

Optimization of the Bavarian Pig Performance Testing and Breeding Scheme

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1 Introduction

The present optimization of performance testing and of the breeding scheme was stimulated by the implementation of a combined breeding value estimation utilizing purebred and crossbred information. Also the breeding objective was updated considering changed market conditions. Another reason is the new testing situation, caused by the change of the traditional pens for two pigs to sized pens with automatic feeding system.

The objective is to maximize profit from breeding by harmonizing the performance testing with the breeding scheme.

2 Idealized selection practice and performance testing

The Piètrain breeders in Bavaria keep about 1400 sows, rearing 9 piglets per litter on average. The first selection takes place at the age of about 12 weeks. First of all, piglets with growth and exterior deficiencies are rejected, followed by a family selection based on breeding values of parents. The second stage proceeds at the age of 7-8 month, where male pigs are judged during breed registration and females at the farms. Criteria are life-time daily gain, ultrasonic back fat thickness as well as exterior characters. Finally, about 400 sires and 600 sows per year participate in central progeny testing. The progenies are delivered in groups of two full sibs out of one litter from herdbook farms and piglet producer farms. Breeding sows have tested one group, natural service sires three groups and AI sires eight groups on average. Presently test capacity for the sire-line is utilized with 20% purebred and 80% crossbred animals respectively. Two thirds of the breeding sows are sired by inaccurately proven natural service sires and only one third by well proven AI sires.

3 Methods

The performance testing was simulated using APL having variable input parameters, like testing capacity, number of sires with purebred and/or crossbred progeny, number of progeny, number of full sibs, housing of related animals, etc. The breeding process is modelled by a three stage selection with the variables estimated breeding values of parents ($EBV_p=I_1$), own performance + EBV_p (I_2) and station testing + own performance + EBV_p (I_3). Truncation selection is conducted to maximize progress in the breeding objective H with

$$H_i = a_{i1}u_{i1} + a_{i2}u_{i2} + \dots + a_{in}u_{in} = \mathbf{a}'\mathbf{u}_i$$

a_i is the economic weight of u_{ij} , the true breeding value of trait j (daily gain, feed conversion, lean meat percentage, pH₁, intramuscular fat) and animal i . Assuming a joint normal distribution of H with all other traits having the following parameters:

$$E \begin{bmatrix} \mathbf{H} \\ \mathbf{I}_1 \\ \mathbf{I}_2 \\ \mathbf{I}_3 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad Var \begin{bmatrix} \mathbf{H} \\ \mathbf{I}_1 \\ \mathbf{I}_2 \\ \mathbf{I}_3 \end{bmatrix} = \mathbf{V} = \begin{bmatrix} \mathbf{V}_{HH} & \mathbf{V}_{HI_1} & \mathbf{V}_{HI_2} & \mathbf{V}_{HI_3} \\ \mathbf{V}_{I_1H} & \mathbf{V}_{I_1I_1} & \mathbf{V}_{I_1I_2} & \mathbf{V}_{I_1I_3} \\ \mathbf{V}_{I_2H} & \mathbf{V}_{I_2I_1} & \mathbf{V}_{I_2I_2} & \mathbf{V}_{I_2I_3} \\ \mathbf{V}_{I_3H} & \mathbf{V}_{I_3I_1} & \mathbf{V}_{I_3I_2} & \mathbf{V}_{I_3I_3} \end{bmatrix}$$

Fraction α of all animals selected

$$\alpha = \int_{k_1}^{\infty} \int_{k_2}^{\infty} \int_{k_3}^{\infty} f(\mathbf{I}) d\mathbf{I}$$

produces the next generation. The superiority of these animals in H is

$$E(\mathbf{H} | \mathbf{I}_1, \mathbf{I}_2, \mathbf{I}_3, k_1, k_2, k_3) = \frac{1}{\alpha} \int_{k_1}^{\infty} \int_{k_2}^{\infty} \int_{k_3}^{\infty} E(\mathbf{H} | \mathbf{I}) f(\mathbf{I}) d\mathbf{I}.$$

The above expression for H and ΔH needs, however, an adjustment for the finiteness of population as well as for the correlation between the estimated breeding values of the candidates. The latter is calculated from diagonal and off-diagonal elements of the covariance matrix of the estimated breeding values. The genetic progress in path ij is consequently

$$E(\mathbf{H} | \text{Selektion}) = \Delta H_{ij} = i_{\mathbf{H}} (1 - \rho_{\hat{\mathbf{H}}\hat{\mathbf{H}}_{ij}})^{\frac{1}{2}} \rho_{\mathbf{H}\hat{\mathbf{H}}} \sigma_{\mathbf{H}}$$

Taking into account generation interval the genetic progress per time unit was calculated by the well known formula of Rendel & Robertson (1950)

$$\frac{\Delta H}{\Delta t} = \frac{\Delta H_{mm} + \Delta H_{mf} + \Delta H_{fm} + \Delta H_{ff}}{\Delta t_{mm} + \Delta t_{mf} + \Delta t_{fm} + \Delta t_{ff}}.$$

To set up the covariance matrix of the estimated breeding values the mixed-model-equations have to be inverted. Since multivariate models are highly demanding on computing power canonical transformation with diagonalization of the covariance matrices of the random effects were used. This enables an efficient absorption of all effects into the additive-genetic equations and thus reduces a lot the computing requirements.

4 Discussion of modelling

An unbiased breeding value estimation implies, that the model includes all proven animals, even the culled ones. Also parents ought to be included, otherwise the accuracy of the estimated breeding values is reduced. However, one has to consider that parents have been selected hence the useable additive-genetic variance is reduced. After some generations this variance converges asymptotically towards a limit. By using the variance of a selected population in equilibrium the Bulmer-effect should be sufficiently accounted for. Proceeding like this the additive-genetic variance between full sibs is underestimated and the assumption of a multivariate normal distribution is then only an approximation. An unbiased solution is only found by Monte Carlo Simulation. Another incorrect assumption is the infinite population, leading to an overestimated intensity of selection. Within a one-dimensional case (correlated) Order Statistics would be appropriate, but there is no discussion in the literature for a multi-stage selection.

5 Model

For modelling fattening and slaughter traits of progenies, a sire-dam-model is implemented where both purebred and crossbred performance information are included. The model consists of two submodels. The first one for purebred performance fits a sire-dam model, whereas that for crossbred information is a sire model. This model neglects dams of crossbred animals, because they cannot be disentangled from the full sib effect (no information on the dam).

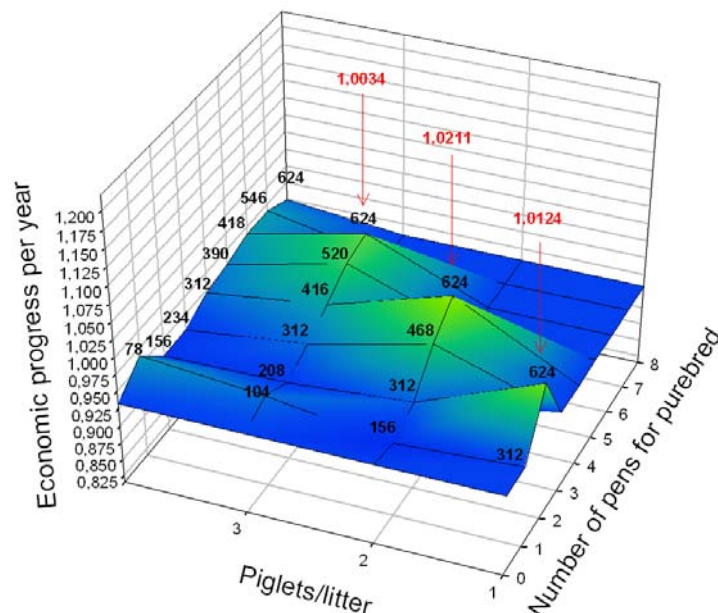
6 Analysis

A first analysis had to answer how many test boars, how many progeny per sire, how many full sibs per test group as well as how many purebred progeny and crossbred progeny respectively are optimal within a given testing capacity and size of breeding population. The crucial factors are the accuracy of estimated breeding values and the selection intensities in the different paths and stages. The weekly capacity constitutes 10 pens to 12 animals each that can be utilized by purebred and crossbred animals. Fraction of animals not finishing the test depends on breed, selection cycle is six months and in crossbred only one piglet/litter is tested, because only the accuracy of sires are of interest. The number of boars being tested varies from 35 to 300 per half year.

7 Results

To find local maxima, results are firstly considered at a given number of sires by varying the number of piglets per litter as well as the number of pens for purebreds. Figure 1 shows the economic progress as a function of the number of piglets and pens for 35 sires.

Fig. 1



Numbering along the axes describes the progeny testing capacity for breeding sows during six months. Three maxima can be detected at the piglet-pen combinations 1/2, 2/4 and 3/6, where the global optimum is 2/4.

Intensity of selection in the male paths is constant and has therefore no effect. By considering the maxima, selection intensity of females is also fixed, thus only the accuracy of the breeding values is decisive. One would expect, that the accuracy of the estimated breeding values of sires decrease with increasing number of piglets/litter (correlation between full sibs) and pens (correlation between purebred and crossbred < 1 , substitution crossbreds by purebreds). However, every sire has 90 progenies, so that appreciable effects arise only if the fraction of purebred animals tested is greater than 50%. The biggest impact has therefore the accuracy of dams, because two piglets tested are better than one. With three piglets, the reliability of sires becomes more important. The differences within number of piglets are mainly influenced by the intensity of female selection. Attention should be paid to the number of pens being not smaller than the number of piglets/litter, otherwise a confounding arises between pen-environment and full sibs, which reduces the accuracy of dams enormously. Therefore with two piglets a fraction of testing of purebreds up to 40 % is advantageous.

If there are 200 boars to be tested in half a year, every sire has fewer progeny and relies more on purebred information. An increasing number of piglets and pens lead to a conspicuous loss in accuracy of sires' estimated breeding values. The local maximum moves to the combination 1/2. The global optimum rests with 35 sires. Responsible for that is a strict selection at the second stage with given half- and full sib information. Even if there is no selection at the third stage, the generation interval can still not be reduced due to testing for genetical defects, but the superiority still remains.

Conclusions

The results presented indicate that a young sire design based on own performance and sib information combined with a strict selection of about 2% at the second stage is superior to the current progeny testing design. The within family breeding value (mendelian sampling) of these selected animals is then estimated by the central progeny testing. It provides sib information for the next generation and enables a further selection. To ensure that all young breeding sows participate with two piglets per litter about 25-30% of testing should be done with purebred animals.

References

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