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Genetic analysis for reproductive and longevity traits in Landlly sows

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ABSTRACT

The rate of reproduction and lifetime productivity of the animals determine the success of a herd. As these features significantly impact sow productivity, welfare, and profitability, there is considerable interest in global swine breeding programmes to genetically select better sows for these attributes. In this scenario, reliable heritability estimates and genetic correlations between traits are essential for the success of genetic selection for such traits. The goals of the current study were to examine the reproductive and longevity traits and to estimate the genetic and phenotypic parameters for these traits in Landlly sows kept at a swine production farm, Izatnagar, Uttar Pradesh, India. The effect of non-genetic factors on different reproductive traits was estimated using SPSS version 16.0 and Bayesian approach which were utilized to estimate the genetic parameters for reproductive and longevity traits. The current study's finding that the year and season of birth significantly affect reproductive traits generally suggests that there is potential for boosting productivity by optimising managemental practices. The heritability estimates were low for the reproductive and longevity traits, indicating a very little additive genetic variance in these traits, and individual selection will not be helpful for improving them. As some traits, such as LSB_FF & LSW_FF and LSB _SF & LSW_SF, have a moderate genetic correlation, indirect selection can be used to improve these two pairs of features.

Keywords: Bayesian, Genetic parameter, Linear model, Longevity, Non-genetics factors, Threshold models

In terms of livestock development, fertility and particularly female reproductive efficiency, rank among the most important factors (Guo *et al*. 2016). The development of a sustainable production system can be achieved by decreasing forced slaughter and improving the life expectancy of animals in herds. Enhancing swine reproduction traits will increase the revenue of commercial swine farms (Uzzaman *et al*. 2018). The lifetime production of a female varies due to genetic variations and environmental factors (Suwanasopee *et al*. 2005). A preference for longevity will increase health and produce more resilient pigs that are best prepared to handle potentially variable farming conditions, making a longer productive life economically valuable and often highly profitable for the farmer as well as the animal (Sobczynska *et al*. 2013). Sow stayability in a herd is affected by a wide range of variables, including health, management, nutrition, and stockbreeder (Knauer *et al*. 2010). Sow longevity is a crucial productivity measure for both sow production and the efficiency of swine management in commercial pig breeding herds. In commercial herds, the culling rate of the sow is about 50% each year in which 15% to 20% of sows are culled because of their poor reproductive potential (Engblom *et al*. 2007). Genetic parameters for reproductive and longevity traits are required to set up a complete swine genetic improvement programme for these traits in crossbred swine. Among the crucial economic traits in pigs are reproductive traits such as litter size, age at first mating, age at first farrowing, and farrowing interval. gestation period, weaning to service interval. and litter uniformity. To achieve the breeding goal of increasing litter size while lowering piglet mortality, swine managemental activities and breeding systems must include piglet uniformity as a crucial necessity (Zhang *et al*. 2016).

Longevity and lifetime production traits are becoming increasingly important in swine breeding systems around the world because they have an impact on sow productivity and wellness and profitability. Hence, enhancing pig reproduction and lifetime production would boost the revenue of commercial swine farms.

Numerous non-genetic factors induce bias in genetic parameter estimation. Therefore, it is challenging to estimate the accurate genetic parameters in the absence of these factors, which determine the optimum selection criteria for the planned improvement of the animals (Tomar

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2004). Based on the above facts, this study was conducted on the Landlly sows maintained at Swine Development Farm.

MATERIALS AND METHODS

Study population and its management: The present study was performed on Landlly sows, i.e. a crossbred of Landrace (exotic) and Ghurrah (local Bareilly pig) developed under AICRP on Pig at Swine Development Farm, situated at 28°N latitude and 79°E longitude, 564 feet above mean sea level. With relative humidity levels ranging from 45% to 85%, the climate in this region is extreme on both sides. Based on the previous year's temperatures and relative humidity, the seasons were classified into three groups: season 1 (November–February), season 2 (March–June), and season 3 (July–October).

The Landrace and Ghurrah breeds' inheritance percentages have been retained in Landlly at 75% and 25%,

Table 1. Least squares means and standard error (SE) for AFM, ASM, AFF, ASF, GL and WSI

		AFM	ASM	AFF	ASF	GL	WSI
	Least squares means (LSM)	342.05±19.44 (146)	539.80±19.92 (88)	455.45±17.70 (149)	652.36±19.98 (88)	113.45±0.56 (146)	49.74±9.5 (87)
Parity		NS	NS	NS	NS	NS	NS
1	LSM	311.35±12.08 (62)	546.04±24.78 (41)	466.71±17.81 (64)	657.88±24.85 (41)	113.24±0.67 (62)	32.74±10.94 (41)
2	LSM	310.16±11.26 (39)	568.88±27.26 (25)	473.95±16.62 (40)	684.31±27.33 (25)	114.16±0.63 (39)	68.88±10.51 (20)
3	LSM	296.39±14.05 (38)	504.48±31.84 (22)	437.28±20.74 (38)	614.88±31.93 (22)	113.86±0.76 (38)	51.49±10.92 (24)
4	LSM	304.54±25.07 (7)	-	434.22±37.13 (7)	-	113.01±1.36 (7)	46.3±28.97 (2)
Year		**	NS	**	NS	NS	*
2014	LSM	338.175±31.23 (10)	545.65±72.50 (4)	471.5±45.68 (11)	660.42±72.69 (4)	115.33±1.71 (10)	34.55±9.1 (3)
2015	LSM	352.24±23.77 (34)	541.59±44.22 (23)	451.78±35.21 (34)	656.93±44.34 (23)	114.11±1.29 (34)	21.20±5.5 (20)
2016	LSM	330.31±20.79 (29)	530.39±35.78 (19)	424.56±30.64 (30)	643.50±35.88 (19)	114.01±1.13 (29)	28.25±5 (17)
2017	LSM	323.87±19.38 (23)	476.86±32.89 (18)	439.28±28.59 (23)	587.47±32.97 (18)	113.53±1.05 (23)	39.65±3.8 (18)
2018	LSM	378.01±18.61 (21)	596.99±38.56 (15)	550.81±27.5 (22)	707.98±38.66 (15)	112.85±1.08 (21)	13.99±5.2 (14)
2019	LSM	160.54±20.17 (19)	547.29±57.49 (9)	468.95±29.9 (19)	657.82±57.64 (9)	112.3±1.1 (19)	22.75±6.22 (11)
2020	LSM	240 ±40.05 (10)	-	364.4±59.34 (10)	-	112.83±2.18 (10)	-
Season		**	NS	**	NS	NS	NS
November-February	LSM	325.62±21.09 (10)	538.72±45.68 (6)	506.75±31.17 (10)	648.88±45.79 (6)	114.57±1.17 (10)	51.1±18.96 (6)
March- June	LSM	280.10±11.28 (95)	518.04±18.57 (61)	391.05±16.59 (98)	631.78±18.62 (61)	112.48±0.62 (95)	47.13±10.74 (61)
July-October	LSM	311.11±12.04 (41)	562.62±28.29 (21)	461.32±17.78 (41)	676.40±28.37 (21)	113.64±0.66 (41)	51.33±11.61 (20)
Generation		NS	NS	NS	NS	NS	*
1	LSM	246.50±19.77 (52)	520.40±39.13 (30)	450.41±29.23 (52)	629.98±39.23 (30)	112.86 ±1.07 (51)	12.27 ±15.93 (30)
2	LSM	289.97±16.3 (34)	552.78±30.69 (24)	454.12±24.09 (33)	665.69±30.77 (24)	112.85±0.89 (32)	42.31±13.55 (24)
3	LSM	261.61±15.85 (31)	547.09±35.17 (21)	439.76±23.39 (31)	659.64±35.26 (21)	113.25 ±0.86 (30)	73.98 ±14.41(20)
4	LSM	334.27±20.92 (23)	538.91±51.83 (13)	450.37±30.92 (23)	654.11±51.96 (13)	114.34±1.14 (23)	70.85±20.12 (13)
5	LSM	395.68±42.86 (10)	-	470.54±63.5 (10)	-	114.53 ±2.33 (10)	-

*, Significant at P<0.05; **, Significant at P<0.01; LSM, Least squares means; NS, Non-significant. No. of observations for the different reproductive traits have been given in brackets along with their least square means.

respectively. Landlly pig is performing well (quality litter size and economical feeding) under various pig farmers' management strategies (Naha *et al*. 2020). This farm has a controlled mating system, and most of the data is kept for both pedigree and individual purposes. Piglets were given ear tags at birth, and data regarding their dam, birthdate, and sex was kept in the farm.

Data collection: The current study analyzed the data from 2014 to 2021, a period of eight years. The fixed variables considered in the study were year of birth (7 levels: 2014-2021), season of birth (3 levels: November-February, March- June, July-October), parity of dam (4 levels: 1-4), and generation of animal (1-6). The date of birth, season of birth, year of birth, parity of dam, date of first farrowing, and date of exits for each animal identity were acquired from the data registers kept at the Institute's Swine Production Unit. In all analyses, the R package 'GeneticsPed' was used to calculate generation numbers (Gorjanc *et al*. 2021).

A total of 14 reproductive traits and 9 longevity and stayability traits were considered in this study. The sizes of the data sets for different reproductive traits are shown in Supplementary Table 1. The reproductive traits include age at first mating (AFM), age at second mating (ASM), age at first farrowing (AFF), age at second farrowing (ASF), gestation length (GL), weaning to service interval (WSI), litter size at birth at first farrowing (LSB_FF), litter size at birth at second farrowing (LSB_SF), litter size at weaning at first farrowing (LSW_FF), litter size at weaning at second farrowing (LSW_SF), within litter weight coefficient of variation at birth during first farrowing (CVB_FF), within litter weight coefficient of variation at birth during second farrowing (CVB_SF), within litter weight coefficient of variation at weaning during first farrowing (CVW_FF), and within litter weight coefficient of variation at weaning during second farrowing (CVW_SF).

The sizes of the data sets for different longevity and stayability traits are shown in Supplementary Table 2. The nine traits were used to assess longevity and stayability: length of life (LL) and length of productive life (LPL) and Stayability for the gilts up to mating for parity 1 (ST1M), Stayability for the gilts up to mating for parity 2 (ST2M), Stayability for the gilts up to mating for parity 3 (ST3M), Stayability for the gilts up to farrowing parity 1 (ST1F), Stayability for the gilts up to farrowing parity 2 (ST2F), Stayability for the gilts up to farrowing parity 3 (ST3F). The accumulated number of piglets born alive up to parity two (ABA2) was also defined as a longevity trait. The failure time for the length of life (LL) was calculated using the difference between the birth date and the exit date. The failure time for the length of productive life (LPL) was calculated using the difference between the dates of the first farrowing and the exit.

The sow's removal parity was considered when defining the stayability traits. For a sow removed before the event (i.e. the farrowing or mating), a value of 0 was given to the stayability traits, while a value of 1 was given to a sow that stayed till the event (i.e. either the mating or farrowing). The traits ST1M, ST2M, ST3M, ST1F, ST2F and ST3F were analyzed as binary traits, while LL and LPL were analyzed as linear traits.

Statistical methods: Using SPSS version 16.0, least-squares estimates for several reproductive traits were generated. Significance testing was performed using differences among least-square means. Year, season, parity, and generation were the fixed effects that were considered for the study.

For both longevity and reproductive traits, the animal was treated as a random effect in linear analyses, whereas the sire was treated as a random effect for stayability traits analysed by threshold model with probit link function, implemented in the 'MCMCglmm' package (Hadfield 2010). Since the majority of the traits had small data sets, the Bayesian technique was employed to estimate the genetic parameters using the MCMCglmm package. If the prior is properly chosen for the analysis, this approach is appropriate for small data sets.

The prior for estimating the heritability of stayability traits was parameter expanded χ^2, while the prior for estimating the variance components and genetic correlation for all reproductive traits and longevity traits (LL, LPL) was inverse gamma prior.

There were 5000000, 9000000, and 2000000–5000000 numbers of iterations for reproductive, longevity and stayability traits respectively. For all analyses, the burn-in and thinning intervals were 10,000 and 100, respectively. Convergence was diagnosed using trace plots, the Heidelberger and Welch diagnosis, autocorrelation, and effective size. The traits also underwent correlation analysis. For the qualities affected by maternal factors, the maternal genetic effect was also employed as a random effect.

Using the R programming environment and R version 4.1.1, all analyses were carried out (R Core Team 2021). The estimation of heritability was performed using the R package MCMCglmm, Version 2.32 (Hadfield 2010). The following mathematical models were used in the analyses.

Linear model for reproductive traits: $Y_{ijklmn} = \mu + FY_i + SE_j + P_k + AFF_l + G_m + A_n + e_{ijklmn}$

Linear model for longevity traits: For the linear analyses of LL, LPL and ABA2 for the estimation of heritability, following model was used: $Y_{ijklmno} = \mu + FY_i + SE_j + P_k + G_m + A_n + D_o + e_{ijklmno}$

Threshold model for stayability traits: The stayability traits were modeled as binary trait using the following model (Jose Lucio 2004): $Y_{ijklmno} = g(x) = \mu + FY_i + SE_j + P_k + AFF_l + G_m + S_n + D_o + e_{ijklmno}$

In all these models, Y_{ijklmn} and $Y_{ijklmno}$, Phenotypic observation for different reproductive/longevity/stayability traits; μ, Population mean common to all the observations; g(x), link function (probit); FY_i, Effect of i^{th} year of birth; SE_j, Effect of j^{th} season of birth; P_k, Effect of k^{th} parity of dam; AFF_l , Age at first farrowing of l^{th} dam; G_m, Effect of m^{th} generation A_n , Random effect of n^{th} animal; D_o,

Table 2. Least squares means and standard error (SE) for litter sizes and coefficient of variation for weights

	LSB_FF	LSB_SF	LSW_FF	LSW_SF	CVB_FF	CVB_SF	CVW_FF	CVW_SF
Least squares means (LSM)	7.92±0.37 (148)	8.39±.61 (85)	7.02±0.45 (148)	7.02±0.67 (85)	0.175±0.01 (146)	0.183±0.02 (86)	0.197±0.2 (140)	0.234±0.02 (85)
Parity	NS	NS	NS	NS	NS	NS	NS	NS
1	8.08±0.45 (64)	8.45±0.68 (42)	6.77±0.53 (64)	7.66±6.44 (42)	0.2±0.01 (63)	0.21±0.02 (42)	0.2±0.03 (60)	0.23±0.02 (42)
2	7.87±0.42 (40)	8.01±0.73 (20)	7.03±0.5 (40)	6.44±0.81 (20)	0.17±0.01 (40)	0.17±0.02 (20)	0.15±0.03 (38)	0.19±0.02 (19)
3	7.93±0.51 (37)	7.69±0.8 (20)	6.7±0.61 (37)	7.16±0.84 (20)	0.16±0.02 (36)	0.17±0.02 (21)	0.22±0.03 (35)	0.23±0.03 (21)
4	7.45±0.91 (7)	9.41±1.72 (3)	7.04±1.09 (7)	6.80±1.91 (3)	0.17±0.03 (7)	0.19±0.05 (3)	0.2±0.06 (7)	0.3±0.06 (3)
Year	NS	NS	NS	NS	NS	NS	NS	NS
2014	7.35±1.13 (11)	9.39±1.84 (4)	6.77±1.35 (11)	6.83±2.04 (4)	0.18±0.04 (10)	0.21±0.05 (4)	0.16±0.07 (10)	0.38±0.06 (4)
2015	7.63±0.87 (34)	8.68±1.15 (23)	7.52±1.04 (34)	7.16±1.28 (23)	0.17±0.03 (34)	0.18±0.03 (23)	0.17±0.06 (33)	0.25±0.04 (22)
2016	8.01±0.75 (29)	7.82±1.04 (18)	7.33±0.9 (29)	7.0±1.15 (18)	0.16±0.03 (28)	0.20±0.03 (18)	0.24±0.05 (26)	0.24±0.03 (18)
2017	7.8 ±0.7 (23)	7.83±0.88 (18)	6.76±0.84 (23)	6.23±0.98 (18)	0.2±0.02 (23)	0.2±0.02 (18)	0.25±0.04 (22)	0.24±0.03 (18)
2018	6.99±0.73 (22)	7.23±1.15 (14)	5.3±0.87 (22)	6.65±1.28 (14)	0.16±0.02 (22)	0.13±0.03 (14)	0.22±0.05 (21)	0.19±0.04 (14)
2019	7.58±0.74 (19)	9.39±1.4 (8)	7.15±0.89 (19)	8.23±1.55 (8)	0.16±0.02 (19)	0.19±0.04 (9)	0.18±0.05 (19)	0.12±0.05 (9)
2020	9.45±1.46 (10)	-	7.36±1.75 (10)	-	0.18±0.05 (10)	-	0.12±0.09 (9)	-
Season	NS	NS	NS	NS	NS	NS	NS	NS
November-February	8.12±0.78 (10)	7.98±1.28 (6)	7.22±0.94 (10)	7.77±1.42 (6)	0.16±0.03 (10)	0.16±0.04 (6)	0.19±0.05 (10)	0.25±0.04 (6)
March- June	7.93±0.42 (98)	8.68±0.69 (57)	7.45±0.5 (98)	7.11±0.77 (57)	0.18±0.01 (97)	0.18±0.02 (58)	0.20±0.03 (93)	0.21±0.02 (58)
July-October	7.45±0.45 (40)	8.51±0.71 (22)	5.98±0.53 (40)	6.18±0.79 (22)	0.18±0.01 (39)	0.22±0.02 (22)	0.18±0.03 (37)	0.24±0.02 (21)
Generation	NS	NS	NS	NS	NS	NS	*	NS
1	7.62±0.73 (51)	7.42±1.02 (29)	6.33±0.87 (51)	6.74±1.14 (29)	0.19 ±0.02 (50)	0.16±0.03 (20)	0.23±0.05 (48)	0.22±0.03 (28)
2	7.71±0.59 (33)	8.64±0.87 (24)	6.66±0.71 (33)	6.94±0.97 (24)	0.16±0.02 (33)	0.16±0.02 (24)	0.12±0.04 (31)	0.19±0.03 (24)
3	8.04±0.58 (31)	8.32±0.99 (20)	7.28±0.69 (31)	7.21±1.1 (20)	0.18±0.02 (30)	0.24±0.03 (20)	0.17±0.04 (29)	0.28±0.03 (20)
4	8.55±0.76 (23)	9.18±1.37 (12)	7.72±0.91 (23)	7.17±1.52 (12)	0.17±0.03 (23)	0.18±0.04 (13)	0.13±0.05 (23)	0.25±0.05 (13)
5	7.24±1.56 (10)	-	6.43±1.87 (10)	-	0.17±0.05 (10)	-	0.31±0.1 (9)	-

*, Significant at P<0.05; **, Significant at P<0.01; NS, Non-significant. No. of observations for different reproductive traits have been given in brackets along with their least square means.

Effect of o^{th} dam; S_n, Random effect of n^{th} sire; e_{ijklmn}, $e_{ijklmno}$, Random residual.

Heritability (h^2) was estimated by following equation for reproductive and longevity traits:

$$h^2 = V_a / V_a + V_r$$

where, V_a , additive variance, and V_r , residual variance.

When maternal genetic effect was fitted in the model, following equation was used for estimation of heritability:

$$h^2 = V_a / V_a + V_m + V_r$$

where V_a , additive variance, V_m , additive variance due to maternal effect and V_r , residual variance.

For stayability traits, heritability was estimated according to the following equation:

$$h^2 = 4V_s / V_s + 1$$

where, V_s is the variance due to random effect of sire, 1 in the denominator is the "variance" of the link transformation (1 for a probit link). All the analyses were performed in R programming environment, R version 4.1.1 (R Core Team 2021).

RESULTS AND DISCUSSION

Effect of non-genetic factors on reproductive traits: Least squares mean with standard errors (SE) for different years (2014-2020), seasons (November-February, March-June, July-October), and parities (1-4) are presented in Tables 1 and 2. Age at first mating (AFM), age at first farrowing (AFF), and weaning to service interval (WSI) were all significantly affected by the year in the current study. Kumari and Rao (2010) and Das *et al*. (2005) also found significant effect of year of birth on the age at first mating (AFM). Season of birth also have significant effect on age

at first farrowing (AFF) and age at first mating (AFM). It is possible to increase output by streamlining the management practices, as the year and season of birth have a significant effect on reproductive traits.

The generation effect was also significant with weaning to service interval (WSI) and within-litter weight coefficient of variation at weaning during first farrowing (CVW FF). In contrast to Pandu Ranga *et al*. (2013), who found that parity had a significant effect on litter traits in crossbred pigs, our study found no significant effect of parity on reproductive traits.

Genetic parameters of reproductive traits: The variance components and heritability estimates for reproductive traits are given in Supplementary Table 3. The estimates of heritability for reproductive traits were 0.01 (AFM), 0.08(ASM), 0.09(AFF), 0.08(ASF), 0.04(GL), 0.34(WSI), 0.07(LSB_FF), 0.06(LSB_SF), 0.07(LSW_FF) 0.06(LSW_SF), 0.25 (CVB_FF), 0.26 (CVB_SF), 0.11(CVW_FF) and 0.26 (CVW_SF).

In comparison to other traits, such as growth traits, the "fitness traits," such as reproductive and survival traits, tend to have lower heritability. This may be because fitness traits have less additive genetic variance than other traits. According to recent studies, the higher residual variances of fitness traits are the cause of their lower heritability. Furthermore, because these traits have more complex genetic structure than other traits, the larger residual variance is caused by higher amounts of non-additive genetic variance (Merilä and Sheldon 1999). Compared to estimates from Merks and Molendijk (1995) and Hanenberg *et al*. (2001) the heritability estimate of our study for age at first mating (AFM) is significantly lower.

Alam *et al*. (2021) reported heritability estimates for age at first farrowing (AFF) in Duroc, Landrace and Yorkshire pigs to be 0.14±0.02, 0.07±0.02, and 0.12±0.01, respectively. The estimated heritability for Landrace (0.07) is comparable to the estimated heritability (0.09) from our study. Haley *et al*. (1988) estimated that the heritability of litter size is approximately 0.09, which is comparable to the estimate from this study (0.07). In the study of Hanenberg *et al*. (2001), heritability estimates for the number of piglets born at first parity in Landrace pigs were 0.09 by the additive model and 0.10 by the repeatability model. This study's estimate (0.07) is similar to the additive model's estimate.

The estimates of heritability reported by Kaufmann *et al*. (2000) in Large White animals were higher than that of the present study.

The heritability estimate for gestation length (0.04) in this study is somewhat higher than that reported by Neopane (2007).

Genetic parameters of longevity and stayability traits: The variance components and heritability estimates for longevity traits are given in Supplementary Table 4. Heritability estimates for traits related to longevity and stayability were 0.18(LL), 0.14 (LPL), 0.05, 0.25 (ST1M), 0.19 (ST2M), 0.54 (ST3M), 0.08 (ST1F), 0.19 (ST2F) and 0.54 (ST3F). According to findings from a previous study, sire model was used in this study as the random effect for the genetic analysis of stayability traits (Luo *et al.* 2001). For Finnish Landrace and Large White pigs, Serenius and Stalder (2004) reported heritabilities ranging from 0.05 to 0.10 for the estimated length of productive life using linear model analyses. The estimated heritabilities by threshold model analysis for the stayability traits for purebred Landrace and Large White pigs, respectively, were 0.136-0.200 and 0.110-0.283, according to the report by Ogawa *et al*. (2021).

The heritability estimates for stayability traits in this study were greater than those of Engblom *et al.* 2015. The estimates of heritability for ST3M/ST3F in the current study were significantly higher than those for other stayability traits, likely as a result of the smaller data sizes for ST3M/ST3F compared to other stayability traits (especially the low number of events/successes), as heritability is overestimated when data sets are small for a binary trait (Hoeschele and Tier 1995).

Correlation between traits: The phenotypic correlations between pair of investigated traits and their significance testing are shown in Figs. 1 and 2. Genotypic correlations between pair of investigated traits are shown in Supplementary Table 5. Between LSB FF and LSW FF, the phenotypic and genotypic correlation were 0.85 and 0.24 respectively while it was 0.87 and 0.56 between LSB_SF and LSW_SF (Supplementary Table 5 and Fig. 1). Likewise, phenotypic and genetic correlations between AFM and AFF were 0.91 and 0.24, respectively, while ASM and ASF trait combinations had phenotypic and genetic correlations of magnitudes 0.99 (~1) and 0.41, respectively. The genetic correlations between pair of investigated traits were higher in second parity as compared to first parity. As per the significant high and positive phenotypic correlations between these two traits, age at first farrowing will be high if age at first mating is high, and vice-versa. Given that both traits are decided by the sow's dates of birth, this is to be expected. Age at second mating and age at second farrowing also showed a

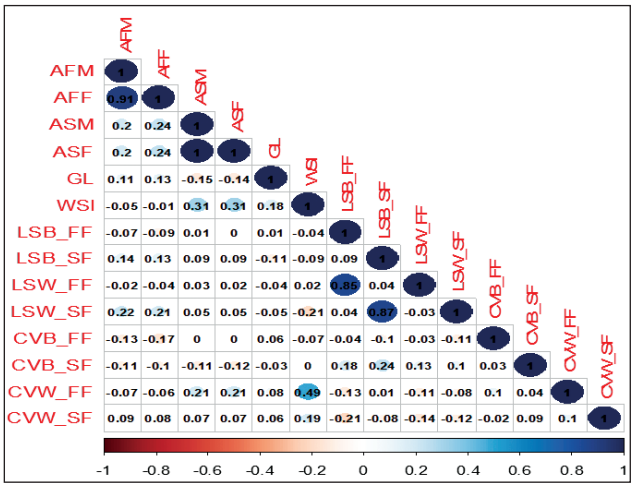

Fig. 1. Phenotypic correlations between the traits.

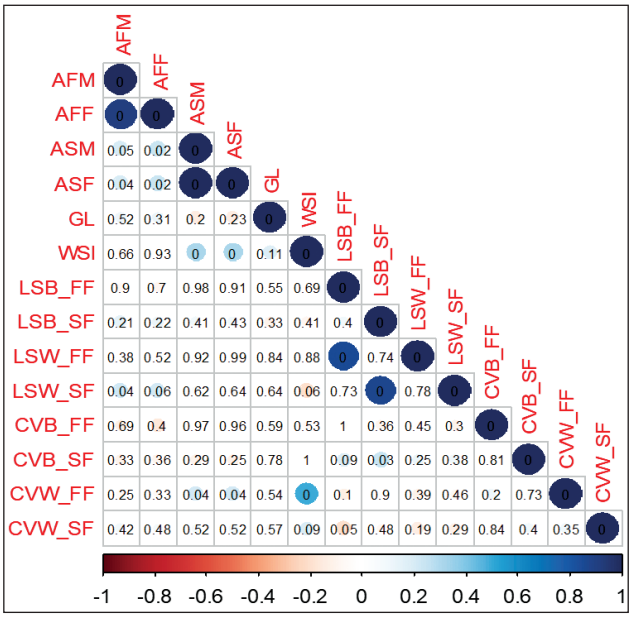

Fig. 2. Significance testing for the phenotypic correlations between investigated traits.

considerable high and favourable phenotypic correlation. Age at first mating (AFM) also had a small but significant effect on age at second mating (ASM) and age at second farrowing (ASF). There were significant high and positive phenotypic correlations between the litter sizes at birth at the first and second farrowings (LSB_FF and LSB_SF) and the litter sizes at weaning at the first and second farrowings (LSW_FF and LSW_SF). They show that the litter sizes at birth are typically maintained during the weaning stage due to management approaches. The genetic correlation between the traits LSB_FF and LSW_FF as well as LSB SF and LSW SF showed that these traits are not controlled by a single gene, but rather by a group of genes.

As per the moderate estimates of the genetic correlations between the two investigated traits, selection on one trait will have a moderate impact on the other linked trait. Several traits displayed negative phenotypic correlations with each other, however these correlations were often of lesser magnitudes. Figs. 1 and 2 illustrate the phenotypic correlations between the traits and their significance testing, respectively.

It can be concluded that the effect of year was highly significant on the age at first mating (AFM) and age at first farrowing (AFF) and significant on weaning to service interval (WSI) in the present study. The season's effect was highly significant on age at first farrowing (AFF) and age at first mating (AFM). The generation effect was significant on the weaning to service interval (WSI) and within litter weight coefficient of variation at weaning during first farrowing (CVW_FF).

As the year and season of birth have a significant effect on reproductive traits, it suggests that there is scope for enhancing productivity by optimising managemental practices. As some traits, such as LSB_FF and LSW_FF, and LSB_SF and LSW_SF, have a moderate genetic correlation, indirect selection can be used to improve these two pairs of features.

The majority of the reproductive, longevity, and stayability traits had low heritability estimates (as expected for fitness traits). This could have been caused by the environment, nonadditive effects, or both, given that the residual variances for these traits were high. Further statistical investigation of the nonadditive influences governing these features using larger sample sizes is possible (as sample sizes were small for many traits). It can be concluded that these traits are influenced by environmental factors if epistatic and dominance effects are found to be insignificant in such future investigations. As a result, by controlling environmental conditions, most reproductive traits, longevity traits, and stayability traits can be improved (such as nutrition and management intervention). Furthermore, since the study is limited by the small data sizes for the majority of the traits, larger data sets are preferred for future validation investigations.

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