

## **Sample size requirements for meat quality evaluations**

Laurence Maignel and Pramod Mathur  
Canadian Centre for Swine Improvement

The number of pigs required for meat quality evaluations depend upon the use of the information. In commercial herds, the meat quality data can be used to validate the effects of selection at nucleus level and for comparison of different groups of pigs that differ with respect to age classes, nutrition levels, breed crosses etc. These data can also serve a resource for several research studies. Another major use of the information, especially from the nucleus herds, is for genetic evaluations. These evaluations are useful to develop pigs that are genetically superior in meat quality traits and contribute to the quality of the pork from commercial herds over several years. The sample size requirements from these uses are described in following sections

### **Genetic evaluations:**

The number of pigs required for genetic evaluations for meat quality traits can be based on the expected genetic progress through their use in the evaluations.

The expected genetic gain is mainly affected by the following factors:

- The selection intensity, generally different for males and females
- The accuracy of genetic evaluation, depending on the amount of information available
- The genetic variability of selected traits

The selection intensity is often determined by testing capacities available on the farm. As a preliminary approach, the expected genetic gain can be estimated according to the number of animals with meat quality measurements.

In the example below (Table 1), a selection herd of 120 sows is considered, using 15 different boars per year. One meat quality trait, with a heritability of 0.30, is measured on slaughtered animals. In addition, following assumptions have been made:

- 20 litters born each month
- 64 gilts and 40 boars probed every month
- 8 gilts and 1 or 2 boars selected every month
- the sires of slaughtered animals are equally represented
- a generation interval of 1.5 years for boars and 2 years for sows is assumed

Table 1: Relationship between number of pigs tested/litter and expected genetic gain

Number of animals (per probed litter) with meat quality measurements	Number of animals with meat quality measurements per month	Average accuracy of meat quality evaluation for the candidates	Expected annual $\Delta G$ (in genetic standard deviation units)
3 per litter	60	0.44	+0.47
2 per litter	40	0.42	+0.45
1 per litter	20	0.37	+0.39
1 every 2 litters	10	0.31	+0.33
1 every 3 litters	7	0.27	+0.28
1 every 4 litters	5	0.22	+0.23
1 every 5 litters	4	0.19	+0.20
1 every 6 litters	3 or 4	0.17	+0.17
1 every 7 litters	2 or 3	0.14	+0.15

The accuracy of the EBVs will depend upon the connectedness between the pigs sent for meat quality evaluations and live pigs in the herd used as selection candidates.

A graphical representation of the above results (Fig .1) suggests a non linear increase in the accuracy of breeding value estimation with the increase in the size of the contemporary group. There is a significant increase in genetic gain as the size of the contemporary group increases from about 2 pig to 20 pigs. Thereafter the increase is gradual and relatively low. It appears that a group size of 20 should be recommended while the minimum should be at 10 pigs.

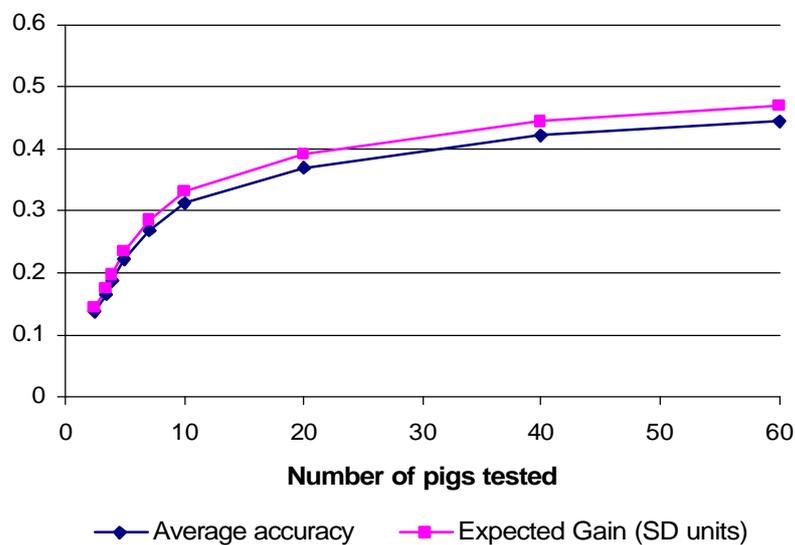


Figure 1: Relationship between contemporary group size and genetic progress

The characteristics of some meat quality traits and the expected genetic gain in the situation where 1 pig from every two litters has meat quality measurements are shown in Table 2

Table 2: Expected annual genetic gain for some meat quality traits, assuming 1 pig with meat quality measurements every two litters

Trait	Phenotypic SD	Heritability	Expected annual genetic gain
Meat colour (Minolta)	4.25	0.28	0.7
24h pH	0.19	0.21	0.03
Drip loss (%)	0.88	0.21	0.12
Marbling score	1.3	0.19	0.16

Pigs for carcass and meat quality evaluations will be selected from the Duroc and Yorkshire breeds. At least one pig will be selected for meat quality evaluations from every two litters probed. A batch of at least 10 pigs from herd will be sent for meat quality analysis (minimum contemporary group size). These pigs will be progeny of at least three different sires.

### Commercial testing

The project will provide useful data to address questions regarding important decisions in commercial herds. For example the producers will be able to compare the effect of higher slaughter weight on meat quality evaluations. Other example of the possible uses are: different feeding regimes, sources of genetics, crosses between different breeds etc.

The minimum sample size to use for comparison of different groups depends upon the minimum difference to be detected, the power of the test and the significance level required. Several methods have been developed to be able to determine the sample sizes needed to settle an experiment with a chosen level of power and sensitivity (Berndtson, 1991). The power of a design is the probability to detect a treatment effect if it exists, and the sensitivity is the smallest response that will be detectable. The following table shows the sample sizes required, using different values of power and differences to be detected.

Table 3: Sample size needed according to power and lowest difference to detect

Difference to be detected as a % of standard deviation	Power (%)					
	70	75	80	85	90	95
5	4938	5552	6279	7181	8408	10397
10	1234	1388	1570	1795	2102	2599
15	549	617	698	798	934	1155
20	309	347	392	449	526	650
25	198	222	251	287	336	416
30	137	154	174	199	234	289
35	101	113	128	147	172	212
40	77	87	98	112	131	162
45	61	69	78	89	104	128
50	49	56	63	72	84	104

In most studies, the classical value considered for power is 80%. A graphical representation of the number of observations required based on the above table (Table 2) is given below (Fig.2) using a power value of 80%.

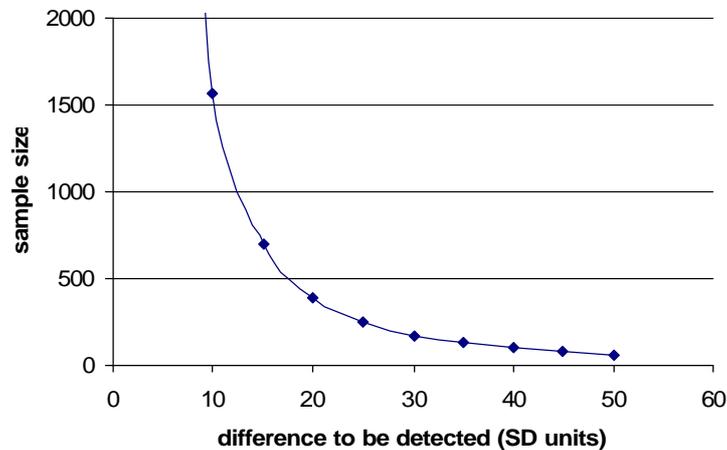


Figure 2 : Relationship between sample size and sensitivity (power=80%)

For small differences, the required sample size is very high, but it decreases rapidly from 5 to 20% standard deviation (SD) units sensitivity. Usually the minimum difference to be detected is about 25% SD, which requires a minimum sample size of 251 animals in each group, but depending on the trait, the relative difference to be detected may vary.