Identifying hypoprolific boars by examining production records

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Summary: *Analysis of litter size performance of 4388 boars used in single-boar matings revealed that 191(4.3%) were hypoprolific according to the criteria of Popescu. Boars classified as normal had sired litters with an average liveborn litter size of 9.984 ± 0.016 standard error (SE) piglets compared to 7.762 ± 0.057 SE (P < 0.0001) for the hypoprolific boars (HPB), a mean reduction of 2.22 piglets. Also, the average number of piglets born dead was significantly greater for the hypoprolific boars as compared to the normal boars (1.0236 ± 0.0309 SE versus 0.9138 ± 0.0085 SE; P = 0.0004). Based on our findings we propose an improved definition of hypoprolificacy based on that of Popescu.*

These data suggest that herd average litter size could be increased substantially by identifying and culling suspected hypoprolific boars as early in their careers as possible, based on farrowing records following single-boar matings. We present a discussion of the necessary number of farrowing records required to do this at various levels of confidence. Since up to half of hypoprolific boars may have a heritable chromosomal abnormality known to cause small litters, we suggest that cytogenetic examinations of hypoprolific boars be the first step in investigating this malady.

A study of parity-specific production values for 68 North American breeding herds revealed that nearly 10% (9.96 [+ 2.1 × 4 SE]) of litters comprised less than seven liveborn piglets.[1] The role of individual sires was not investigated. In European countries, notably France, the negative impact of hypoprolific boars (HPB) on swine reproduction is well known from over two decades of research to identify and control this condition. Popescu[2] analyzed data on 6467 boars and determined the HPB prevalence to be 1.5 per 1000. For that study, a HPB was defined as one having sired six or more homospermic litters in a 12-month period of service with an average litter size of less than eight liveborn piglets. However, their analysis did not consider the possible effects of farm or parity.

Several factors contribute to the HPB condition. Recent data from European countries[3] indicates that approximately 50% of HPBs result from chromosomal aberrations, principally reciprocal translocation. At least 50 different reciprocal translocations have been reported; all were diagnosed in relation to studies of boars with reproductive disorders.[3]

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In a study of 84 United States swine breeding herds,[4] the mean annual culling rate for boars was 59.4%. Approximately 18% of the boars culled were removed for reproductive reasons, including infertility and poor libido. The incidence and cause(s) of the reported infertility among those culled was not determined.

In our initial cytogenetic surveillance for HPBS,[5] one of 15 boars in one herd was found to be hypoprolific. This boar averaged 7.1 (+ 2.5 SE) total piglets per litter when single-boar-mated to 51 sows. Comparable herd mates, when single-mated to other boars, averaged 10.8 + 2.6 SE piglets per litter. Examination of chromosomes of cultured blood lymphocytes (see Appendix) revealed that only the hypoprolific boar had an abnormal karyotype in the form of a 1/14 reciprocal translocation (38XY, t(1;14) (q2.12, q2.2)). This is the only report of an reciprocal translocation for swine in the United States. Earlier, McFeely, et al.,[6] reported a 13/17 centric fusion-type of translocation in a sow with a history of reduced litter size.

The recent trend toward use of artificial insemination (AI) by the United States swine industry heightens the need for early screening of boars for undesirable traits. The high prevalence of chromosomal aberrations related to low fertility in swine described by us[5] and others[2,3,6,9] further emphasizes this need.

Herds practicing natural mating typically maintain sow:boar ratios of 20:1 or less. During estrus, most sows and gilts are mated on 2 consecutive days with different boars. While this practice of heterospermic matings may have advantages in improving farrowing rates and total-born litter sizes, it makes it impossible to identify HPBs early in their careers.

Artificial insemination, which usually involves extending and diluting semen, results in AI herds having lower sow:boar ratios than those using natural service. Thus, individual boars exert greater influence on overall herd performance in AI herds. However, reduced boar numbers, and the concomitant increase in daily matings by individual boars, improves the opportunity for homospermic matings, and thus the early detection of HPBs. Even in herds where a general policy of heterospermic matings is mandated, it may be advantageous to use young boars exclusively for homospermic matings until sufficient farrowing records accrue to allow them to be compared with overall herd performance.

As with any testing procedure, there is an inherent risk of erroneously classifying a normal boar as hypoprolific (Type I error), or failing to

identify a truly hypoprolific boar (Type II error). The decision maker must make a judgment between the probabilities of making Type I and Type II errors. The higher the significance level (α) chosen, the more likely that a Type I error will be made. The greater the power (1–ß) of a statistical test, then the lower the likelihood that a Type II error will be made. Generally, the probabilities of making either type of error can be reduced by increasing the number of observations in the study.

The purposes of our study were to determine whether hypoprolific boars exist in the United States, and, if present, estimate the extent of their prevalence. Our third objective was to develop a practical strategy that producers may follow to quickly identify hypoprolific boars and minimize their effect on herd productivity.

Materials and methods

Definitions for this study were those used by the PigCHAMP® computer record system[7] and the French National System for Sow Herd Management,[2] as follows:

- Hypoprolific boar (HPB): A HPB is defined as one that has sired six or more litters with an average litter size of eight or fewer liveborn piglets within 12 months of service.
- Qualified boar: Any boar with six or more single mated litters within 12 months of service.
- Qualified herd: Any herd with at least one qualified boar.
- Average piglets born live per litter: The sum of piglets born live divided by the number of farrowings.
- Single-mated litter: Any litter sired by only one boar.
- Positive herd: Any herd with at least one HPB.
- Negative herd: Any herd without any HPBs.

Data for this study came from North American users (largely United States) of a computerized health and management program developed at the University of Minnesota (PigCHAMP®).[7] Each herd file included the dates of mating events with identified boars and sows, and farrowing events during calendar years 1987 through 1989. These performance reports were used to make comparisons between individual boars, and between individual boars and the overall herd averages. They include total matings attributed to a specific boar, the average parity of females at service for single-boar services, and the total single-boar services for each boar. Boar performance was measured by farrowing rate, liveborn litter size, and average number of pigs born dead.

Statistical analysis consisted of an analysis of covariance with a block treatment design to determine differences between normal and HPB.[11] Because the parity of farrowed sows was significantly ($P < .0001$) different between normal and HPB groups, covariates were parity and parity squared. Farm was the block.

Table 1

Means (± standard errors) of parity of sows, number of single-boar services evaluated, liveborn litter size, and number of pigs born dead for normal and hypoprolific boars

	Normal (n=4197)		Hypoprolific (n=191)		*P*
	Mean	SE	Mean	SE	
Parity of sows	3.31	0.03	2.39	0.10	<.0001
Single boar services evaluated	26.33	0.51	17.84	1.88	<.0001
Live-boar litter size	9.984	0.016	7.762	0.057	<.0001
Pigs born dead	0.9138	0.0085	1.0236	0.0309	.0004

Results

Objective 1

At least one HPB was detected in 97 (41.8%) of 232 qualified herds studied. Of 8203 boars listed, 4388 were qualified, and among the qualified boars, 191 (4.3%) were found to be hypoprolific (Table 1).

Objective 2

When the effects of parity and farm were eliminated, the pigs born live from sows mated to normal boars averaged 9.984 (+ 0.016 SE), versus 7.762 (+ 0.057 SE) ($P < .0001$) for HPB, a mean reduction of 2.22 piglets per litter. These data also reveal that the average number of pigs born dead was greater in the HPB-sired litters as compared to that of the normal boar litters (1.0236 [+ 0.0309 SE] versus 0.9138 [+ 0.0085 SE]; $P = .0004$).

Objective 3

For a herd with a mean total-born litter size of 11 pigs, and a standard deviation of 2.9 pigs per litter, the number of litters sired by an individual boar required to detect a significant difference from the herd average is shown in Table 2. Numbers in the body of the table have been calculated assuming that the one-sample Student's t-test will be used with a one-tailed hypothesis.

For example, assume that the true mean total born in litters sired by the boar being tested is 10.0. At $\alpha = 0.05$ and ß = .90, data from 74 farrowings would be needed to determine whether the mean litter size of 10.0 was significantly different from the herd average performance. At this level, there would still be a 10% chance (1 - ß = .90) of failing to detect a truly hypoprolific boar (Type II Error), and a 5% chance ($\alpha = 0.05$) of erroneously classifying a normal boar as hypoprolific (Type I Error). If the boar being evaluated was mated with three females per week (six copulations), it would take at least one year for sufficient farrowing records to accrue in order to generate the desired sample size.

Discussion

It is important to identify and remove hypoprolific boars from breeding herds.[8] According to Gustavsson,[3] approximately 50% of HPBs may

Table 2

Number of farrowings for a boar required to detect a significant difference between a total-born litter size of 11 with a standard deviation of 2.9 and an average total-born litter size of 10, 9, and 8 with a 5%, 10%, and 20% chance of a Type I error and a power of 90%, 80%, 70%, 60%, and 50%

Average of test boar	Power (1 - ß)	Type I Error (α) .05	.10	.20
10	.90	74	57	38
	.80	54	39	24
	.70	41	29	16
	.60	32	21	9
	.50	25	15	4
9	.90	20	15	10
	.80	15	11	7
	.70	12	8	5
	.60	10	6	3
	.50	8	5	3
8	.90	10	8	5
	.80	7	6	4
	.70	6	5	3
	.60	5	4	3
	.50	5	3	3

have heritable chromosomal aberrations, principally reciprocal translocations. This type of chromosomal anomaly is known to cause a widely varied reduction in litter size, with an average reduction of 42%, depending on the chromosomes involved. If these percentages are valid for pigs in the United States, the finding of 41.8% HPB-positive swine herds with a 4.3% HPB prevalence in the 4388 boars studied in these herds, it could be that the occurrence of cytogenetic aberrations may be much more extensive and result in greater economic losses than generally suspected.

In practice, herd managers are less conservative than scientific researchers, and are willing to make decisions based on fewer observations. In this case, the cost of replacing a suspect boar is relatively cheap compared with longer-term litter size reductions associated with hypoprolificacy. Thus, the number of homospermic farrowing records required to evaluate a boar with a true mean litter size of 10.0 is reduced to 29 at $\alpha = 0.10$ and $ß = 0.3$. At this level, there would be 30% chance of failing to detect a truly hypoprolific boar (Table 2).

Where the true mean litter size of a hypoprolific boar and the desired target differs by 2.0, only 20 or fewer observations are needed to detect it. Only 10 farrowing records are required to be highly confident of properly identifying a boar that has a total litter size more than one standard deviation below the mean (8.0 where the desired target is 11.0).

However, in carrying out these evaluations, care must be taken to ensure that comparisons are unbiased. Possible biases occur where young, lighter boars are used exclusively on gilts, which would be expected to farrow smaller litters than older sows. Also, because of the possibility of short or weak estrus behavior by sows and gilts, farrowings resulting from single-mating services should be ignored where a double-mating policy is practiced. In addition to failing to address these biases, Popescu's definition of a HPB uses liveborn rather than total-born litter size.[2] As the majority of the risk factors for stillbirth are sow- rather then boar-related, and herdspeople have difficulty in properly classifying stillborn piglets,[10] statistics regarding total-born litter sizes may provide a fairer means of identifying HPBs. Therefore, we propose the following modification of the definition of hypoprolificacy as stated by Popescu[2]:

> A hypoprolific boar is one whose mean total-born litter size from farrowings resulting from homospermic matings is at least one standard deviation below the desired target mean total-born litter size for the herd. Such evaluation must be based on at least 10 farrowing records resulting from matings with a representative population of sows and gilts.

We also suggest that, since half of the hypoprolific boars have a heritable chromosomal abnormality known to cause small litters,[3] making a cytogenetic examination of hypoprolific boars is a logical and prudent initial step in attempts to determine the cause of the condition.

Implications

- Heterospermic matings can mask boar hypoprolificacy. New boars should initially be used in homospermic matings long enough to accumulate at least 10 farrowing records so that their prolificacy can be assessed.
- Investigation of small litter size problems should begin with examination of the chromosomes of the boars involved.

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Appendix

Cytogenetic procedures involved in detection of chromosomal abnormalities in hypoprolific boars

- Send 10 mL of freshly drawn anticoagulated (green-top Vacutainer® tubes) blood, collected aseptically and sent by overnight mail, Monday through Thursday to:
  Cytogenetics Laboratory
  Veterinary Diagnostic Laboratory
  University of Minnesota
  1333 Gortner Avenue
  St. Paul, MN 55108
- The lymphocytes are cultured, stimulated to divide, treated to maximize chromosomal length, fixed, stained, and karyotyped to identify any reciprocal translocations.
- Response time is 2–4 weeks.
- Results are reported to the submitter.
- Cost is US$135.