51 ± 0.90	61.24 ± 1.11	--	17.8 ± 0.5
		50%	26.07 ± 0.62	31.80 ± 1.20	57.87 ± 1.34	--	18.1 ± 0.6
		33%	24.06 ± 0.76	31.12 ± 0.74	55.19 ± 1.14	--	17.9 ± 0.4
		25%	22.17 ± 0.60	32.48 ± 1.06	54.65 ± 0.88	--	18.9 ± 0.5
	NSC	100%	25.06 ± 0.44	28.82 ± 0.91	53.87 ± 1.01	58.09	11.0 ± 0.2
		50%	23.38 ± 0.45	29.52 ± 0.70	52.90 ± 0.80	57.31	11.2 ± 0.2
		33%	20.80 ± 0.59	30.50 ± 1.01	51.30 ± 1.01	55.79	11.8 ± 0.2
		25%	19.87 ± 0.35	30.48 ± 0.64	50.35 ± 0.83	54.04	12.5 ± 0.2
	SC	100%	26.36 ± 0.43	30.50 ± 0.94	56.86 ± 1.04	--	11.9 ± 0.2
		50%	23.42 ± 0.49	31.01 ± 0.88	54.43 ± 1.04	--	12.3 ± 0.2
		33%	20.59 ± 0.50	31.03 ± 0.79	51.62 ± 0.97	--	12.9 ± 0.3
		25%	19.56 ± 0.50	31.79 ± 0.63	51.35 ± 0.80	--	12.6 ± 0.2

1) Number of sows/annual number of boars.

2) NSC: no sequential culling; SC: sequential culling of sows.

3) Proportion of boars selected in first stage.

4) Standard error.

3.4. Theoretical predictions of selection response

Values of parameters used to calculate predicted cumulative overall responses (equations 14 - 16) are in Table 8. These values were derived from the two extra populations that were simulated without the mild independent culling of pigs on own performance production index, without sequential culling of sows and with $p_1=100\%$.

Selection intensity of males after test was equal to 1.94 with 20 boars per year (population 200/20) and 1.62 with 40 boars per year (200/40). Predicted cumulative overall responses in year 25 (R_p) were then equal to Dfl. 63.86 (200/20) and 58.09 (200/40) (Table 7).

With 20 boars per year, reductions in overall responses due to first stage selection of boars were higher than predicted (Table 7). For $p_1=25\%$ (relative to $p_1=100\%$), a reduction of 3% was expected with the theoretical formulas, while the realized reduction (averaged over NSC and SC) was 11%. With 40 boars per year, the predicted reduction was 7%, while the average realized reduction was 8%.

Table 8. Parameters used for theoretical predictions of overall selection response.

	Population:	200/20	200/40
Proportion of males selected ($p_1 \times p_2$)		0.067	0.134
Selection intensity of females (i_f)		1.23	1.23
Stand. dev. of overall aggregate genotype in Dfl. (σ_H)		7.10	7.22
Accuracy of 1st stage overall index for boars ($r_{I1H,m}$)		0.227	0.223
Accuracy of 2nd stage overall index for boars ($r_{I2H,m}$)		0.346	0.348
Correlation between 1st and 2nd stage overall indexes of boars ($r_{I1I2,m}$)		0.617	0.621
Accuracy of overall index for gilts ($r_{IH,f}$)		0.288	0.289
Generation interval in years (L)		1.31	1.31

3.5. Inbreeding coefficient

Sequential culling (SC) gave higher coefficients of inbreeding (F) in year 25 (Table 7), which can be explained mainly by the reduced generation interval. Generation interval (based on selected animals) was reduced from 1.30-1.31 to 1.25-1.27 years.

A lower proportion of boars selected in first stage gave on average a small increase in rate of inbreeding. This increase resulted from higher variances in family size for males to males and for females to males due to more emphasis on pedigree information (relative to own performance data).

4. DISCUSSION AND CONCLUSIONS

4.1. First stage selection

Theoretical predictions of response (section 2.6) were used to explain the influence of first stage selection on overall response. A simplification in the predictions was that the small proportion of independent culling at the end of test on own performance production index was ignored. A truncation point of one standard deviation below average (Table 3) means a culling proportion of 16%. Because of this small proportion, it was expected that reductions in overall response due to this culling would be limited.

In the population with 20 boars per year, the reductions in overall response due to first stage selection were higher than theoretically predicted (Table 7). Selection at this stage was within batches, and mainly based on pedigree indexes for reproduction traits. Within these batches sometimes very few families were available. This reduced selection intensity (Hill, 1976, 1977). The theoretical predictions of response assumed infinite population size, which means that they did not account for reductions in selection intensity due to family structure.

With 40 boars used per year, the predicted reductions in response due to first stage selection were in agreement with the realized reductions. Optimization of first stage selection in dam lines with 40 boars or more (used per year) is possible with a deterministic model, as in these

populations selection response will not be much affected by family structure.

The influence of first stage selection of boars on response depends on the number of boars tested per litter. In the present study, a maximum of two boars per litter was tested (Table 3). On average four boars per litter were available. With more boars tested per litter, selection intensity after the test is higher. Based on the theoretical prediction formulas (section 2.6) a smaller influence of first stage selection on response is then expected. The same holds for increase of the number of sows with a fixed number of boars.

In the present study, only individual test results and pedigree information (indexes of parents) were used for selection on production traits. Use of half-sib information will increase accuracy of second stage production indexes, and thus decrease the correlation between first and second stage overall indexes. As a result, response will be more affected by first stage selection.

Another consequence of the use of half-sib information would be that accuracy of (second stage) production indexes becomes dependent on the number of boars tested. First stage selection will then reduce accuracy of selection. However, half-sib information does not only come from tested boars but also from tested gilts. Due to the large number of tested female half-sibs, effects of first stage selection of boars on accuracy of selection would be small.

First stage selection of boars reduces response to selection, but also costs of the breeding programme. The reduction in costs can be derived from the difference in profit between a boar fattened in a test division and a pig fattened under commercial conditions. The difference in profit can be due to lower returns for entire boars and higher costs for housing and labour.

Selection before the test makes it possible to increase nucleus population size without large extra costs. Some breeding organizations have a small nucleus and use subnucleus herds to produce the required number of purebred gilts for the multiplier herds. However, enlargement of the nucleus can give a considerable improvement in response, while also rate of inbreeding can be reduced. Webb and Bampton (1987) report on a breeding programme with dam lines which were enlarged to 1000 sows. In these lines

40% of the progeny is performance tested. Moreover, the enlarged nucleus removed the need for subnucleus herds, which resulted in a reduced time lag between nucleus and commercial levels.

The optimum proportion of first stage selection of boars (p_1) depends on the marginal costs and returns of a test place. In a breeding pyramid with a large nucleus (relative to the number of commercial sows), a low proportion of boars tested can be justified because of the relatively large reduction in costs for testing.

4.2. Sequential culling

Richard et al. (1973) suggested that sequential culling could improve genetic gain in pig breeding programmes. Hagenbuch and Hill (1978) used the methods of Hopkins and James (1977) to quantify the benefits of sequential culling of boars and sows for selection on production traits. They found only 2-3% extra response, and stated that such a small improvement might be not sufficient to compensate for the operational difficulties involved. However, in the study of Belonsky and Kennedy (1988) 41% extra response in production traits (with $h^2=0.3$) was found. This was probably mainly due to the high maximum age of boars (3 years). Wray (1989) used boars for a maximum of 30 weeks, and found 6% extra response from sequential culling (with $h^2=0.2$).

In the present study, sequential culling was not applied for boars. Such a system was expected to have a very small influence on selection response, as breeding boars were only used for a short time period (8 weeks). Moreover, when boars are culled as soon as a better replacement is available, variation in number of progeny born per boar will be high. This will reduce effective population size, and thus increase rate of inbreeding.

For selection on reproduction traits, use was made of an animal model for estimation of breeding values. As a result, family information was used and genetic trend was accounted for. This was not the case for selection on production traits. Individual test data were expressed as deviations from phenotypic batch means. As a result, production indexes of older animals were overestimated compared to younger potential replacements. If genetic trend had been taken into account for production traits, response

from alternatives with sequential culling (SC) would have been somewhat higher. However, the same holds for the alternatives without sequential culling (NSC). Based on the results of Hagenbuch and Hill (1978), only a small increase in the difference between SC and NSC is expected when corrections would have been made for genetic trend.

In the present study, fixed proportions of boars and gilts were culled for conformation (Table 3). Also sows were culled (after each parity) for conformation or health problems (section 2.4). Culling on conformation is expected to improve longevity of sows. Response to this type of culling was not taken into account in the evaluations of the alternative selection systems. The influence of sequential culling of sows on the genetic improvement of longevity traits is difficult to predict. It might be expected that it will give a small reduction in improvement of longevity traits, as culling on conformation is probably more effective at higher parities.

The relative benefits from sequential culling depend on the culling rates for non-genetic reasons and on the maximum number of age classes (Hopkins and James, 1977). In the present study, sequential culling of sows improved overall selection response only by 2-3%. This was probably mainly due to the high culling rates of sows for non-genetic reasons (about 40%) and the low maximum number of parities per sow (5). A further explanation is that sequential culling reduced accuracy of selection on reproduction traits (Table 5), which was due to the increase of accuracy of the reproduction index with parity number.

Sequential culling of sows increases the proportion of first parity sows. Litters from first parity sows are smaller than from older parity sows, which means a lower number of pigs born under sequential culling (Hagenbuch and Hill, 1978). However, in the simulated herds, this had hardly any effect on the number of boars and sows tested, because number of animals tested per litter (Table 3) was restricted.

Sequential culling had limited effects on rate of inbreeding. Main disadvantages of the system are the higher costs for the breeding scheme due to the higher replacement rate of sows. Average number of replacement gilts needed per sow place per year in the present study was 1.5 for NSC and 2.1 for SC. However, the extra costs of sequential culling of sows depend on the destination of the culled sows. They are high when these sows

are slaughtered, as the lower number of pigs born per litter (due to parity distribution) and the higher number of replacement gilts needed reduce the output of purebred animals for subnucleus purposes. When culled sows are used for subnucleus purposes, extra costs from sequential culling can be limited.

4.3. Conclusions

From $p_1=100\%$ to $p_1=50\%$ the reduction in response was on average 3.5%, while from $p_1=50\%$ to $p_1=25\%$ the reduction was an additional 6%. The optimum of p_1 depends on the costs for testing, and on the size of the nucleus population relative to the total breeding pyramid. With a relatively large nucleus breeding herd, a low proportion of boars tested can be justified.

Sequential culling gave on average 2-3% extra response for production and reproduction traits. It had limited influence on rate of inbreeding.

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APPENDIX

Derivation of weighting factors for production indexes.

Optimal weighting factors for the pedigree index ($-0.5(I_{\text{prod,sire}} + I_{\text{prod,dam}})$) and the own performance index ($I_{\text{prod,own}}$) in equations (11) and (13) were derived from selection index theory.

$$\begin{pmatrix} b_p \\ b_o \end{pmatrix} = P^{-1} G = \begin{pmatrix} r^2_{IH_p} \sigma^2_H & r^2_{IH_p} r^2_{IH_o} \sigma^2_H \\ r^2_{IH_p} r^2_{IH_o} \sigma^2_H & r^2_{IH_o} \sigma^2_H \end{pmatrix}^{-1} \begin{pmatrix} r^2_{IH_p} \sigma^2_H \\ r^2_{IH_o} \sigma^2_H \end{pmatrix}$$

where b_p and b_o are weighting factors for the pedigree index and the own performance index, P is the variance-covariance matrix of indexes, G is

the covariance matrix of indexes with aggregate genotype, r_{IH_p} and r_{IH_o} are accuracies of the indexes.

This leads to:

$$b_p = (1 - r_{IH_o}^2) / (1 - r_{IH_p}^2 r_{IH_o}^2)$$

$$b_o = (1 - r_{IH_p}^2) / (1 - r_{IH_p}^2 r_{IH_o}^2).$$

Accuracy of the own performance index (r_{IH_o}) was 0.5804 for boars and 0.3716 for gilts. Accuracy of the pedigree index (r_{IH_p}) was equal to $\sqrt{(0.25(r_{IH,sire}^2 + r_{IH,dam}^2))} = \sqrt{(0.25(0.5804^2 + 0.3716^2))} = 0.3446$.

For boars this gives $b_p = 0.6907$ and $b_o = 0.9180$, and for gilts $b_p = 0.8763$ and $b_o = 0.8959$.

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Chapter 6

OPTIMAL USE OF NUCLEUS AND TESTING CAPACITY IN A PIG BREEDING SYSTEM WITH SIRE AND DAM LINES

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ABSTRACT

In the short term, total nucleus and testing facilities of a pig breeding organization are fixed, but distributions over sire and dam lines can be varied. The objective of this study was to optimize these distributions.

Effects of alternative distributions of nucleus places for sows and testing capacity for boars on total selection response were studied with a semi-deterministic model. Parameters used in this model were derived from stochastic simulation studies.

Conclusions (for four-way crossbreeding systems) were as follows:

- The optimum ratio of sow places for sire lines to sow places for dam lines was about 1 : 2.
- The optimum ratio of boar testing capacity for sire lines to boar testing capacity for dam lines was about 1 : 1.
- Optimum ratios depended on total testing capacity relative to total number of sow places in the nucleus. Optimum ratios were also sensitive to testing system (maximum number of boars tested per litter). Culling rate of boars after test (for conformation or semen quality) and crossbreeding system (three-way vs. four-way cross) had only slight influence.

1. INTRODUCTION

Many pig breeding organizations have a closed nucleus with specialized sire and dam lines. Sire lines are selected for production traits (growth and carcass traits), dam lines for production and reproduction traits (litter size). Test places are important for selection on production traits, while sow places in the nucleus are important for selection on reproduction traits. In the short term, total nucleus facilities and testing capacity of a breeding organization are fixed, but distribution over lines can be varied. Therefore, optimization of this distribution is very relevant. This has been studied before, among others by Minkema (1973), Niebel and Fewson (1979) and Schmid (1984). However, these studies were focussed on production traits. They did not include the important influence of number of nucleus sows on selection response for reproduction traits.

The objective of this study is to optimize the distribution of sow places

in the nucleus and boar testing capacity over sire and dam lines in a breeding programme with selection for production and reproduction traits. For this purpose, effects of alternative distributions on predicted total selection response were studied.

Predictions of selection response with a stochastic approach was not suitable due to the large number of alternatives that had to be evaluated. A deterministic approach based on parameters of unselected populations was too complicated, as it was difficult to account for the influence of selection, inbreeding and the variation in information available for selection (number of parities, number of relatives). Therefore another approach was followed, which might be referred to as semi-deterministic. Selection responses were predicted with a deterministic model, while parameters used in this model were derived from stochastic simulation. This approach appeared to give good predictions, provided that enough families were available for selection (De Vries et al., 1989b).

2. MATERIAL AND METHODS

2.1. Model

Two stages of selection were distinguished for males. First stage selection was before the performance test (at two months of age), while second stage selection took place after the test at sexual maturity (at eight months of age). Selection before the performance test was not considered for females, as in many breeding programmes testing costs for these animals are relatively low. Moreover, a large number of tested gilts can be used for subnucleus purposes.

Predicted annual response (R_p) was calculated from expected genetic selection differentials for males (S_m) and females (S_f). To take two-stage selection into account, S_m was calculated using the method of Cochran (1951).

$$R_p = (S_m + S_f) / (2 \times L) \quad (1)$$

$$S_m = \sigma_H \times (r_{I1H,m} \times z_1 \times p_2' + r_{I2H,m} \times z_2 \times p_1') / (p_1 \times p_2) \quad (2)$$

$$S_f = i_f \times r_{IH,f} \times \sigma_H \quad (3)$$

where L is the generation interval;
 σ_H is the standard deviation of overall aggregate genotype;
 $r_{IH,m}$ and $r_{IH,f}$ are the accuracies of first and second stage overall selection indexes of boars;
 $r_{IH,f}$ is the accuracy of the overall selection index for gilts;
 p_1 and p_2 are proportions of boars selected in first and second stage; and
 i_f is the selection intensity for females.

Variables z_1 and z_2 are the ordinates of a univariate normal curve corresponding to truncation points (k_1 and k_2) for first and second stage of selection. Values for k_1 and k_2 were derived with a bivariate normal distribution function with correlation r_{II12} , while the proportions p_1' and p_2' are the integrals of a univariate normal curve corresponding to truncation points k_1' and k_2' :

$$k_1' = (k_1 - r_{II12} \times k_2) / \sqrt{(1 - r_{II12}^2)}$$

$$k_2' = (k_2 - r_{II12} \times k_1) / \sqrt{(1 - r_{II12}^2)}$$

2.2. Parameters from simulation

Parameters were derived from simulations with a stochastic model developed for closed pig populations (De Roo, 1987 and 1988; De Vries et al., 1989a). The simulations described by De Vries et al. (1989b) were done for dam lines. In addition, similar simulations were done for sire lines, with the exception that the breeding goal for sire lines did not include reproduction traits. Values derived from the simulations are given in Table 1.

The simulated populations consisted of 200 sows. In dam lines a higher annual number of boars is optimal than in sire lines. Annual number of boars used was 20 in the sire lines and 40 in the dam lines. These numbers of boars were needed for an acceptable rate of inbreeding (about 0.5% per year) (De Roo, 1988, De Vries et al., 1989a).

Production traits in the breeding goal were growth rate, feed intake and

Table 1. Parameters used for predictions of selection response.

	Population:	Sire line	Dam line
Selection intensity of females (i_f)		1.23	1.23
Stand. dev. of aggregate genotype in Dfl. (σ_H)		3.30	7.22
Accuracy of 1st stage index for boars ($r_{11H,m}$)		0.143	0.223
Accuracy of 2nd stage index for boars ($r_{12H,m}$)		0.532	0.348
Correlation between 1st and 2nd stage indexes of boars ($r_{1112,m}$)		0.301	0.621
Accuracy of index for gilts ($r_{1H,f}$)		0.343	0.289
Generation interval in years (L)		1.31	1.31

lean percentage in the carcass. Boars and gilts were performance tested from 23-100 kg. Traits in the production indexes of boars were growth rate, feed intake and estimated lean percentage, while the production indexes of gilts contained growth rate and side fat thickness. Only own performance data were used in the production indexes.

Reproduction traits in the breeding goal for dam lines were size of the first litter and average size of later litters. Breeding values for these traits were estimated with an animal model taking all relevant family relationships into account (De Vries et al., 1989a). Genetic and phenotypic correlations between production and reproduction traits were assumed to be zero (Brien, 1986)

First stage selection of males was before the test. Selection was on pedigree index, which contained the production indexes (and in dam lines also the reproduction indexes) of sire and dam. Selection before the test was not applied for females.

Sows produced two litters per year. A maximum of two boars per litter was tested. At the end of test and at sexual maturity, some males (40%) and females (20%) were culled for reasons not related to the breeding goal (conformation, semen quality). Culling chances for these reasons were independent of production and reproduction traits.

Selection between the remaining males and females at sexual maturity

(second stage of selection for males, and the only stage of selection for females) was on an index that combined the production indexes (and in dam lines also the reproduction indexes) of parents with the own performance index for production traits.

Sows with one or more litters were not culled on index (no sequential selection). Culling was related only to conformation or fertility problems. The sows could stay in the herd for a maximum of 5 parities. Proportion of litters from first parity sows was 44%.

2.3. Basic situation

The basic situation studied with the semi-deterministic approach corresponded to the characteristics of the simulated populations.

Number of boars used per year was 20 for the sire lines and 40 for the dam lines. Maximum number of boars tested per litter was two. Culling rate of boars was 40% at the end of test (conformation) and again 40% at sexual maturity (conformation, semen quality), which means a total culling rate of 64%.

The nucleus consisted of two sire and two dam lines (four-way cross-breeding system).

2.4. Alternative situations

Optimization of distribution of nucleus and testing facilities under alternative situations is interesting because of the differences in breeding schemes between pig breeding organizations. The optimal distributions were expected to be sensitive to testing system (maximum number of boars tested per litter), culling rate of boars for conformation or semen quality, and the crossbreeding system. Therefore, three alternative situations were studied:

- An increase of maximum number of tested boars per litter from 2 to 3.
- An increase of the number of boars available for selection on index after test by 50% due to a decreased culling rate of tested boars from 64% to 46%.
- A three-way cross (one sire line) instead of a four-way cross (two sire lines).

3. RESULTS

3.1. Basic situation

A breeding programme with 1200 sow places in the nucleus and testing capacity for 2400 boars per year is used to show the influence of alternative distributions of nucleus and testing facilities on total selection response (Table 2). Number of nucleus sows for each of the two

Table 2. Effects of distribution of sow places in the nucleus over lines ($SP_s/SP_d^{1)}$) and first stage selection of boars in sire lines ($pl_s^{2)}$) on predicted total selection response (expressed in % relative to the optimum) in basic situation³⁾. Corresponding proportions of boars selected in first stage in dam lines are given between brackets.

$SP_s/SP_d^{1)}$	$pl_s^{2)}$					
	0.50	0.60	0.70	0.80	0.90	1.00
50/550	89.3 (0.50)	90.8 (0.49)	91.8 (0.48)	92.6 (0.47)	93.2 (0.46)	93.5 (0.45)
100/500	95.5 (0.50)	96.5 (0.48)	97.1 (0.46)	97.6 (0.44)	97.9 (0.42)	98.1 (0.40)
150/450	97.9 (0.50)	98.6 (0.47)	99.1 (0.43)	99.5 (0.40)	99.6 (0.37)	99.6 (0.33)
200/400	99.0 (0.50)	99.5 (0.45)	99.9 (0.40)	100.0 (0.35)	99.9 (0.30)	99.4 (0.25)
250/350	99.2 (0.50)	99.7 (0.43)	99.7 (0.36)	99.4 (0.29)	98.4 (0.21)	96.0 (0.14)
300/300	98.9 (0.50)	99.1 (0.40)	98.6 (0.30)	97.0 (0.20)	89.7 (0.10)	--- (0.00)

1) Number of sow places for sire line / Number of sow places for dam line.

2) Proportion of boars selected in first stage in sire line.

3) For a breeding programme with 1200 sow places in the nucleus and 2400 test places (per year) for boars.

sire lines (SP_s) was increased from 50 to 300 sows, which implied that size of the dam lines (SP_d) decreased from 550 to 300 sows. For each alternative distribution of sow places, proportion of boars selected in first stage in the sire lines (pl_s) was varied. The optimum combination (i.e. the combination with maximum predicted total response) was $SP_s/SP_d=200/400$ and $pl_s=0.80$. The corresponding proportion of tested boars in dam lines (pl_d) was then equal to 0.35. Table 2 gives the predicted responses for alternative combinations relative to the maximum response.

An increase of SP_s/SP_d from 50/550 to 200/400 (with optimal levels for pl_s) gave 6% improvement of response (Table 2). Within the range between 150/450 and 300/300, effects of variation of SP_s/SP_d were limited. The influence of pl_s on selection response was small when no extreme values were chosen. The optimum value for pl_s depended on the distribution of sow places. An increased size of the sire lines decreased the optimum value for pl_s (from 1.00 to 0.60), but the corresponding absolute number of test places for each of the sire lines was increased (from 200 to 720).

The larger optimal size of dam lines compared to sire lines (Table 2) is due to inclusion of reproduction traits in the breeding goal. This increased possibilities for selection, especially for first stage selection (Table 1). Another aspect is the number of boars used per year, which was higher in dam lines (40) than in sire lines (20). A higher number of boars makes selection intensity more sensitive to the number of sows, which means a larger optimal population size.

First stage selection gave in dam lines only a small reduction in selection response, due to the high accuracy of selection in this stage (Table 1). This explains the low optimal value of pl_d (0.35) compared to pl_s (0.80).

Table 3 shows the optimum distributions of nucleus and testing facilities for breeding programmes with 600 to 1800 sow places and 1200 to 4800 test places (per year). It was assumed that sows produce 2 litters per year. A maximum of 2 boars per litter was tested in the basic situation. This means 4 boars available for testing per sow per year.

The breeding programme with 600 sow places and 1200 test places per year had the highest selection response when 32% of the sow places and 49% of the test places were used for the sire lines. The proportion of boars

Table 3. Optimal fractions of sow places (SP_s/SP_t) and test places (TP_s/TP_t) for sire lines, together with corresponding proportions of boars selected in first stage in sire and dam lines (pl_s , pl_d) and predictions of total annual selection response (R_p) (Dfl.) for basic situation.

$SP_t^{1)}$	$TP_t^{2)}$	SP_s/SP_t	TP_s/TP_t	pl_s	pl_d	R_p
600	1200	.32	.49	0.77	0.37	3.988
	2400	.40	.40	1.00	1.00	4.116
1200	1200	.28	.50	0.44	0.18	4.327
	2400	.33	.53	0.80	0.35	4.573
	3600	.38	.51	0.99	0.60	4.640
	4800	.40	.40	1.00	1.00	4.650
1800	1200	.27	.50	0.31	0.12	4.495
	2400	.31	.54	0.58	0.22	4.772
	3600	.34	.55	0.81	0.34	4.872
	4800	.37	.54	0.96	0.49	4.915

1) Total number of sow places in the nucleus.

2) Total number of boars tested per year.

tested in this situation was 77% in the sire lines $((0.49 \times 1200)/(0.32 \times 600 \times 4))$ and 37% in the dam lines.

The optimal values for SP_s/SP_t ranged between 0.27 and 0.40. The values in Table 3 show that the optimal distribution of sow places was sensitive to total testing capacity relative to total number of sow places. Increase of total testing capacity (TP_t) resulted in an increase of the optimal value for SP_s/SP_t (i.e. larger optimal size of the sire lines), while increase of total number of nucleus sows (SP_t) gave a decrease of this ratio (Table 3). These effects can be explained by the low accuracy of first stage selection in sire lines (Table 1). Extra sow places with fixed testing capacity increases intensity of first stage selection, which has only a small impact on selection response in sire lines. The impact on selection response in dam lines is much larger. Therefore, most of the extra sow places are used for dam lines.

The optimal value for TP_s/TP_t was in most situations close to 0.50. Special situations are the alternatives with $SP_t=600$ and $TP_t=2400$ and with $SP_t=1200$ and $TP_t=4800$. In these situations all boars can be tested, which implies that TP_s/TP_t has to be equal to SP_s/SP_t .

The values of R_p in Table 3 show the influence of SP_t and TP_t on total selection response. Increase of SP_t from 600 to 1200 sow places improved response with 9-11% (dependent on TP_t). The influence of TP_t on response was quite small.

3.2. Alternative situations

Table 4 and 5 give the optimal distributions of nucleus and testing facilities for the alternative sets of parameters. Comparison of these values with the values for the basic situation (Table 3) reveals the influence of the parameters that were varied.

A higher maximum number of boars tested per litter (alternative A in Table 4) had exactly the same influence as an increase of the total number of sows (SP_t). It reduced the optimal ratio of SP_s/SP_t , while the optimal ratio for TP_s/TP_t was increased. The breeding programmes with 1200 sows in this alternative situation were similar to the breeding programmes in Table 3 with 1800 sows, as the number of boars available for selection was similar. Results for breeding programmes with a maximum of one boar tested per litter can be derived from Table 3 and 4. For example, nucleus herds with 1200 sows and one boar tested per litter will give exactly the same results as the herds in Table 3 with 600 sows (maximum of two boars tested per litter).

A lower culling rate of boars after test (alternative B in Table 4) hardly affected optimal distribution of sow places, while for the optimal ratio of TP_s/TP_t a small increase was found. Note that alternative B with 2400 test places was similar to alternative A with 3600 test places, as they lead to similar proportions of boars selected.

The optimal size of the sire line in a three-way cross (Table 5) is somewhat lower than the optimal total size of the two sire lines in a four-way cross (Table 3). The same holds for testing capacity. The reduction can be explained by the reduced annual number of boars needed for sire lines (20 in three-way cross; 2 x 20 in four-way cross). A lower number of boars

Table 4. Optimal fractions of sow places (SP_s/SP_t) and test places (TP_s/TP_t) for sire lines, together with corresponding proportions of boars selected in first stage in sire and dam lines (pl_s, pl_d) and predictions of total annual selection response (R_p) (Dfl.) for alternative situations (A: maximum of 3 boars tested per litter; B: culling rate of boars equal to 46%).

$SP_t^{1)}$	$TP_t^{2)}$	SP_s/SP_t	TP_s/TP_t	pl_s	pl_d	R_p
Alternative A						
600	1200	.30	.50	0.56	0.24	4.196
	2400	.36	.52	0.95	0.51	4.409
1200	1200	.27	.50	0.31	0.12	4.495
	2400	.31	.54	0.58	0.22	4.772
	3600	.34	.55	0.81	0.34	4.872
	4800	.38	.54	0.96	0.49	4.915
1800	1200	.25	.50	0.22	0.08	4.647
	2400	.29	.54	0.41	0.15	4.946
	3600	.31	.56	0.60	0.21	5.066
	4800	.33	.57	0.76	0.29	5.129
Alternative B						
600	1200	.33	.52	0.79	0.36	4.343
	2400	.40	.40	1.00	1.00	4.437
1200	1200	.29	.52	0.45	0.17	4.674
	2400	.34	.55	0.81	0.34	4.872
	3600	.39	.51	0.99	0.60	4.925
	4800	.40	.40	1.00	1.00	4.931
1800	1200	.27	.52	0.32	0.11	4.838
	2400	.31	.56	0.60	0.21	5.066
	3600	.35	.57	0.82	0.33	5.149
	4800	.38	.55	0.97	0.48	5.184

1) Total number of sow places in the nucleus.

2) Total number of boars tested per year.

Table 5. Optimal fractions of sow places (SP_s/SP_t) and test places (TP_s/TP_t) for sire lines, together with corresponding proportions of boars selected in first stage in sire and dam lines (pl_s , pl_d) and predictions of total annual selection response (R_p) (Dfl.) for a three-way crossbreeding system.

$SP_t^{1)}$	$TP_t^{2)}$	SP_s/SP_t	TP_s/TP_t	pl_s	pl_d	R_p
600	1200	.31	.46	0.75	0.39	4.222
	2400	.37	.37	1.00	1.00	4.330
1200	1200	.27	.46	0.42	0.19	4.558
	2400	.32	.50	0.79	0.37	4.772
	3600	.36	.48	0.99	0.61	4.831
	4800	.38	.38	1.00	1.00	4.839
1800	1200	.26	.46	0.30	0.12	4.725
	2400	.30	.51	0.57	0.23	4.970
	3600	.33	.52	0.80	0.35	5.058
	4800	.36	.51	0.96	0.51	5.096

1) Total number of sow places in the nucleus.

2) Total number of boars tested per year.

reduces the impact of extra sow places on selection intensity, which means a smaller optimal population size.

Responses to selection (R_p) in the alternative situations (Table 4 and 5) were higher than in the basic situation (Table 3). This was due to higher selection intensities. Intensity of first-stage selection was affected by testing system. Intensity of second-stage selection depended on culling rate of boars after test and crossbreeding system.

4. DISCUSSION

In this study, distributions of nucleus and testing facilities over lines were optimized by maximization of total selection response. It was assumed that the distributions over lines have no influence on the costs of a breeding programme. This assumption is justified when alternative

distributions of sow places in the nucleus do not lead to changes in the total number of purebred animals of each line in the total production pyramid. This means that an increase of the size of a line at nucleus level is accompanied by a decrease of the size of this line at subnucleus level. However, this will not always be possible.

Optimal distributions of sow places depended on the relations between selection response and selection intensity in the sire and dam lines. Without first stage selection (i.e. all boars tested), equations (1)-(3) with the parameters in Table 1 lead to the following relations:

$$\begin{array}{ll} \text{sire lines:} & R_p = 0.53 + 0.67 \times i_m \quad (4) \\ \text{dam lines:} & R_p = 0.98 + 0.96 \times i_m \quad (5) \end{array}$$

where R_p is the predicted annual selection response; and
 i_m is the selection intensity of males.

The regression factors for i_m in these theoretical formulas show that the influence of selection intensity on selection response was in dam lines 43% larger as in sire lines. This resulted in the larger optimal size of dam lines (Table 3 and 4). Empirical formulas derived from realized selection responses in stochastic simulation studies with dam lines (De Vries et al., 1989a) and with sire lines (De Roo, 1988) showed almost the same difference in regression factors (45%). This means that an approach with stochastic simulation would have given the same optimal distributions of sow places as the present semi-deterministic approach.

The relations between selection response and proportion of first stage selection were important for optimization of the distribution of test places over lines. Again use was made of stochastic simulation to validate these relations. Provided that enough half-sib families were available for selection, the theoretical formulas (equations 1-3) appeared to give good predictions for dam lines (De Vries et al., 1989b). The same could be concluded for sire lines. Problems with a small number of half-sib families (resulting from a small annual number of boars) are that responses to first stage selection are overestimated, as the theoretical predictions do not account for reductions in selection intensity due to family structure (Hill, 1976, 1977).

The parameters in Table 1 were derived from simulated populations.

Selection on production indexes in these populations was based only on individual test results and pedigree information (indexes of parents). However, use of sib information can increase accuracy of second stage production indexes. This will have a relatively larger effect on the regression factor for i_m in sire lines (equation 4) than in dam lines (equation 5), as the breeding goal for dam lines also includes reproduction traits. Optimal size of sire lines will then be somewhat larger.

The generation interval in sire lines was equal to the generation interval in dam lines (Table 1). In the simulated herds, sows could be used for a maximum of 5 parities. However, some breeding organizations have in sire lines a shorter maximum stay of sows. Selection intensity of females and generation interval are then reduced. The reduced generation interval results in a higher regression factor in equation (4), and thus in a larger optimal size of sire lines.

Selection against congenital effects was not taken into account in this study. This type of culling reduces intensity of first stage selection. When the proportions of animals culled for this reason would be equal in sire and dam lines, it would have the same effects as a reduction of the total number of sow places. The sensitivity of optimal distributions of nucleus and testing capacity to total number of sow places was shown in Table 3.

For breeding organizations, it is important to know the optimum distributions of facilities over lines. However, in some situations these distributions can give practical problems. For example, a line can become too small to produce enough purebred animals for the breeding pyramid. In such situations, the consequences of deviations from the optimum need to be considered. The results in Table 2 showed that reductions in selection response at suboptimal distributions can be limited as long as no extreme values are chosen.

CONCLUSIONS

The conclusions that could be drawn from the results of this study were as follows:

- The optimum ratio of sow places for sire lines to sow places for dam lines was about 1 : 2.

- The optimum ratio of boar testing capacity for sire lines to boar testing capacity for dam lines was about 1 : 1.
- Optimum ratios depended on total testing capacity relative to total number of sow places in the nucleus. Optimum ratios were also sensitive to testing system (maximum number of boars tested per litter). Culling rate of boars after test (for conformation or semen quality) and crossbreeding system had only slight influence.

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GENERAL DISCUSSION

1. Definition of the breeding goal

The first part of optimization of selection for production and reproduction traits in pigs was definition of the breeding goal. This was studied in the first two chapters of this thesis. Definition of the breeding goal involves the derivation of weighting factors for the traits that can be changed by selection. The weighting factor of a trait should reflect the economic value of improvement of the trait for the organization that is responsible for the breeding programme (Elsen et al., 1986).

Weighting factors of traits in the breeding goal usually are derived by calculation of economic values at the commercial level, which is the level where slaughter pigs are produced. This approach was also followed in Chapter 1. An economic model was developed to estimate economic values of production and reproduction traits.

Traits directly selected on (measured traits) as well as genetically correlated traits were evaluated. Tess et al. (1983) directly included changes in correlated traits (e.g. mature weight of sows) in the economic values of selection traits (i.e. growth rate). This may also be done with the economic values derived in Chapter 1. Some of the relations for the model of Tess et al. (1983) could be used for this purpose. However, more research on relations between traits is needed.

Smith et al. (1986) imposed two conditions for derivation of economic values. The first was that extra profit resulting from extra output should not be included in the economic values. The second was that changes that correct previous inefficiency in the production enterprise should not be counted. With the strategy in Chapter 1, these two conditions could be coped with. Evaluation of traits was based on herd efficiency, and all costs were regarded as variable with the level of output.

In many situations, calculation of economic values at the commercial level will lead to an optimal breeding goal for the commercial herds as well as for the breeding organizations. However, direct use of these economic values as weighting factors in the breeding goal will not always be optimal. Four aspects may affect the breeding goal:

(1) competitive position of a breeding organization relative to other

- organizations;
- (2) expressions of traits at nucleus and sub-nucleus level;
 - (3) differences in time of expression between production and reproduction traits;
 - (4) biological interactions between traits.

The first aspect, the influence of competitive position on the value of improvement of a trait, was dealt with in Chapter 2. It was demonstrated that a trait with a low performance level (compared to other breeding organizations) should get more weight in the breeding goal. This aspect is especially relevant for the balance between selection for production and for reproduction traits. Reproduction traits are expressed in sow herds, whereas production traits are expressed in fattening herds. The breeding stock of an organization needs to be acceptable for both groups of herds.

Concerning the second and third aspect, De Vries and Van der Steen (1987) showed that the importance of reproduction traits relative to production traits increases when nucleus and sub-nucleus expressions of genetic improvement and differences in time of expression are taken into account. However, they also demonstrated that the two aspects influenced the relative weights of traits only to a small extent. Therefore, efficiency of selection was not much affected by inclusion of these aspects in the breeding goal. This conclusion does not hold for investment decisions. When financial returns from a certain investment have to be predicted, expressions of traits at all levels in the breeding pyramid have to be considered. Time lag between investment and returns then is also important.

Biological interactions between traits form the last aspect that can be important for definition of the breeding goal. A trait like daily feed intake has a negative economic value in the economic model in Chapter 1, because extra feed means extra production costs. Reduction of feed intake is therefore profitable in the short-term. However, in the long-term a reduced feed intake capacity can limit the genetic improvement of lean tissue growth rate (Fowler, 1986; Webb, 1986). Kanis (1988) showed that the economic value of feed intake capacity in a breeding goal with biological traits (feed intake capacity, maximum protein deposition rate and minimum fat to protein ratio) becomes positive when feed intake capacity is not high enough to realize potential protein deposition rate.

Genotype x Environment (G x E) interactions do not affect the breeding

goal, because the traits in the breeding goal should be defined at the commercial level (Brascamp et al., 1985). However, a low correlation between traits at the commercial level and corresponding traits at the nucleus level reduces the weighting factors for the index traits (measured at nucleus level). As a result, the balance between selection for production and for reproduction traits can be affected by G x E interactions, especially when they would exist for only one group of traits. G x E interactions for production traits were found among others by Merks (1988). For reproduction traits, no studies on G x E interactions within breeds could be found in literature, but the Crossbred type x Environment interactions reported by Knap (1989) give an indication that G x E interactions are also relevant for this group of traits. Further research on this subject is needed.

The aspects mentioned in this section show that definition of the optimal breeding goal for production and reproduction traits can be quite complicated, especially because of the large differences between these two groups of traits. From the studies on these aspects, however, it can be concluded that values derived with the economic model in Chapter 1 give a proper general basis for an optimal breeding goal. As shown in Chapter 2, some modification of the breeding goal can be necessary for the short-term benefits of a breeding organization when performance level of a trait deviates much from competitors. However, frequent and severe modifications are not recommended, because they will reduce long-term selection response (Chapter 2, Figure 3).

2. Evaluation of alternative breeding programmes

Optimization of several factors that determine the method of selection for production and reproduction traits in dam lines of pigs was dealt with in Chapters 3 to 5. In Chapter 6, distributions of nucleus and testing capacity over sire and dam lines were optimized.

The stochastic simulations in these chapters were done with a model developed by De Roo (1987) for closed pig populations (in particular for sire lines) and adapted for dam lines as described in Chapter 3. The model was quite suitable, because it was constructed specifically for nucleus populations of current pig breeding programmes. However, a few properties

of the model require some discussion:

- (1) stochastic approach;
- (2) biological plateaus for lean percentage and litter size;
- (3) selection for production on individual performance data;
- (4) correctness of data-sets;
- (5) no quantification of costs.

The first property, the stochastic approach, had the disadvantage of high computational requirements, especially after inclusion of the breeding value estimation procedure for reproduction traits in the model (described in Chapter 3). This limited the number of alternative breeding programmes that could be evaluated and prevented sensitivity analyses from being done (e.g. comparison of different heritabilities of traits).

A deterministic model would not have had high computational costs. It was not possible, however, to derive a proper deterministic model for the studies in this thesis. The model would have had to account for: linkage disequilibrium (i.e. reduced genetic variance due to selection in previous generations), deviations of breeding values from normality (due to earlier stages of selection), and differences in accuracy of selection between candidates for selection (e.g. because of different age classes). In addition, aspects of small populations were relevant: reductions of genetic variance due to inbreeding, reductions of selection intensity due to small numbers (small number of selection candidates, small number of families), and influence of selection on inbreeding and drift variance (De Vries et al., 1988). All these aspects, however, were automatically taken into account with the stochastic model.

The aspects of small populations cannot be ignored for optimization of current pig breeding programmes. Inbreeding can even be relevant in large populations, because selection using family information can heavily reduce effective size of a pig population (Belonsky and Kennedy, 1988; Toro et al., 1988). Reduction of selection intensity due to small numbers is mainly a result of the continuous selection process, which means that animals of a single generation are not available for selection at the same time. This reduction can be substantial when few families are available (resulting from a low number of boars) and when indexes of family members are highly correlated (due to using family information) (Hill, 1976, 1977).

Lean percentage and litter size were modelled with biological plateaus

(De Roo, 1987, 1988), which made the simulations more realistic. However, a disadvantage was that it made interpretation of results sometimes more difficult. For example, effects of inbreeding on selection response were confounded with the effects of the biological plateaus.

In the simulations, breeding values for reproduction traits were estimated with an animal model (described in Chapter 3); as a result, all relevant information from relatives was taken into account. For selection on reproduction traits, this information is very important because of the low heritability of these traits (Avalos and Smith, 1987). For production traits, no family information was included. This made results from the simulated dam lines in Chapter 3 easier to compare with those from the sire lines in the study of De Roo (1988). However, in the near future many breeding organizations probably will use family information also for selection on production traits. The consequences of this information for the optimization studies in this thesis were discussed in some chapters. The main conclusion was that selection response will be more affected by testing capacity, because accuracy of selection after the test will be increased (relative to accuracy before the test) and accuracy of selection will depend on the number of sibs tested.

During simulation, all data for the breeding value estimations were assumed to be correct. In practice, however, data-sets will never be without errors, which may have consequences for the optimal size of nucleus populations, especially when the frequency of errors would increase with population size (Franklin, 1982; Bichard and David, 1984)

The simulation model predicted selection responses, drift variance and inbreeding. However, alternative breeding programmes can also differ in costs, for example when testing capacity is varied. In this thesis, costs were discussed at relevant places, but never quantified, because they were difficult to estimate. Moreover, costs for nucleus and test places may vary between breeding organizations. For investment decisions (e.g. increase of nucleus size or testing capacity), breeding organizations need to compare additional returns from increased selection response to the additional costs involved. These additional returns (extra sales or better prices for breeding stock) will depend on the competitive position of the breeding organization (Chapter 2). The relation between returns and selection response will be non-linear (Hill, 1971).

The study in this thesis was limited to factors that determine the method of selection (breeding goal, intensity of selection, family size in selection, multi-stage selection). Therefore, no attention was given to factors such as mating policy. However, not all factors that determine the method of selection were covered. The choice of selection criteria was not studied, although it is an important step in the optimization of breeding programmes (Harris et al., 1984). An interesting subject for further research in this optimization step is the use of production and reproduction records from sub-nucleus and commercial herds for breeding value estimations. The relevance of this subject is due to the existence of Genotype x Environment interactions (Merks, 1988) and to the possibilities of selection for non-additive gene effects (Sellier, 1982; Wei and Van der Steen, 1989). Research on the value of sub-nucleus and commercial records should not focus on their effects on accuracy of selection but rather on their effects on selection response, because reduction in selection intensity due to high correlations between indexes of family members (Hill, 1976, 1977) can be high in situations with selection based mainly on family information. Effects on inbreeding also should get attention.

Even without Genotype x Environment interactions and non-additive gene effects, records from sub-nucleus and commercial herds are expected to be useful. Avalos and Smith (1987) predicted 15% higher accuracy of selection for reproduction when sub-nucleus records were included ($h^2 = 0.10$, mating ratio = 1:10, all males used from selected litters). In breeding pyramids, with multiplication of purebred gilts at sub-nucleus level, it is also possible to integrate the sub-nucleus herds with the nucleus herd. This will have the same impact on accuracy, but moreover, it will increase intensity of selection.

Alternative methods for the estimation of breeding values were also not studied in this thesis. The benefits of the use of an animal model for selection on production traits were demonstrated by Belonsky and Kennedy (1988), Sorensen (1988) and Wray (1988). For reproduction traits, this method is even more important. Efficient use of family information is vital for these traits because of their low heritability (Avalos and Smith, 1987). Stochastic simulation with the model in Chapter 3 showed that exclusion of reproduction data from relatives (i.e. reproduction indexes

of young boars and gilts were based only on records of their dam) reduced selection response for reproduction traits by 34%, whereas response for production traits increased by 10%. As a result, 15% reduction in overall response was found (De Vries, 1988, unpublished results).

Results in Chapters 3 to 6 sometimes showed that differences between alternative breeding programmes can be small. From Table 2 in Chapter 6, for example, it could be concluded that reduction in selection response at suboptimal distributions of nucleus and testing capacity over lines could be limited if no extreme values were chosen. For breeding organizations, it is important to know the optimal design of the breeding programme, but information about the consequences of deviations from the optimum design can also be useful. This information helps to find the best alternative design when the optimum design gives practical problems.

As soon as the breeding programme with the best design is operational, the various parts of the programme need to be evaluated regularly, because there might be possibilities for improvement (e.g. more accurate predictions of lean content, better recording of data, more efficient use of facilities). After a number of years, the entire breeding programme should be evaluated by estimating the genetic trends in the nucleus lines. In addition to the data from the nucleus, also data from sub-nucleus and commercial level would be useful for this purpose.

For investment decisions, breeding organizations first have to compare the benefits of alternative ways to change the breeding programme. For example, an increase in testing capacity needs to be compared with an increase in the size of the nucleus populations. Another aspect is the distribution of the additional facilities over the sire and dam lines. When the optimal adaptation of the breeding programme is found, its expected returns and costs must be examined to see whether the proposed investment is justified.

3. Main conclusions

From the studies in this thesis (and from some related studies), the following main conclusions can be drawn for current pig breeding programmes:

- The breeding goal should be based on economic efficiency of piglet production and fattening herds; the model in Chapter 1 can be used for this purpose. For the short-term benefits of a breeding organization, some modification of the breeding goal can be necessary when performance level of a trait deviates much from that of competitors (Chapter 2). For the long-term benefits, modification can be necessary when the level of a trait would become a biological limit for further improvement of other traits (Kanis, 1988).
- Selection response for production and reproduction traits in dam lines can be much increased by enlargement of the nucleus (Chapter 3). Additional nucleus sows do not necessarily have to be accompanied by additional test places for boars, because efficient selection of young boars (on pedigree index) is possible before the test. From a large proportion of the litters in dam lines, no boars have to be tested (Chapter 5).
- For dam lines, a high turn-over of breeding boars is necessary (Chapter 3). This is a better option for limiting the rate of inbreeding than restrictions on family size in testing and selection (Chapter 4). With 40 boars per year, rate of inbreeding can be limited to 0.5% per year.
- In a pig breeding programme with specialized sire and dam lines, sire lines can be much smaller ($\pm 50\%$) than dam lines. Testing capacity should be equally distributed over sire and dam lines (Chapter 6).

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SUMMARY

Introduction

Reproduction traits are important for piglet production, whereas production traits are important for fattening. Pig breeding organizations improve both groups of traits by selection in nucleus populations. Optimization of selection in these nucleus populations is important, because these populations determine the performance in all levels of the breeding pyramid, including the piglet production and fattening herds.

Optimization of selection in pigs requires a careful study, because many complicating aspects have to be dealt with (multi-trait and multi-stage selection, overlapping generations, inbreeding, reductions in selection intensity due to small numbers, continuous selection process).

Production traits can be measured on young boars and gilts during a performance test. Reproduction traits can be measured only on sexually mature sows. The difference in expression between the two groups of traits form an additional complication for the optimization of pig breeding programmes.

Most of the previous optimization studies for pig breeding have focussed on selection for only one group of traits. However, an important question at the moment, for the majority of pig breeding organizations, is how to improve production and reproduction traits simultaneously.

The objective of this study is optimization of combined selection for production and reproduction traits in pig breeding programmes. The research is focussed on genetic response to selection and rate of inbreeding.

Definition of the breeding goal

The first two chapters of this thesis deal with definition of the breeding goal. In Chapter 1, a deterministic model was developed to estimate economic values of traits in pig breeding programmes. The model describes efficiency of pig meat production as a function of breeding goal traits. Traits in the breeding goal were: oestrus and litter traits, mature weight, feed requirements and longevity of sows, growth rate and daily feed intake of young pigs and of fatteners, mortality rate of pigs, carcass

traits and incidence of PSE-meat.

The model was applied to the Dutch situation. Economic values (Dfl. per slaughter pig) of most important traits were:

- 0.09 (per day) for age at first oestrus,
- 0.32 (per day) for interval weaning-oestrus,
- 8.90 (per pig litter⁻¹) for litter size born alive,
- 1.10 (per %) for mortality rate of piglets in suckling period,
- 2.30 (per farrowing) for longevity of sows,
- 0.26 (per g day⁻¹) for growth rate of fatteners,
- 0.06 (per g day⁻¹) for daily feed intake of fatteners,
- 3.10 (per %) for lean content of the carcass.

Sensitivity of economic values was tested to changes in production circumstances (changes in feed prices, price of replacement gilts, labour and management costs and technical performance).

After estimation of the economic values of traits, the breeding goal can be defined. However, direct use of the economic values as weights in the breeding goal is not always optimal. One of the aspects that can play a role is the competitive position of a breeding organization (i.e. the performance of its breeding stock relative to other organizations). This aspect is dealt with in Chapter 2.

The value of improvement of a trait for a breeding organization is determined by its impact on saleability of the breeding stock. This impact is influenced by the competitive position of the organization. This is especially relevant for the optimal balance of selection between production and reproduction traits, because breeding stock needs to be acceptable for piglet production as well as for fattening herds. No method could be found in literature to quantify effects of competitive position on values of traits.

A generally applicable method was developed to take effects of competitive position into account. With an example it was shown that modification of the breeding goal can be necessary (for the short-term benefits of a breeding organization) when performance levels of traits deviate widely from competitors. Traits with a relatively low performance would need a higher weight in the breeding goal than traits with a high performance.

In the General Discussion of the thesis, attention was given to aspects that can affect the breeding goal. It was concluded that, in addition to competitive position, biological interactions between traits can be important (e.g. when the level of feed intake capacity becomes a limit for genetic improvement of protein deposition rate). Genotype x Environment interactions do not affect the breeding goal, but they may change the optimal balance between selection for production and for reproduction traits.

Evaluation of alternative breeding programmes

Chapters 3, 4 and 5 deal with the optimization of selection for production and reproduction traits in dam lines of pig breeding programmes. For this purpose, an existing stochastic simulation model for sire lines was adapted for dam lines. Several factors of the breeding programme that determine the way of selection were studied.

With the simulation model, effects of selection over 25 years were evaluated. Attention was focussed on changes in production and reproduction traits and on increase of inbreeding coefficient. Traits were assumed to be affected by many unlinked loci, each of small additive effect. Selection of boars and gilts was on an index that combined estimated breeding values for production and reproduction traits. Estimated breeding values for production traits were based on individual performance data, whereas estimated values for reproduction traits were based on family information, using a multi-trait animal model.

Effects of size of the nucleus population and sow/boar ratio were examined in Chapter 3. Population size was varied between 50 and 400 sows, and annual number of boars varied between 10 and 40.

Increasing the number of sows had a large positive effect on selection response: an increase from 200 to 400 sows gave 11% more response. For most breeding organizations, this might be high enough to offset the extra costs for sow and test places.

Variation in annual number of boars had a small influence on selection response, especially for large populations. A high number of boars was needed to keep the rate of inbreeding acceptably low. Therefore, use of a

high annual number of boars (40) is recommended for dam lines.

The objective of the study in Chapter 4 was to evaluate alternative selection and testing systems in dam lines. The stochastic simulation model was used to study effects of alternative systems on variances in family size, rate of inbreeding and response to selection.

Two alternative testing systems were evaluated. A system of one boar tested per litter gave about 10% lower response to selection than a system of two boars tested per litter. The only advantage of the first system is that testing costs are lower.

Differences in selection response between alternative selection systems were small. A restriction on the number of boars selected per litter (within full-sib family selection) had little influence on rate of inbreeding and on selection response. A restriction on the number of boars per sire (within paternal half-sib family selection) gave a small reduction in rate of inbreeding and in response to selection. Based on these results and those in Chapter 3, it could be concluded that increasing the number of boars is a better option for limiting the rate of inbreeding than within family selection.

Multi-stage selection in dam lines is dealt with in Chapter 5. The simulation model was used to study effects of time of selection on accuracy of selection, response to selection and rate of inbreeding.

First stage selection of boars was before the performance test. The proportion of boars selected in the first stage (p_1) was varied between 100% and 25%. From $p_1=100\%$ to $p_1=50\%$ the reduction in overall response was on average 3.5%, while from $p_1=50\%$ to $p_1=25\%$ the reduction was an additional 6%. The optimum of p_1 depends on the costs for testing, and on the size of the nucleus population relative to the total breeding pyramid. With a relatively large nucleus breeding herd, a low proportion of boars tested can be justified.

Breeding schemes with sequential culling of sows (weaned sows competing with replacement gilts) were compared to schemes without sequential culling (no genetic culling after weaning). Sequential culling gave on average 2-3% extra response.

Most pig breeding organizations have a nucleus with sire as well as dam lines. In the short term, total capacity of the nucleus herds (number of sow places) and testing capacity are fixed, but the distribution over lines can be varied. Therefore, optimization of population size and testing capacity must be done simultaneously for sire and dam lines. The objective of the study in Chapter 6 was to optimize distributions of nucleus and testing capacity over lines in various situations.

Effects of alternative distributions of nucleus places for sows and testing capacity for boars on total selection response were studied with an approach that might be referred to as semi-deterministic. The distributions were optimized with a deterministic model, whereas parameters used in this model were derived from stochastic simulation.

Conclusions (for a four-way crossbreeding system) were as follows:

- The optimum ratio of sow places for sire lines to sow places for dam lines was about 1 : 2.
- The optimum ratio of boar testing capacity for sire lines to boar testing capacity for dam lines was about 1 : 1.
- Reductions in total selection response at suboptimal distributions were limited as long as no extreme values were chosen.
- Optimum ratios depended on total testing capacity relative to total number of sow places in the nucleus. Optimum ratios were also sensitive to testing system (maximum number of boars tested per litter). Culling rate of boars after test (for conformation or semen quality) and crossbreeding system (three-way vs. four-way cross) had only slight influence.

Main conclusions

From the studies in this thesis (and from some related studies), the following main conclusions could be drawn for current pig breeding programmes:

- The breeding goal should be based on economic efficiency of piglet production and fattening herds; the model in Chapter 1 can be used for this purpose. For the short-term benefits of a breeding organization, some modification of the breeding goal can be necessary when performance level of a trait deviates much from that of competitors. For the long-term benefits, modification can be necessary when the level of a trait would

become a biological limit for further improvement of other traits.

- Selection response for production and reproduction traits in dam lines can be much increased by enlargement of the nucleus. Additional nucleus sows do not necessarily have to be accompanied by additional test places for boars, because efficient selection of young boars (on pedigree index) is possible before the test. From a large proportion of the litters in dam lines, no boars have to be tested.

- For dam lines, a high turn-over of breeding boars is necessary. This is a better option for limiting rate of inbreeding than restrictions on family size in selection and testing. With 40 boars per year, rate of inbreeding can be limited to 0.5% per year.

- In a pig breeding programme with specialized sire and dam lines, sire lines can be much smaller ($\pm 50\%$) than dam lines. Testing capacity should be equally distributed over sire and dam lines.

SAMENVATTING

Inleiding

Produktiekenmerken zijn van belang voor bedrijven met mestvarkens, terwijl reproductiekenmerken van belang zijn voor vermeerderingsbedrijven. Varkensfokkerij-organisaties werken aan de erfelijke verbetering van beide groepen kenmerken door te selecteren in topfokpopulaties. Het optimaliseren van de selectie-strategie in deze topfokpopulaties is belangrijk, aangezien deze populaties de technische resultaten in alle lagen van de produktie-kolom bepalen, inclusief de vermeerderings- en mestbedrijven.

Voor het optimaliseren van de selectie-strategie bij varkens is nauwgezet onderzoek nodig, aangezien er met veel complicaties rekening gehouden moet worden (selectie op meerdere kenmerken en in meerdere fasen, overlappende generaties, inteelt, reducties in selectie-intensiteit als gevolg van kleine aantallen, continu selectie-proces).

Produktiekenmerken kunnen worden gemeten aan jonge beren en gelten tijdens een prestatietoets. Reproductiekenmerken kunnen alleen aan geslachtsrijpe zeugen gemeten worden. De verschillen in expressie tussen de twee groepen kenmerken vormen een extra complicatie voor de optimalisatie van varkensfokkerijprogramma's.

De meeste studies op het gebied van optimalisatie van varkensfokkerijprogramma's hebben zich tot dusver gericht op de genetische verbetering van slechts één groep kenmerken. Echter, voor de meeste fokkerij-organisaties is op het ogenblik een belangrijke vraag, hoe er tegelijkertijd op produktie- en reproductiekenmerken geselecteerd moet worden.

Het doel van deze studie is de optimalisatie van gecombineerde selectie op produktie- en reproductiekenmerken in varkensfokkerijprogramma's. Het onderzoek is met name gericht op genetische vooruitgang en inteelttoename.

Bepaling van het fokdoel

De eerste twee hoofdstukken in dit proefschrift gaan over het opstellen van het fokdoel. In Hoofdstuk 1 wordt een model beschreven dat ontwikkeld is voor het schatten van economische waarden van kenmerken in varkensfokkerijprogramma's.

Het model beschrijft de efficiëntie van varkensvleesproductie als een functie van fokdoelkenmerken. De kenmerken in het fokdoel waren: bronst- en worpkenmerken, volwassen gewicht, voerverbruik en levensduur van zeugen, groei, voeropname en sterfte-percentages van jonge biggen en van mestvarkens, karkaskenmerken en frequentie van PSE-vlees.

Het model werd toegepast voor Nederlandse omstandigheden. Economische waarden (fl. per slachtvarken) van de belangrijkste kenmerken waren:

- 0,09 (per dag) voor leeftijd bij eerste bronst,
- 0,32 (per dag) voor interval spenen tot bronst,
- 8,90 (per big/worp) voor aantal levend geboren biggen,
- 1,10 (per %) voor sterfte van biggen tijdens de zoogperiode,
- 2,30 (per. worp) voor levensduur van zeugen,
- 0,26 (per gram/dag) voor groei van mestvarkens,
- 0,06 (per gram/dag) voor voeropname van mestvarkens,
- 3,10 (per %) voor vlees-percentages.

De effecten van veranderende productie-omstandigheden op de economische waarden werden bestudeerd in een gevoeligheidsanalyse (veranderingen in voerprijzen, aankoop prijs van opfokgelten, arbeidskosten en technische resultaten).

Nadat de economische waarden van kenmerken geschat zijn, kan het fokdoel opgesteld worden. Echter, het direct gebruiken van deze waarden als wegingsfactoren in het fokdoel is niet in alle gevallen optimaal. Eén van de aspecten die hierbij een rol kunnen spelen is de concurrentiepositie van een fokkerij-organisatie (d.w.z. de kwaliteit van het eigen fokmateriaal ten opzichte van andere organisaties). Dit aspect wordt behandeld in Hoofdstuk 2.

De waarde van het verbeteren van een kenmerk voor een fokkerij-organisatie wordt bepaald door de invloed ervan op de verkoopbaarheid van het fokmateriaal. Deze invloed hangt af van de concurrentiepositie van de betreffende organisatie. Dit is met name relevant voor de optimale balans van selectie tussen productie- en reproductiekenmerken. Fokmateriaal moet immers zowel voor vermeerderings- als voor mestbedrijven acceptabel zijn. In de literatuur kon geen methode gevonden worden om de effecten van de concurrentiepositie op de waarde van een kenmerk te kwantificeren.

Een algemeen toepasbaar model werd ontwikkeld om met de effecten van de

concurrentiepositie rekening te kunnen houden. Met een voorbeeld werd aangetoond dat aanpassingen van het fokdoel nodig kunnen zijn (ten behoeve van de korte termijn opbrengsten van een fokkerij-organisatie) wanneer de niveaus van kenmerken veel verschillen van concurrenten. Kenmerken met een relatief laag niveau zouden ten opzichte van kenmerken met een hoog niveau zwaarder in het fokdoel ingewogen moeten worden.

In de Algemene Discussie van het proefschrift wordt aandacht besteed aan aspecten die van invloed kunnen zijn op het fokdoel. Geconcludeerd werd dat, naast concurrentiepositie, biologische interacties tussen kenmerken van belang kunnen zijn (b.v. wanneer het niveau van de voeropnamecapaciteit een beperkende factor wordt voor de genetische verbetering van eiwit-aanzet). Genotype x milieu interacties hebben geen invloed op het fokdoel, maar ze kunnen wel een effect hebben op de optimale balans van selectie tussen produktie- en reproductiekenmerken.

Evaluatie van alternatieve fokprogramma's

De hoofdstukken 3, 4 en 5 gaan over de optimalisatie van selectie op produktie- en reproductiekenmerken in moederlijnen van varkensfokkerij-programma's. Hiervoor werd een bestaand stochastisch simulatiemodel voor vaderlijnen aangepast aan de situatie van moederlijnen. Verschillende factoren van het fokprogramma die de wijze van selectie bepalen werden bestudeerd.

Met het simulatiemodel werden de effecten van selectie over een periode van 25 jaar nagegaan. Hierbij werd vooral aandacht besteed aan de veranderingen in produktie- en reproductiekenmerken en de toename van de inteeltcoëfficiënt. Verondersteld werd dat de kenmerken beïnvloed werden door een groot aantal ongekoppelde genen, die elk op zich een klein effect hadden. Beren en gelten werden geselecteerd op grond van een totaal-index welke de geschatte fokwaarden voor produktie- en reproductiekenmerken combineerde. De geschatte fokwaarden voor produktiekenmerken waren gebaseerd op eigen prestatie-gegevens, terwijl voor reproductiekenmerken familie-informatie meegenomen werd via een statistisch diermodel voor meerdere kenmerken.

In Hoofdstuk 3 werden de effecten van de omvang van de topfokpopulatie en de verhouding tussen het aantal beren en zeugen bestudeerd. De populatie-omvang werd gevarieerd van 50 tot 400 zeugen, terwijl het jaarlijks aantal ingezette beren tussen de 10 en 40 beren varieerde.

Een verhoging van het aantal zeugen gaf een grote verbetering van het selectieresultaat. Een toename van 200 tot 400 zeugen leidde tot een extra genetische vooruitgang van 11%. Dit is voor de meeste fokkerij-organisaties waarschijnlijk voldoende om de extra kosten voor zeugenplaatsen en toetsruimte terug te verdienen.

Variatie van het aantal beren had weinig invloed op het selectieresultaat. Vooral in de grote populaties waren de effecten gering. Wel bleek een groot aantal beren nodig te zijn om de inteelttoename aanvaardbaar te houden. Om die reden is het aan te raden om jaarlijks een groot aantal beren (40) in moederlijnen in te zetten.

Het doel van het in Hoofdstuk 4 beschreven onderzoek was het vergelijken van alternatieve selectie- en toetssystemen voor moederlijnen. Met behulp van het stochastische simulatiemodel werden de effecten van alternatieve systemen op de varianties in familie-omvang, de inteelttoename en het selectieresultaat bestudeerd.

Twee alternatieve toetssystemen werden geëvalueerd. Een systeem waarbij 1 beer per toom getoetst werd gaf 10% minder selectieresultaat als een systeem waarbij 2 beren per toom werden getoetst. Het enige voordeel van het eerste systeem is de lagere toetskosten.

De verschillen in selectieresultaat tussen de alternatieve selectiesystemen waren gering. Een beperking van het aantal geselecteerde beren per toom (selectie binnen full-sib families) had weinig invloed op de inteelttoename en het selectieresultaat. Een beperking van het aantal beren per vader (selectie binnen half-sib families) resulteerde in een kleine reductie van de inteelttoename en het selectieresultaat. Op basis van deze resultaten en de resultaten uit Hoofdstuk 3 werd geconcludeerd dat een verhoging van het jaarlijks aantal ingezette beren een betere manier is om inteelttoename te beperken dan selectie binnen families.

Meerfasen-selectie in moederlijnen werd bestudeerd in Hoofdstuk 5. Met behulp van het simulatiemodel werd nagegaan wat de effecten van het moment

van selectie zijn op de nauwkeurigheid van selectie, het selectieresultaat en de inteelttoename.

De eerste fase selectie van beren vond plaats voorafgaand aan de prestatietoets. De geselecteerde fractie beren in de eerste fase (p_1) werd gevarieerd tussen 100% en 25%. Een verlaging van $p_1=100\%$ naar $p_1=50\%$ leidde tot 3,5% reductie in selectieresultaat, terwijl een verlaging van $p_1=50\%$ naar $p_1=25\%$ een reductie van 6% te zien gaf. De optimale waarde van p_1 hangt af van de toetskosten, en van de omvang van de topfokpopulatie ten opzichte van de totale produktie-pyramide. Met een relatief grote topfokpopulatie kan het verantwoord zijn om slechts een klein deel van de beren te toetsen.

In het onderzoek werden fokprogramma's waarin zeugen voortdurend uitgeselecteerd konden worden (gespeende zeugen moesten concurreren met opfokgelten) vergeleken met fokprogramma's zonder selectie in elke cyclus (geen afvoer na het spenen om genetische redenen). Deze laatste vorm van selectie leverde gemiddeld 2-3% extra selectieresultaat op.

De meeste varkensfokkerij-organisaties hebben op hun topfokbedrijven zowel vader- als moederlijnen. Op korte termijn kan de totale capaciteit van de topfokbedrijven (aantal zeugenplaatsen) en de toetscapaciteit niet veranderd worden, maar het is wel mogelijk om de verdeling ervan over de lijnen te variëren. Daarom dient de optimalisatie van populatie-omvang en toetscapaciteit voor vader- en moederlijnen tegelijkertijd uitgevoerd te worden. Het doel van het in Hoofdstuk 6 beschreven onderzoek was om de verdeling van topfok- en toetscapaciteit over lijnen voor verschillende situaties te optimaliseren.

De effecten van alternatieve verdelingen van topfokplaatsen voor zeugen en toetscapaciteit voor beren op het totale selectieresultaat werden bestudeerd met een benadering die semi-deterministisch genoemd zou kunnen worden. De verdelingen werden geoptimaliseerd met een deterministisch model, terwijl de parameters voor dit model ontleend werden aan stochastische simulatie-studies.

De conclusies (voor een 4-weg kruisingssysteem) waren als volgt:

- De optimale verhouding van het aantal zeugenplaatsen in de topfokkerij voor vader- en moederlijnen was ongeveer 1 : 2.
- De optimale verhouding van het aantal te toetsen beren van vader- en

moederlijnen was ongeveer 1 : 1.

- De reducties in het selectieresultaat bij suboptimale verdelingen waren gering zolang geen extreme waarden werden gekozen.
- De optimale verhoudingen waren afhankelijk van de totale toetscapaciteit (relatief t.o.v. het aantal topfokplaatsen voor zeugen). Ze waren tevens afhankelijk van het toetssysteem (maximum aantal getoetste beren per toom). Het uitval-percentages van beren na de toets (op grond van exterieur of sperma-kwaliteit) en het kruisingssysteem (3-weg t.o.v. 4-weg kruising) bleken niet veel invloed te hebben.

Belangrijkste conclusies

De belangrijkste conclusies uit dit proefschrift (en uit een aantal eraan gerelateerde studies) voor de huidige varkensfokkerijprogramma's zijn als volgt:

- Het fokdoel moet gedefinieerd worden op het niveau van vermeerderings- en mestbedrijven en gericht zijn op economische efficiëntie; hiervoor kan het model uit Hoofdstuk 1 gebruikt worden. Voor het korte termijn belang van een fokkerij-organisatie kunnen er enkele veranderingen in het fokdoel nodig zijn, wanneer het niveau van een kenmerk afwijkt van dat van de concurrenten. Aanpassing voor het belang op de lange termijn kan nodig zijn, wanneer het niveau van een kenmerk biologisch beperkend zou worden voor de verdere verbetering van andere kenmerken.
- Het selectieresultaat voor produktie- en reproductiekenmerken in moederlijnen kan sterk verbeterd worden door uitbreiding van de topfokkerij. Extra zeugenplaatsen voor de topfokkerij hoeven niet noodzakelijkerwijs gepaard te gaan met extra toetsplaatsen voor beren, aangezien een efficiënte selectie van beertjes voorafgaand aan de toets (op basis van afstammings-index) mogelijk is. Van een groot deel van de tomen in moederlijnen hoeven geen beren te worden getoetst.
- In moederlijnen dienen jaarlijks veel beren ingezet te worden. Dit is een betere manier om inteelt te beperken dan het opleggen van restricties op familie-omvang bij het selecteren en toetsen. Met 40 beren per jaar kan inteelttoename beperkt worden tot 0.5% per jaar.
- In een varkensfokkerijprogramma met vader- en moederlijnen kunnen de vaderlijnen veel kleiner zijn ($\pm 50\%$) dan de moederlijnen. De toetscapa-

citeit dient gelijkelijk verdeeld te worden over de vader- en moederlijnen.

Curriculum vitae

Alfred Gerard de Vries werd op 24 maart 1961 geboren te Drogeham (gemeente Achtkarspelen). In 1979 behaalde hij het diploma aan het Stedelijk Gymnasium te Leeuwarden. In datzelfde jaar begon hij met de studie Zoötechniek aan de Landbouwhogeschool te Wageningen. Het doctoraalexamen werd afgelegd in 1984 met als hoofdvak Veeteelt en als bijvakken Veevoeding, Agrarische Bedrijfseconomie en Pedagogiek en Didactiek.

Na zijn afstuderen werkte hij anderhalf jaar als docent aan het Opleidingscentrum voor Dierveredeling te Almelo. In februari 1986 werd hij als promotie-assistent aangesteld bij de vakgroep Veefokkerij van de Landbouwniversiteit voor het in dit proefschrift beschreven onderzoek. Sinds 1 september 1989 werkt hij als wetenschappelijk medewerker op het gebied van de varkensfokkerij bij het Instituut voor Veeteeltkundig Onderzoek "Schoonoord" te Zeist.