

Genetic aspects of Wood's lactation curve parameters in Jersey crossbred cattle using Bayesian approach

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SUPPLEMENTARY FILE

Supplemental Table S1. Mathematical descriptions of lactation curve traits estimated by Incomplete gamma function

Peak Milk Yield (Y_{\max})	$a(b/c)^b e^{-b}$
Time of Peak Milk Yield (N_{\max})	b/c
Persistency of milk yield (P)	$c^{-(b+1)}$

a =Initial milk yield after calving; b =Ascending slope up to peak yield; c =Descending slope after peak yield

Model used:

The following repeatability animal model was used:

$$y = Xb + Za + Wp + e$$

Where,

y = n × 1 vector of observations for each trait/parameter

b = Vectors of fixed effect

a = Vectors of direct additive genetic effect

c = Vectors of permanent environmental effect

e = Vectors of residual effect

X, Z and W= Incidence matrices of fixed effect, direct additive genetic effect and permanent environmental effect

The three random effects have the following distribution

$$\text{Var} \begin{pmatrix} a \\ p \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{pmatrix} = \begin{pmatrix} G & 0 \\ 0 & R \end{pmatrix}, \quad G = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_{pe}^2 \end{pmatrix}$$

Where, A= Additive numerator relationship matrix

I= Identity matrix

σ_a^2 = Direct additive genetic variance

σ_{pe}^2 = Permanent environmental variance

σ_e^2 = Residual variance

The total phenotypic variance (σ_p^2) is the sum of the three variance components.

$$\sigma_p^2 = \sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2$$

Estimation of genetic and phenotypic parameters

The heritability (h^2) of the studied traits were estimated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

The repeatability (r) of the studied traits were estimated as

$$r = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

The genetic correlations (r_g) between the studied traits were estimated as

$$r_g = \frac{Cov(a_X, a_Y)}{\sigma_a(X) \times \sigma_a(Y)}$$

Where, $Cov(a_X, a_Y)$ =additive genetic covariance between trait X and Y

$\sigma_a(X)$ and $\sigma_a(Y)$ = additive genetic standard deviation of trait X and Y respectively.

The phenotypic correlations (r_p) between the studied traits were estimated as

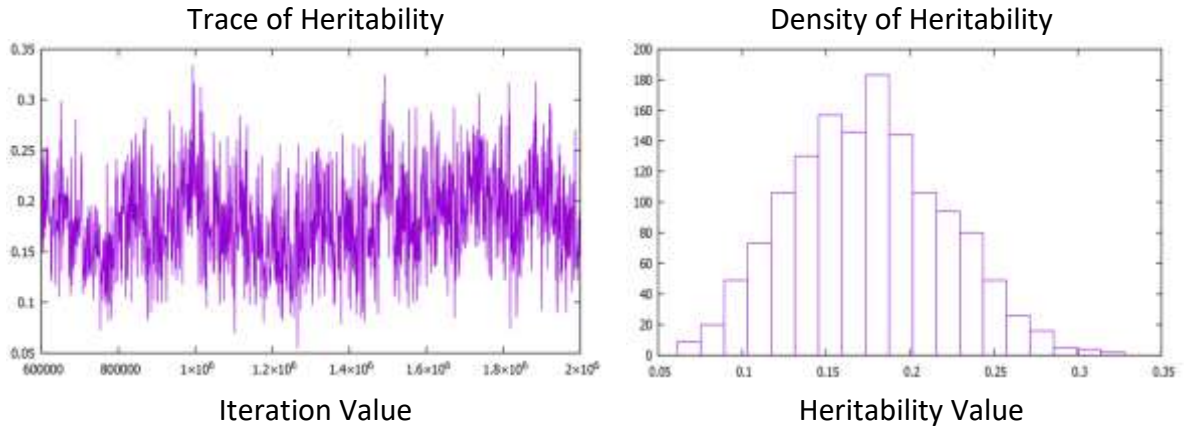
$$r_p = \frac{Cov(P_X, P_Y)}{\sigma_p(X) \times \sigma_p(Y)}$$

Where,

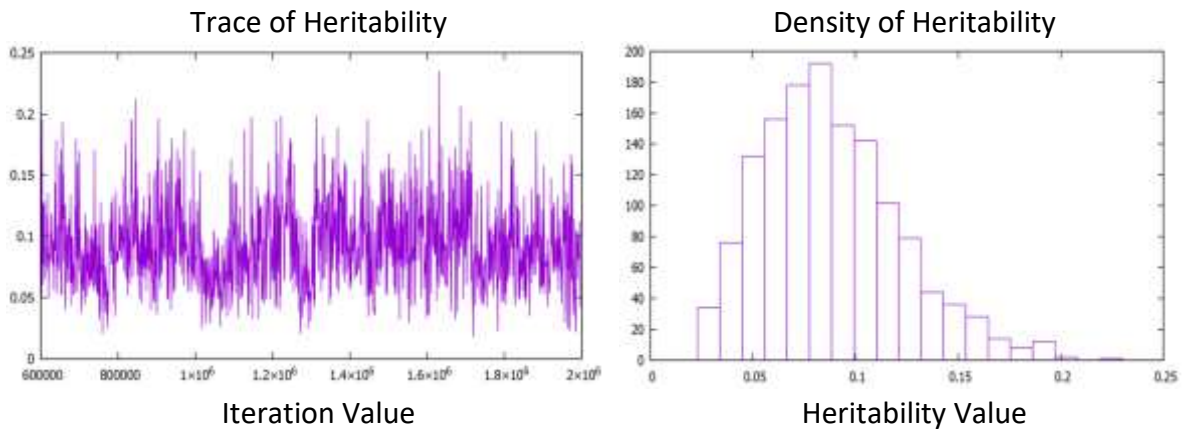
$Cov(P_X, P_Y)$ =Phenotypic covariance between trait X and Y

$\sigma_p(X)$ and $\sigma_p(Y)$ = Phenotypic standard deviation of trait X and Y respectively.

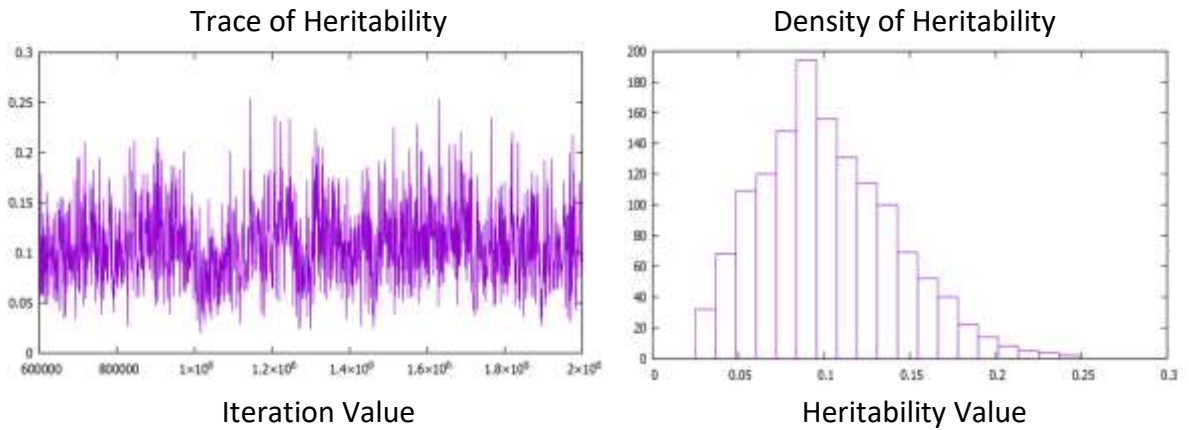
Figure S1 : Trace and density function of heritability of lactation curve parameters of Jersey crossbred cows estimated by Bayesian analysis.



Initial milk yield after calving (a)



Ascending slope up to peak yield (b)



Declining slope after peak yield (c)

Figure S2 : Trace and density function of repeatability of lactation curve parameters of Jersey crossbred cows estimated using Bayesian analysis

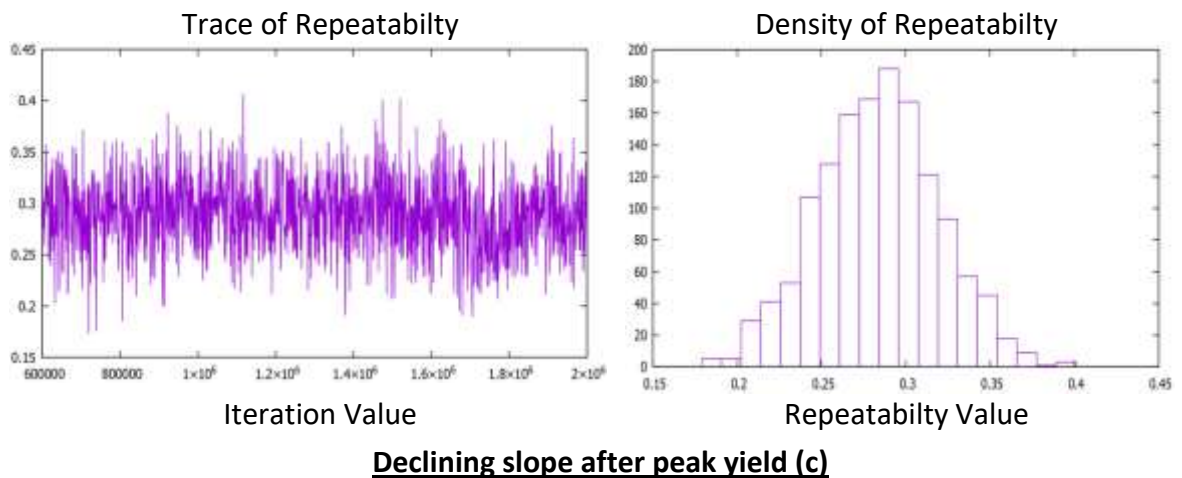
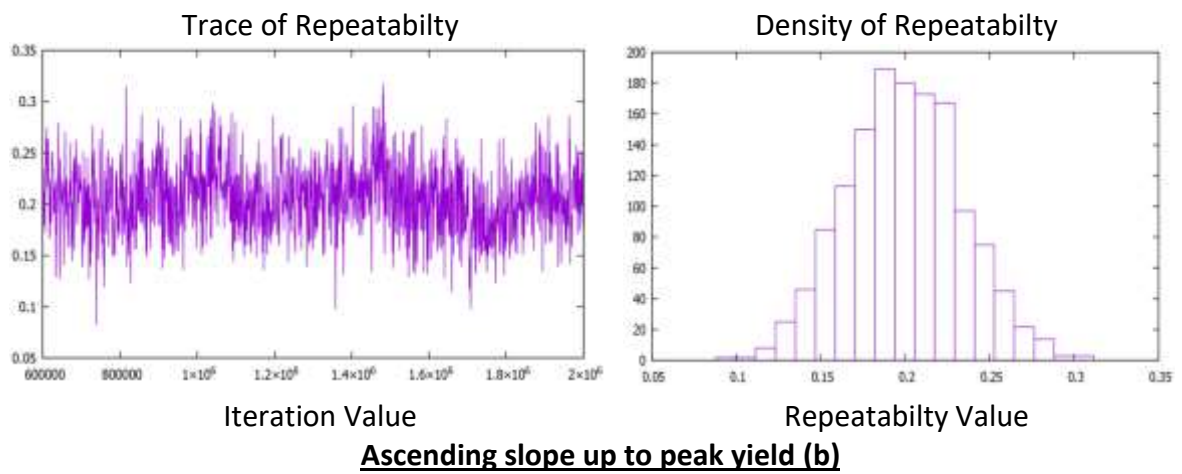
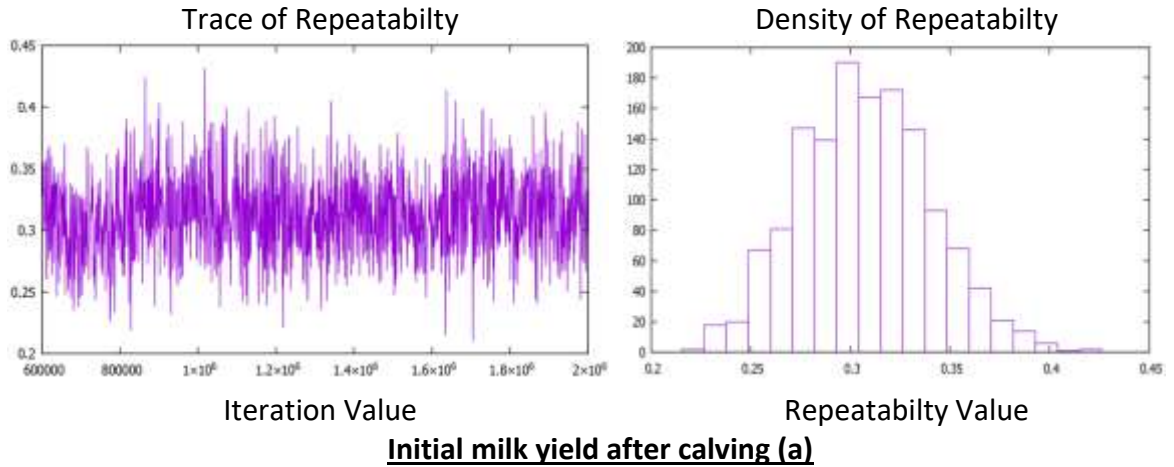
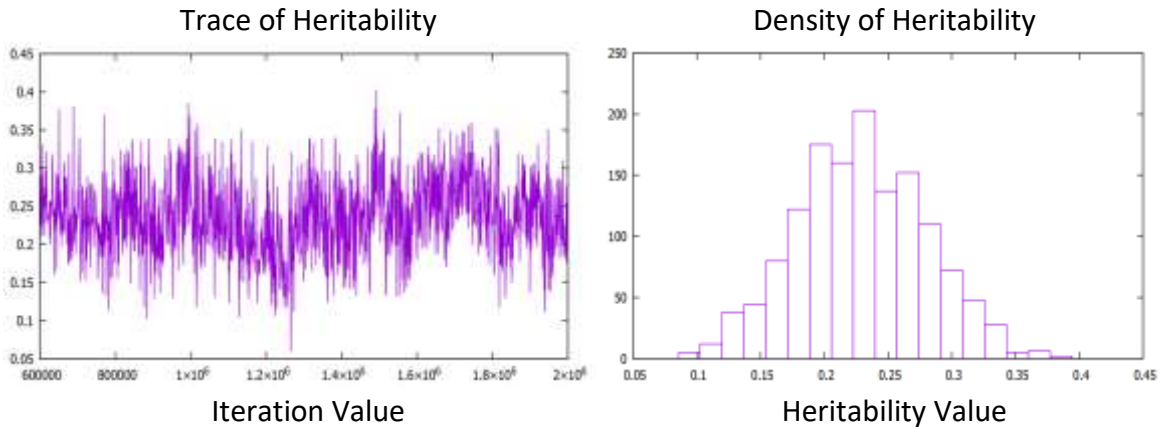
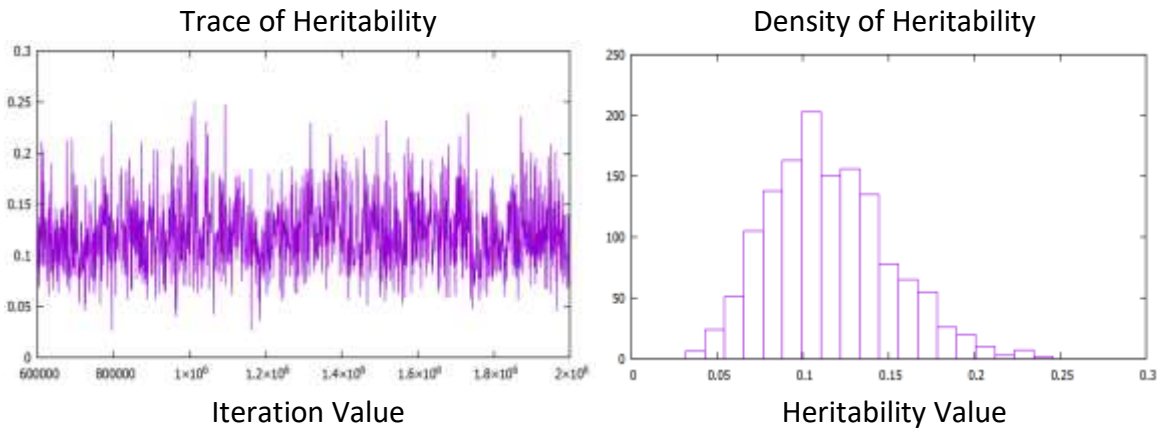


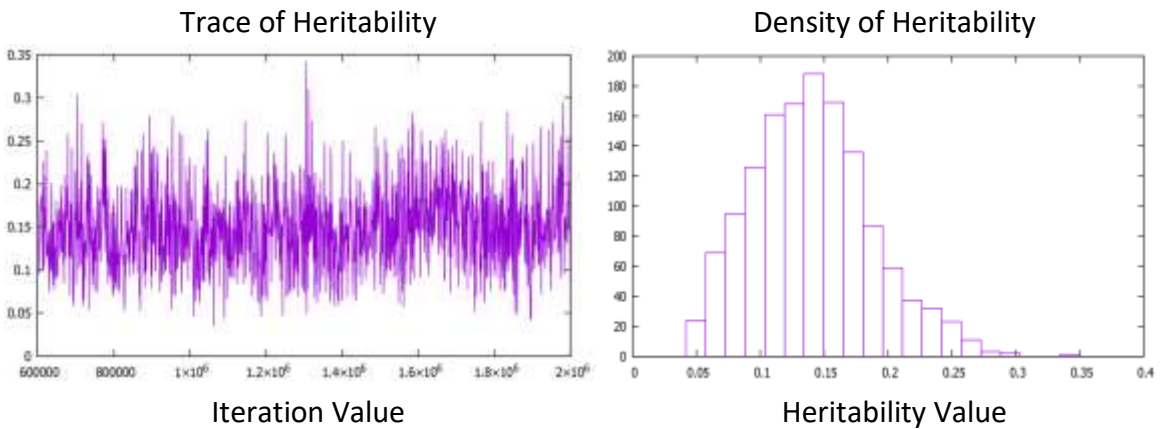
Figure S3: Trace and density function of heritability of lactation curve traits of Jersey crossbred cows estimated using Bayesian analysis



Peak milk yield (n_{max})



Days to attain Peak Yield (t_{max})



Persistency of milk yield (P)

Figure S4: Trace and density function of repeatability of lactation curve traits of Jersey crossbred cows estimated using Bayesian analysis

