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# Boar genotype as a factor shaping age-related changes in semen parameters and reproduction longevity simulations



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#### ABSTRACT

The aim of this study was a detailed analysis of the boar genotypes used in Al stations with an indication of their production capacity, including age and a precise analysis of their culling time and reason. The study included 334 boars: 81 Polish Large White (PLW), 108 Polish Landrace (PL), 49 Pietrain (P), 56 Duroc  $\times$  Pietrain (D  $\times$  P) and 40 Hampshire  $\times$  Pietrain (H  $\times$  P). Semen volume, spermatozoa concentration, total number of spermatozoa, number of motile spermatozoa, and number of insemination doses were analyzed. Quadratic regression was used to illustrate the selected sperm parameters at specific ages. Among all the studied boars the lowest motilities of spermatozoa were identified in white breeds PLW and PL, and the difference between motility extremes was 3.53% (P < 0.01). The highest number of insemination doses were produced from D × P crossbreed boars: about 0.7 portions more compared to PL, 1.13 to PLW, 1.18 to H  $\times$  P and 1.8 to P (all differences P < 0.01). It has been shown in the case of ejaculate volume that for PLW and  $H \times P$  boars the culling moment was far too early in terms of production capacity and differences were, respectively, 16.35 ml for PLW and 12.61 ml for H  $\times$  P. Based on the developed regression equations, the earliest maximum number of motile sperm (73.82  $\times$  10<sup>9</sup>) was obtained by  $H \times P$  crossbreed boars as early as at age 24 months. The highest values for this parameter were achieved, however, by other D  $\times$  P crossbreed boars: 74.30  $\times$  10 $^9$  at the later age of 32 months. A consequence of the high number of motile sperm in young H x P boars was that the theoretical maximum value of the number of AI doses was produced as early as the 14th month (25.59 portions). Curves of similar shape were obtained for PL and D  $\times$  P boars; the difference in maximal values was 0.54 portions in favor of crossbreeds, at a later age of 7 months. It was noted that for PLW and D  $\times$  P boars the highest number of cullings were due to reduced demand (24.47% and even 31.19%, respectively). Other boars - PL, P and H × P - were most frequently culled because of low semen values. Regardless of the genotype, high survival probabilities (over 0.96) were noted for the age of 12 months. The highest probabilities (still over 0.96) were noted in the longest time period (up to 18 months) for P boars. The results of our study can be used in AI stations as reference points for the exploitation and culling of boars with different genotypes.

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## 1. Introduction

AI stations have still reserves which should be used to increase the profitability of their activity. The use of AI is still the most popular reproductive technique in pig production, with particularly significant developments being noted in the late 90s and early 00s. Therefore, the consumer market for AI doses is more demanding in terms of the product on offer. AI stations now need to be technically

highly specialized to maintain a large number of healthy, high-performance boars of various breeds and genetic lines [1].

The genotype structure of boars used in insemination programs depends on the demand, and the popularity of crossbreeds in AI stations results in their increasing numbers due to their high libido and easy semen collection [2]. However, there is no single boar type that represents the best of all possible semen parameters, because some studies indicate the superiority of crossbreeds [3,4] and others pure-breed boars [5]. Maintenance of the optimal participation of boar genotypes in AI stations is required by the market situation related to the demand from domestic customers for material for fattening [6]. Increasing the efficiency of production is one

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of the main activities currently undertaken by AI stations with the highest product quality.

The quantity and quality of semen are the primary determinants of boar fertility and represent measurable progress achieved by sires in pig production [7]. AI station economic profitability depends on boar capacity and the production of live/motile spermatozoa during exploitation [8], and this is limited by dysfunctions impacting upon a later culling [9]. Accordingly, the interest of AI stations is focused on maximizing the longevity of boar reproduction to achieve lower production costs for the AI doses offered for sale. Early identification of boars characterized by falling production capacity, or diagnosed health or behavioral problems is the essence of the proper functioning of AI stations. Specialized stations should maintain strict control of sires and ejaculates.

Tracking reproductive longevity together with production parameters is the first step in the effective replacement in a herd [10]. According to Szostak and Przykaza [11], research on controlling productivity, the prediction of effective production capacity at given ages and the time moment of culling remain economically significant. However, insightful analyses of boars with different genotypes used in AI stations are rarely published. Such an analysis would include age-dependent performance, specific culling reasons and a survival analysis.

Based on the above considerations, the aim of this study was a detailed analysis of the boar genotypes used in AI stations, with an indication of their production capacity including age and a precise analysis of culling time and reason.

#### 2. Materials and methods

# 2.1. Experimental location and design

The study was carried out between 2010 and 2015 at the Boar Exploitation Station in Częstochowa and included 334 boars in 5 genotypes: 81 Polish Large White (PLW), 108 Polish Landrace (PL), 49 Pietrain (P), 56 Duroc  $\times$  Pietrain (D  $\times$  P) and 40 Hampshire  $\times$  Pietrain (H  $\times$  P). The total number of analyzed ejaculates was 41,935. The presented population was representative in proportion to the most common breed components used for AI in Poland.

# 2.2. Semen data

Semen collection started at the age of 8 months. Before the start of semen collection, all boars were held in quarantine, the length of which was approximately  $36.85 \pm 4.87$  days. The boars were trained to ejaculate on a dummy sow. Additionally, all boars were exploited in the same way, developed and adopted according to the methodology of the AI station. Collection interval was almost identical between the genotypes, i.e.  $5.11 \pm 2.94$  days. Ejaculates that were not acceptable and did not qualify for use in AI were not included in the analysis. The following quantity and quality parameters were analyzed: semen volume (ml), spermatozoa concentration ( $\times 10^6$  ml<sup>-1</sup>), total number of spermatozoa in ejaculates  $(\times 10^9)$ , number of motile spermatozoa in ejaculates  $(\times 10^9)$ , and number of insemination doses obtained from one ejaculate (n). Ejaculates were collected by the gloved hand method using a container with a filter [12]. The gelatinous fraction was separated. Immediately after collection, semen volume was measured using a scalar cylinder. The spermatozoa concentration was evaluated using a SpermaCue device, Model 12300/0500 (Minitube International, Verona, USA). Based on the semen volume and spermatozoa concentration, the total number of spermatozoa in the ejaculate was calculated and expressed as 10<sup>9</sup> spermatozoa per ejaculate. Semen dilution was effected using the same short-term semen extender, BTS boar semen extender (Version 13525/0100 Antibiotic free, Minitube International, Verona, USA). Motility of spermatozoa was assessed under an optical microscope at a magnification of  $\times 200$  (Nikon Eclipse E100, Nikon Instruments, Japan). For the assessments, aliquots of semen samples were placed on prewarmed slides, covered with a glass cover slide (20  $\times$  20 mm). The total number of motile spermatozoa in the ejaculate was calculated by multiplying the total number of spermatozoa in the ejaculate by the percentage of motile spermatozoa. All normal insemination doses (80 ml) were used for production.

# 2.3. Culling data

The moment for culling boars was determined based on individual exploitation histories from birth until death. Reasons for culling fell into 7 groups: low semen value, low or lack of libido, leg problems, infectious diseases, old age, reduced demand for semen from the given boar, and others.

# 2.4. Housing and feeding

Boars were single-housed and maintained in accordance with the principles of animal welfare [13]. Preventive care and vaccination was carried out regularly for all boars at the same time intervals and in accordance with the methodology of the unit. The individual pen area was 8 m²/boar. The air temperature in all boar pens was close to 15 °C (min 12 °C, max 20 °C). Relative humidity was close to 75% (min 65%, max 85%). The air circulation inside the building was equal to 0.15 m/s in winter and 0.20 m/s in summer. Over the whole study period, boars were fed the same all-mash mixture, dosed according to the recommended nutrition standards for boars [14], with permanent access to water.

# 2.5. Statistical analysis

Numeric materials were analyzed statistically using the Statistical 12.5 software package [15]. The values set out in the tables determine the arithmetic means  $(\bar{x})$  and standard deviations (SD). Factor analysis (ANOVA) was used for precise determination of the possible genotype effect on selected semen parameters based on the GLM advanced mixed model. The collected data were checked for normality with the Kolmogorov-Smirnov test with Lilliefors correction. The homogeneity of variances was checked with the Brown-Forsythe test. The significance of differences was calculated on the basis of Tukey's multiple range test.

Adoption procedures for quadratic regression generated the best fit. Linearized non-linear regression based on data transformation was applied. Charts were generated separately for each genotype based on the partial data and additionally marked maximum values. The overall square regression model was as follows:

$$y=ax^2+bx+c$$

where: y - dependent variable (semen parameter).

x – independent variable (age of boar in months).

a, b, c – real coefficient adjustment on the basis of partial results. Survival analysis was performed using the Cox proportional hazard model for each genotype of boar. The time variable was defined as age in months from birth.

### 3. Results

The effects of boar genotype on selected semen parameters are presented in Table 1. The highest semen volumes were noted in

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