Design and standards for genetic evaluation of swine seedstock populations[1]

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ABSTRACT: The purpose of this article is to describe a program for evaluation of seedstock populations in the swine industry. Differences among seedstock populations for economically important traits must be identified in order for pork producers to efficiently use available genetic resources. National genetic evaluation programs have the potential to identify the important differences among populations and to increase the rate of genetic improvement in a population. Program results provide performance benchmarks that stimulate testing and selection procedures by seedstock suppliers that further increase the rate of genetic improvement. A Terminal Sire Line Genetic Evaluation Program was designed and conducted in the United States by the National Pork Producers Council (Des Moines, IA) to compare seedstock populations for use in crossbreeding systems. High levels of statistical accuracy for program results were established; the ability to detect differences of 0.25 SD per trait, a power of test of 75%, and a 5% significance level were selected. Pure breeds and breeding company sire lines were nominated for the program. Semen was collected from nominated boars and distributed to cooperating commercial producers during eight 1-wk breeding periods. Pigs were produced in 136 commercial herds and transported to testing facilities at 8 to 23 d of age. Nine of the 11 sire lines originally entered in the program completed the sampling requirements for statistical analysis. High levels of statistical accuracy and a large, representative sample of boars with restrictions on genetic relationships ensured that the program results included unbiased, highly accurate sire line data for growth, carcass, meat quality, and eating quality traits of economic importance. This program has shown commercial producers that they have several choices of sire lines for changing their crossbreeding programs in desired trait areas. Commercial product evaluation must be an ongoing process, and this program serves as a model for future testing and evaluation of diverse genetic seedstock populations.

Key Words: Animal Genetic Resources, Design, Genetic Variation, Standards, Swine

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Introduction

In order for pork producers to use available genetic resources efficiently, differences among seedstock populations for economically important traits must be identified. A national genetic evaluation program would identify the important differences among populations and increase the rate of genetic improvement. Commercial producers could increase the use of the superior lines, and the mean performance of the industry would be improved. Program results provide performance benchmarks that stimulate testing and selection procedures by seedstock suppliers, which further increase the rate of genetic improvement.

Many of the breed evaluations and crossbreeding experiments that have been reported were conducted 20 to 30 yr ago (Johnson and Omtvedt, 1973; Johnson, 1981; Wilson and Johnson, 1981). These experiments compared only the largest purebred populations, and few included breeding company lines. Few production traits were evaluated extensively, and meat and eating quality traits were generally not included. Because selection objectives and populations change genetically over time, data from past research may not accurately reflect present-day differences.

[1]Journal paper No. J-19711 of the Iowa Agriculture and Home Economics Experiment Station, Ames; Project No. 3600, and supported by Hatch Act and State of Iowa funds. Funding provided through producer check-off monies of the National Pork Board and administered by the National Pork Producers Council.

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Received March 13, 2002.

Accepted June 3, 2002.

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Although some data on breeds and lines are available from private production recording systems, these data are not adequate to compare seedstock populations. These programs do not require any sampling of lines and breeds and do not require a uniform test environment to ensure unbiased genetic comparisons. Comparison of these records could easily result in genetic differences that are confounded with environmental effects.

The Terminal Sire Line Genetic Evaluation Program was designed and conducted in the United States by the National Pork Producers Council (NPPC; Des Moines, Iowa), to compare seedstock populations for use in terminal crossbreeding systems. This article outlines details of the program and provides information to researchers on potential application to future evaluations.

Materials and Methods

Terminal Sire Line Genetic Evaluation Program Development and Rationale

Producer leadership within the NPPC appointed a Genetic Evaluation Task Force of six producers and six geneticists in 1990. The mission of this task force was to "evaluate the commercial pork producer's needs for genetic information and design comprehensive evaluation programs to provide sound information to the commercial pork industry" (NPPC, 1991). This task force had many public meetings to gather industry comments and design scientifically sound programs for producer goals.

Four points of consensus guided the task force and succeeding Genetic Programs Committees (GPC): 1) to provide unbiased, clearly presented results of genetic evaluations to producers of all business sizes; 2) to compare seedstock populations for crossbreeding use instead of pure line use; 3) to use industry resources to reduce program costs and increase industry participation; and 4) to reduce environmental differences, particularly related to health, among seedstock sources entering the program.

Seedstock Populations

Seedstock populations that met the definition of a freely interbreeding population of pigs were needed to accomplish the objectives of this experiment. Broadly defined, a seedstock population is a resource population of boars used to test a reference population of commercial sows. A seedstock population can encompass pure breeds and synthetic breeds but must be a distinctly different source of male germplasm that is distinguishable from other populations. Upon repeated sampling, seedstock populations must provide samples of similar genotypes.

The following criteria were set by the GPC to define a seedstock population for the program: Of the litters produced in the last 5 yr, 90% had dams that were produced within the population and 90% had sires that were produced within the population. Of the litters produced in the most current year, 90% had dams that were produced within the population and 90% had sires that were produced within the population.

This defined pure breeds and breeding company synthetic breeds. For the purposes of this program, lines were pure or crossbred/hybrid seedstock populations. The corporate managers of the lines (i.e., breed association or breeding company personnel) entered pure lines into the program. Crossbred lines, such as F_1 or F_2 animals, were entered by corporate managers of the parent lines. The parent lines of these crossbred lines were required to meet the definition of a seedstock population.

It was the responsibility of the seedstock breeder to document the genetic history of their population if requested by the GPC. Minimum requirements were three-generation pedigrees of all litters born in the last 5 yr.

Seedstock Sampling

The terminal sire line evaluation required a large number of boars to be tested with sufficient progeny to be assured that significant differences would be detected if they exist. Genetic relationships among boars were limited to half sibs or greater to ensure a wide range of variability. Breeders were prevented from any contact with test pigs to avoid bias of test results.

The objective was to test sufficient animals to ensure that if differences between sire lines were detected, true differences did exist. High levels of statistical accuracy for program results were established: the ability to detect differences of 0.25 SD per trait, a 75% power of test, and a 5% significance rate were selected.

Design of Program

Figure 1 outlines the structure of the complete evaluation program.

Breed association executives or breeding company administrators applied to the GPC for entry. Pedigree files were submitted to and evaluated by GPC geneticists to meet program definitions. The committee then determined how many boars per line would need to be sampled. Eleven populations entered the program, and nine completed the sampling with the required number of boars.

Eight contemporary breeding groups (1 wk in duration) were established, and semen collected at one of eight commercial boar studs was distributed to cooperating commercial producers. Semen from individual boars was distributed across breeding groups and farms to ensure connectivity across farms and breeding groups. Two doses of semen were sent for each sow entered in the program. Pigs farrowed from each contemporary breeding group made up a separate nursery and finishing contemporary group.

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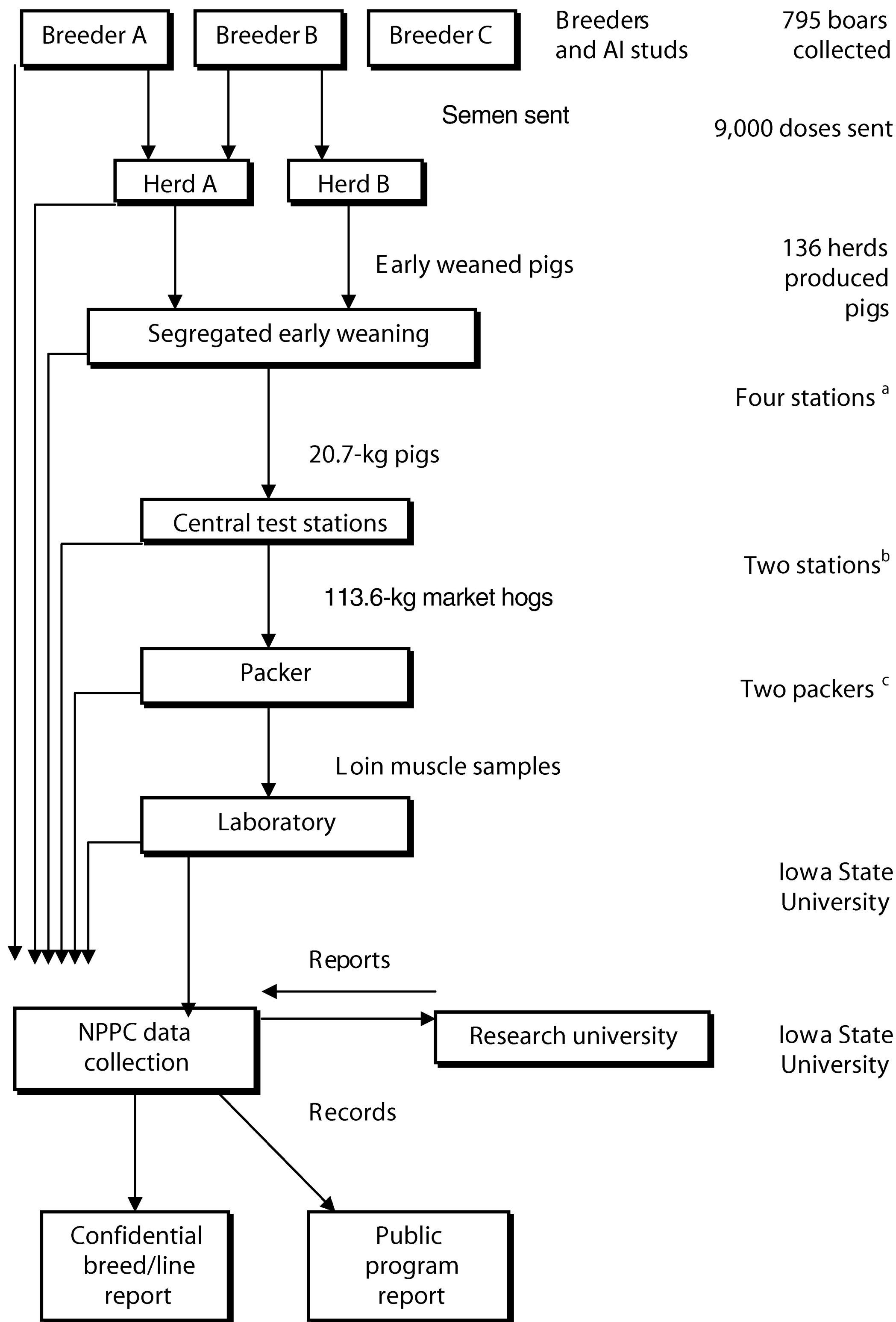

Figure 1. Terminal Sire Line National Genetic Evaluation Program. [a]Minnesota Pork Producers Association Segregated Early Weaning Station, Waseca, MN; Iowa Pork Producers Association Segregated Early Weaning Nursery, Ames, IA; Purdue University Segregated Early Weaning Nursery, West Lafayette, IN; Carroll Foods Segregated Early Weaning Nursery, Clinton, NC. [b]Minnesota Swine Testing Station, New Ulm, MN; Western Illinois University Testing Station, Macomb, IL. [c]Hormel Foods, Austin, MN; Rochelle Foods, Dubuque, IA.

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Table 1. Segregated early weaning entry protocol in the Terminal Sire Line Genetic Evaluation Program

Day	Treatment
1	Establish pig identification—numbered tag placed in right ear Pig weight and sex recorded Ivomec administered at label dose[a] Naxcel administered at label dose[b] Pigs penned by sire genetic line and weight Fresh water and feed available
2	Naxcel administered at label dose Denagard[c] added to water at 180 ppm
3	Denagard in water at 120 ppm
4–7	Denagard in water at 60 ppm

[a]Merial, Duluth, GA.
[b]Pharmacia & Upjohn Co., Kalamazoo, MI.
[c]Boehringer Ingelheim Vetmedica, Inc., Ridgefield, CT.

Table 2. Segregated early weaning nursery diets in the Terminal Sire Line Genetic Evaluation Program

Ingredient	Diet 1, percentage of diet	Diet 2, percentage of diet
Corn	36.6	39.1
Soybean meal (48% CP)	13.1	31.6
Soybean oil	5.0	3.0
Dried whey	20.0	20.0
Dried skim milk	10.0	—
Spray-dried plasma	7.5	—
Fish meal	3.0	—
Spray-dried blood meal	1.75	2.50
Limestone	0.325	0.687
Monocalcium phosphate	1.225	1.550
Methionine	0.05	0.05
Vitamins, trace minerals, antibiotic[a]	1.45	1.40
Copper sulfate	0.075	0.075

[a]Composition provided in NPPC (1995).

Participating commercial producers were required to meet the following standards: 1) the herd must be pseudorabies federal-monitored or validated-free status; 2) there must be no swine dysentery; 3) no clinical signs of Porcine Reproductive and Respiratory Syndrome; 4) no active transmissible gastroenteritis or other contagious disease prior to collection of pigs; 5) single genetic type in sow herd (terminal crossbreeding); 6) ability to use AI and identify litters; 7) willing to provide to the program one or two pigs per litter at feeder pig prices; and 8) sows should be grouped by genetic type for breeding within 1 wk.

Pigs were purchased from producers at 8 to 23 d of age and transported to a segregated early weaning (**SEW**) nursery. Pig group health status was standardized in the SEW program. Pigs were moved to two environmentally controlled testing stations with partially slotted-floored pens at 20.7 kg of weight. Pigs started the test at 29.5 kg and completed the test at 113.6 kg.

Pig Management

The GPC implemented SEW technology to standardize health among the test pigs originating from many source herds. The goal of the SEW procedures was to minimize the use of medications and to standardize pig health into a single, high-health status and not necessarily to eliminate all diseases. Pilot projects to evaluate SEW procedures were completed prior to implementation of the program (Goodwin et al., 1993).

One to four pigs per litter from each breeding group were delivered to one of four SEW nurseries on a single day to form a contemporary group. Transportation distance from the commercial herds to the SEW nurseries ranged from 80 to 1,000 km. During transport, four pigs were placed in a 0.6- × 0.6- × 0.4-m plastic ventilated box bedded with wood shavings or paper. Boxes were stacked in a covered van for transport. Temperature monitors were used to monitor air temperature surrounding the pigs during transit. Three SEW nurseries had 1.2- × 1.2-m pens, and pigs were allowed 0.15 to 0.19 m^2/pig. One nursery had 1.5- × 3.0-m pens and pigs were allowed 0.23 to 0.28 m^2/pig.

Table 1 gives the SEW entry protocol that was used. Ambient air temperature in the SEW nurseries was maintained at 29.5 to 31.0°C at pig level for 10 d after entry. After d 10, air temperature was decreased 0.28°C/d until the air temperature reached 22.0°C. Specific health situations were treated by an attending veterinarian.

Table 2 gives two diets that were fed during the nursery phase of the program. Diet 1 was fed until pigs weighed approximately 8.2 kg. Diet 2 was fed until pigs completed the nursery phase at approximately 20.7 kg. Both diets were pelleted and contained Mecadox (Pfizer, Inc., New York, NY) at 55 mg/kg.

Upon completion of the nursery phase of the program, pigs were transported to one of two central testing stations and penned by sire genetic line and weight. Station 1 included two finishing barns. The first barn was an environmentally controlled, solid concrete-floored building with 1.8- × 3.4-m pens. Pens were bedded with wood shavings and manually cleaned each day. The second barn was a naturally ventilated, curtain-sided building with 2.4- × 7.6-m partially slatted, concrete-

Table 3. Grow-finish diets in the Terminal Sire Line Genetic Evaluation Program

Ingredient	Diet 1, percentage of diet	Diet 2, percentage of diet
Corn	60.2	70.1
Soybean meal (48% CP)	33.6	24.8
NPPC G-F Base Mix[a]	3.0	3.0
Choice white grease	3.0	2.0
Tylan 10[b]	0.2	0.1

[a]Composition provided in NPPC (1995).
[b]Elanco Animal Health, Greenfield, IN.

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Table 4. Definition of growth, efficiency, and carcass traits in the Terminal Sire Line Genetic Evaluation Program

Trait	Definition
Days to 113.6 kg	Age of pig when it weighs 113.6 kg, calculated from birth
Average daily gain, kg/d	Weight gain/days on test
Feed efficiency, g/kg	Feed efficiency expressed as gain/feed
Soundness, 1 to 10	Leg structure and movement score of pigs; 10 is ideal
Carcass length, cm	Carcass length
Last lumbar midline backfat, cm	Midline backfat measured at the last lumbar vertebra on the carcass
Last rib midline backfat, cm	Midline backfat measured at the last rib on the carcass
Tenth-rib backfat, cm	Off midline backfat at the 10th rib
Loin muscle area, cm^2	Longissimus muscle area measured at the 10th rib on the carcass
Dressing percentage	(Carcass weight/live weight) × 100

floored pens. Station 2 had two barns that were partially slatted, naturally ventilated buildings with manually operated side doors to control air flow. Pen dimensions were 1.8 m × 5.5 m. Each pig was allotted 0.75 m^2/pig.

Feeding of nursery Diet 2 was continued at the testing station for the first 7 d, and pigs were changed to a grower diet on d 8. Pens were placed on test when pigs weighed an average of 29.5 kg. Table 3 gives the diets used in the grow-finish phase. Diet 1 was fed from approximately 22.7 to 68.2 kg, and Diet 2 was fed from 68.2 kg to market weight.

Table 4 gives definitions of the growth, efficiency, and carcass traits that were evaluated. Pigs were weighed and marketed weekly upon reaching an off-test weight of 112 kg. Leg soundness was evaluated prior to slaughter by a trained panel of pork producers. Leg movement and leg structure were each evaluated on a five-point scale and these scores added to give the soundness score. A score of 10 is ideal. Carcass data were obtained at two commercial abattoirs. A three-rib section of loin (10th to 12th ribs) was removed from each carcass and taken to a university meat laboratory for meat quality and eating quality evaluation. Table 5 gives definitions of the meat quality and eating quality traits that were evaluated.

Results and Discussion

Information given in Tables 6 to 8 was used to determine the number of animals that needed to be tested to meet specification standards for each trait. Size of differences to be detected are given in Table 6 as a percentage of the SD, which allows Table 6 to be used for all traits. Values in Table 6 are based on a single comparison of a pair of means. For comparisons of multiple means, appropriate methods should be used. If more comparisons are made, results will be less conclusive unless larger numbers are tested.

Standard deviations for traits are from NSIF (1997). Actual differences used in the program, expressed as a percentage of the SD (25%), are 3.25 d for days to 113.6 kg, 0.0227 kg/d for ADG, 0.0625 g/kg for feed efficiency, and 0.0635 cm for backfat depth. The number of obser-

Table 5. Definition of meat quality and eating quality traits in the Terminal Sire Line Genetic Evaluation Program

Item	Definition
	Meat quality
Marbling, 1 to 5	Subjective marbling score of longissimus in packer cooler
Color, 1 to 5	Subjective color score of longissimus in packer cooler
Firmness, 1 to 5	Subjective firmness score of longissimus in packer cooler
Minolta, %	Minolta light reflectance reading taken in packer cooler
Hunter	Hunter "L" score taken with Minolta in packer cooler
pH	Ultimate pH of longissimus muscle (24 to 48 h after slaughter)
Protein solubility, mg/g	Protein solubility of uncooked longissimus muscle
	Eating quality
Juiciness, 1 to 5	Juiciness score of cooked longissimus
Tenderness, 1 to 5	Tenderness score of cooked longissimus
Chewiness, 1 to 5	Chewiness score of cooked longissimus
Instron tenderness, kg	Instron universal testing machine pressure reading of cooked longissimus
Drip loss, %	Drip loss from filter paper method
Cooking loss, %	Difference in weight before and after cooking
Moisture percentage, %	Moisture percentage of cooked longissimus muscle
Cholesterol, mg/100 g	Cholesterol content of uncooked longissimus muscle on a wet or "as is" basis
Lipid, %	Total lipid percentage of uncooked longissimus muscle on a wet or "as is" basis

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Table 6. Number of observations required per sire line in the Terminal Sire Line Genetic Evaluation Program[a,b]

Size of difference as a percentage of SD	Significance level	Power of test				
		95	85	80	75	60
5	5%	8,428	7,161	6,302	5,570	3,938
10		2,122	1,815	1,590	1,408	999
15		954	818	718	637	455
20		545	469	413	367	265
25		356	307	271	242	177
30		254	219	195	174	129
35		192	167	148	133	100
40		151	132	118	107	81
45		124	109	98	89	68
50		104	92	83	76	59
5	10%	6,854	5,770	4,968	4,322	2,902
10		1,733	1,458	1,257	1,096	740
15		782	659	570	498	340
20		448	379	329	289	200
25		294	250	218	192	135
30		210	178	157	140	100
35		160	137	121	108	79
40		127	110	97	87	65
45		105	91	81	73	56
50		89	78	69	63	49

[a]Cochran and Cox (1957).
[b]Based on assumption of one record per animal and one progeny per sire.

vations needed for any level of testing depends on the ratio of differences to be detected and the variation in the trait.

A basic assumption in Table 6 is that only one progeny per sire is tested. If more than one half-sib progeny per sire is tested, the numbers in Table 6 must be augmented by using the values shown in Table 7.

Consider the case of using an 80% probability of detecting a 0.5 pig-per-litter difference and testing observed differences at the 5% level. A 0.5 pig difference is 20% of the SD (NSIF, 1997). From Table 6, a 20% difference as a percentage of the SD at the 5% significance level and under the 80% power of test means that 413 animals per group are needed. Table 7 is used if more than one half-sib progeny per sire is to be tested. For litter size, testing 10 half-sibs per sire requires 632 animals (1.53×413) per sire line group.

Genetic population size in this study was determined by the average number of paternal half-sib families in 2 yr, 1991 and 1992, prior to the initiation of the trial. Only sires represented by three or more litters were considered to be half-sib families when determining the number of boars to be sampled. The design of the program was to have each sampled boar sire four litters. One pig from each of these litters would be tested. For large populations, a minimum of 85 boars entered and 340 progeny tested was required.

From Table 6, differences of 0.25 SD per trait, 75% power of test, and a 5% significance rate could be achieved with 242 observations with one progeny per

Table 7. Percentage increase in numbers needed for more than one progeny per sire (half-sibs only) in the Terminal Sire Line Genetic Evaluation Program[a,b]

Number per sire	Trait[c]				
	LS	Days	ADG	FE	BF
2	111	118	120	115	120
4	121	135	140	130	140
6	132	153	160	145	160
8	142	170	180	160	180
10	153	188	200	175	200

[a]Assume one record per individual. These values depend on heritabilities. Heritabilities used are those from National Swine Improvement Federation (NSIF) guidelines (1997).
[b]Cochran and Cox (1957).
[c]LS = litter size; Days = days to 113.6 kg; ADG = average daily gain; FE = feed efficiency; BF = backfat.

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Table 8. Minimum number of sires per line represented by progeny needed to meet statistical requirements in the Terminal Sire Line Genetic Evaluation Program[a]

Annual paternal half-sib families (N_t)	Number of sires (N_s)
100	46
200	60
300	67
400	71
500	73
600	75
700	76
800	77
900	78
1000	78
Large	85

[a]See Appendix.

sire. The number of required observations was adjusted using data in Table 7. Average daily gain and backfat require the greatest increase in number of observations for four progeny per sire (140%), resulting in 340 observations (85 sires with four pigs tested per sire). The Yorkshire, Hampshire, and Duroc breeds qualified as large populations.

Table 8 shows the number of paternal half-sib families per year (number of sires with three or more litters per year) and the number of boars with tested progeny needed before results would be published. The minimum population size was set at 46 sires (100 paternal half-sib families in the two most recent years). If a genetic population was too small to provide 46 boars that had genetic relationships of less than half-sibs, more closely genetically related boars could be used with GPC approval. The number of boars to be entered for smaller populations was calculated by the following formula (derivation given in Appendix):

$$N_S = NN_t/(N + N_t)$$

where N_s is the number of sires in a small sample mean, N is the number of boars a large genetic population would enter (85), and N_t is the total number of sires in a small population from the past 2 yr.

Nine of the 11 sire lines originally entered in this program completed the sampling requirements for statistical analysis. Two lines did not submit adequate numbers of boars to meet program requirements.

Table 9 gives the number of boars sampled, litters born, and test pigs per sire line. Pigs farrowed in 136 commercial herds were tested in the program. Twenty producers had multiple sow genetic types in their herds, and the remaining herds had only one genetic type in their herd. There were 45 sow genetic types reported, and these genetic types were grouped into 11 classes for the trait evaluations. Table 10 gives the number and percentage of litters produced by sow genetic type. Sire lines were used randomly across commercial herds, and all matings were made to produce 100% heterosis in the test pigs.

The numbers of tested progeny per sire and litters per sire are given in Tables 11 and 12, respectively. The original sampling goal was to test one pig from each of four litters per sire. The requirement that boars had to be less than 15 mo of age to enter the program resulted in highly variable amounts of semen produced by each boar. Semen from boars was collected and distributed during several breeding periods to increase the probability of litters produced. Low semen volume and quality restricted the doses of semen produced by several of the young boars, resulting in fewer than four litters by 75.4% of sires used in the program. Use of semen from boars that produced large volumes of semen was limited, and progeny tested by boars with lower semen output was maximized. The percentage of dams that produced one, two, three, and four tested progeny

Table 9. Number of boars, litters, and test pigs in each sire line in the Terminal Sire Line Genetic Evaluation Program

Sire line	Boars used	Boars with progeny	Litters[e]	Test pigs
Danbred[a]	49	45	151	222
Berkshire	57	50	127	233
Duroc	127	111	297	554
Hampshire	105	95	314	580
NE SPF Duroc[b]	75	65	168	278
Newsham Hybrid[c]	57	49	128	216
NGT Large White[d]	55	42	78	184
Spotted	94	82	213	389
Yorkshire	110	87	192	411
Other lines	66	49	112	194
Total	795	675	1,780	3,261

[a]Danbred NA, Seward, NE.
[b]Nebraska SPF, Lincoln, NE.
[c]Newsham Hybrids, Colorado Springs, CO.
[d]National Genetic Technologies, Columbus, NE.
[e]Not all litters born were available for testing due to specific source herd health problems or because all pigs in a source herd were from the same line.

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Table 10. Number and percentage of litters produced by sow genetic type in the Terminal Sire Line Genetic Evaluation Program

Type	Litters	%
Yorkshire-Landrace F_1	445	23.6
PIC Camborough 15[a]	324	17.2
Yorkshire-Hampshire F_1	133	7.0
Farmers Hybrid[b]	86	4.6
Yorkshire-Large White	84	4.4
DeKalb DK-30[c]	82	4.3
Yorkshire-Chester F_1	79	4.2
Yorkshire-Hamp × Landrace F_2	78	4.1
PIC Camborough[a]	61	3.2
Yorkshire-Farmers Hybrid[b]	55	2.9
Babcock[d]	45	2.4
DeKalb DK-33[c]	42	2.2
Yorkshire-various crosses	155	8.2
Landrace-various crosses	111	5.9
Hampshire-various crosses	60	3.2
Other	48	2.5
Total	1,888	100.0

[a]PIC USA, Berkeley, CA.
[b]Farmers Hybrid Company, Des Moines, IA.
[c]Monsanto, Chesterfield, MO.
[d]Babcock Genetics, Rochester, MN.

were 32.9, 50.9, 14.8, and 1.6%, respectively. The average number of tested progeny per sire was 4.83 and per dam was 1.85.

Pigs were removed from the program upon death or advice of the attending veterinarian that the pig was injured or severely ill. Table 13 lists the pig performance by contemporary group in the SEW nurseries. Average daily gain for the eight contemporary groups over a 40-d test period ranged from 341 to 405 g/d. Mortality rates in the nursery period ranged from 0.93 to 3.08%. Average grow-finish performance by contemporary group is given in Table 14. Average daily gain for the eight contemporary groups ranged from 803 to 900 g/d and days to 113.6 kg ranged from 165 to 180. Mortality rates in the finisher phase ranged from 0.10 to 2.18%.

Pork producers have and will continue to choose among available seedstock populations for use in commercial swine production. These decisions are often based on limited experimental comparisons, subjective evaluation, and potentially biased promotional material. A comprehensive genetic evaluation that accurately evaluates genetic differences among seedstock populations provides an objective basis for making choices among a large number of seedstock populations.

Table 11. Tested progeny per sire in the Terminal Sire Line Genetic Evaluation Program

Progeny per sire	Percentage of sires
1	6.1
2	15.1
3	14.2
4	15.4
5	9.6
6	20.1
7	5.3
8	4.9
9	3.4
10	2.2
11 to 16	3.6

Table 12. Tested litters per sire in the Terminal Sire Line Genetic Evaluation Program

Litters per sire	Percentage of sires
1	29.6
2	25.5
3	20.3
4	12.0
5	7.1
6	3.4
7	1.3
8	0.4
9	0.3

Characterization of numerous beef cattle breeds has been accomplished through the Germplasm Evaluation Program as reported by Koch et al. (1976; 1979; 1982) and Wheeler et al. (1996). Breed differences in production traits have been identified as important genetic resources for improving efficiency, composition, and quality. Evaluation of carcass traits and meat palatability has been completed to assist in determining the potential value of these alternative genetic resources (Wheeler et al., 1996). Large differences among and within sire breeds can be exploited by producers to improve carcass and quality traits and increase the rate of genetic improvement.

Random sample testing has been used very successfully by the poultry industry (Anderson, 2001; Hartman, 1985; Working Group 3, 1999). It provided data for unbiased comparisons of performance of commercial poultry stocks. Strict and representative sampling procedures were established as fundamental prerequisites for unbiased comparisons. The first random sample egg-laying test established in California in 1947 was followed by rapid growth in the number of testing stations for egg-laying and broiler and turkey stocks (Hartman, 1985). Some programs are still in existence today (e.g., the North Carolina layer performance program has been in existence since 1957). The European Community continues to publish a combined summary of information from several countries (Working Group 3, 1999). Without question, random sampling had an impact on the rate of improvement in poultry production efficiency since objective information concerning the relative quality of commercial stocks was readily available.

A very high level of statistical accuracy and extensive genetic sampling of lines was built into this program so that producers could have confidence in using the results to change their breeding programs. The results

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Table 13. Pig performance summary in segregated early weaning nurseries in the Terminal Sire Line Genetic Evaluation Program

Contemporary group	In weight, kg[a]	Off weight, kg[b]	Mortality, %	ADG, g/d
1	5.32	18.86	2.44	341 ± 4
2	5.00	21.45	1.99	405 ± 5
3	5.23	19.82	1.05	355 ± 4
4	5.14	20.64	3.08	379 ± 5
5	5.41	20.45	1.69	378 ± 5
6	5.27	20.86	0.93	384 ± 5
7	5.55	21.59	0.95	383 ± 5
8	5.27	22.18	1.37	400 ± 4

[a]In weight = Live weight at start of nursery period.
[b]Off weight = Live weight at end of nursery period.

Table 14. Pig performance summary in the grow-finish period in the Terminal Sire Line Genetic Evaluation Program

Contemporary group	Number of pigs	Mortality, %	Off weight, kg[a]	ADG, g/d	Days to 113.6 kg
1	560	0.50	115.0	900 ± 7	167 ± 1.0
2	338	0.88	113.2	803 ± 8	177 ± 1.3
3	470	1.05	112.7	860 ± 7	172 ± 1.1
4	310	1.61	113.2	821 ± 8	177 ± 1.3
5	291	1.03	113.2	893 ± 7	165 ± 1.1
6	321	2.18	113.2	822 ± 7	180 ± 1.1
7	519	1.34	114.1	858 ± 8	174 ± 1.3
8	504	0.10	114.1	867 ± 7	169 ± 1.1

[a]Off weight = Live weight at end of test.

apply to crossbreeding use because that is how commercial producers use seedstock.

Implications

The Terminal Sire Line Genetic Evaluation Program of the National Pork Producers Council is the most comprehensive and unbiased evaluation of swine breeds and lines ever conducted. Program results have shown commercial producers that they have several choices of sire lines to change their crossbreeding programs in desired trait areas. Producers can use the information generated to know which trade-offs they can profitability make among production, carcass, and quality traits, and where to find the genetics that match their goals. Because selection objectives and populations change genetically over time, data from past research may not accurately reflect present-day differences among lines. Commercial product evaluation must be an ongoing process. This program serves as a model for future testing and evaluation of diverse genetic seedstock populations.

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Appendix

Let μ_1 be the true mean of large population 1, and μ_2 be the mean of large population 2. A random sample from each population produces sample means of $\overline{X}_1$ and $\overline{X}_2$. Then $C_L = \overline{X}_1 - \overline{X}_2$ is the contrast of sample means from two large populations. The variance of C_L is:

$$V(C_L) = V[(\overline{X}_1 - \mu_1) - (\overline{X}_2 - \mu_2)]$$

Then $V(C_L) = V(\overline{X}_1) + V(\overline{X}_2)$ because $V(\mu_1) = V(\mu_2) = 0$, and thus covariances of sample means with population means are also zero. It was determined that the number of sires should be 85 (N = 85) to test sample mean differences $(\overline{X}_1 - \overline{X}_2)$ with a 5% significance rate and 75% power of test, and samples of two dams per sire and two pigs per dam (n = 4, and total per population = Nn = 340).

All populations are not large, however, so the variance of their mean and covariance of the population mean and sample mean are not zero. Let the population mean and sample mean of a small population be μ_S and $\overline{Y}_S$, respectively. The contrast of the mean difference between a large population (e.g., population 1) and the small population is:

$$C_{S-L} = [(\overline{Y}_S - \mu_S) - (\overline{X}_1 - \mu_1)]$$

The variance of this contrast is:

$$V(C_{S-L}) = V[(\overline{Y}_S - \mu_S) - (\overline{X}_1 - \mu_1)] = V(\overline{Y}_S) + V(\mu_S) + V(\overline{X}_1) - 2Cov(\overline{Y}_S, \mu_S)$$

The variance of any one of the means with N_i sires and n = 4 can be expressed as:

$$\frac{\sigma_w^2 + 2\sigma_d^2 + 4\sigma_S^2}{4N_i} = \text{(Mean square sires)/(number of progeny)}$$

where N_i is number of sires in the sample or in the total population. If nN_i is large, the coefficients on the within litter and dam components of variance are small, and the variance of the mean depends mostly on the sire component of variance and the number of sires. As a result, the equation can be reduced to:

$$\frac{\sigma_w^2 + 2\sigma_d^2 + 4\sigma_s^2}{4N_S} \cong \frac{\sigma_S^2}{4N_S}$$

Because in a small population, all sires in the sample mean are also in the population mean, there is a covariance between the small population sample mean and the population mean. Let N_s = number of sires in the small sample mean, and N_t = total number of sires in the small population. Then,

$$V(\overline{Y}_s) = \frac{\sigma_s^2}{4N_s} \text{ and } V(\mu_S) = \frac{\sigma_s^2}{4N_t}$$

A covariance between the means occurs because the N_s sires in the sample are part of the N_t total sires. The covariance between two progeny of the same sire, one in the sample mean and the other in the population mean, is the sire component of variance. With n progeny per sire in each mean, there are n^2 covariances within each sire, and $N_s n^2$ total covariances. The divisor for the sample mean is $n(N_s)$, the number of observations in the sample, and the divisor for the population mean is $n(N_t)$. Then, the covariance between small population sample and population means is:

$$Cov(\overline{Y}_S, \mu_S) = \frac{N_S n^2 \sigma_S^2}{nN_S nN_t} = \frac{\sigma_S^2}{N_t}$$

The variance of the contrast of small and large population means is:

$$V(C_{S-L}) = V(\overline{Y}_S) + V(\mu_S) + V(\bar{X}_1) - 2Cov(\overline{Y}_S, \mu_S) = \frac{\sigma_S^2}{N_S} + \frac{\sigma_S^2}{N_t} + \frac{\sigma_S^2}{N} - 2\frac{\sigma_S^2}{N_t}$$

Given that N = 85 for large populations, $V(C_{S-L})$ should equal $V(C_L)$. Then,

$$V(C_{S-L}) = \frac{\sigma_S^2}{N_S} + \frac{\sigma_S^2}{N_t} + \frac{\sigma_S^2}{N} - 2\frac{\sigma_S^2}{N_t} \text{ and } V(C_L) = 2\frac{\sigma_S^2}{N}$$

The next step is to equate the two variances and solve for N_s.

$$2\frac{\sigma_S^2}{N} = \frac{\sigma_S^2}{N_S} + \frac{\sigma_S^2}{N_t} + \frac{\sigma_S^2}{N} - 2\frac{\sigma_S^2}{N_t}$$

$$N_S = \frac{NN_t}{N + N_t}$$

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