

Autoregressive and random regression models in multiple lactations of Holstein cattle

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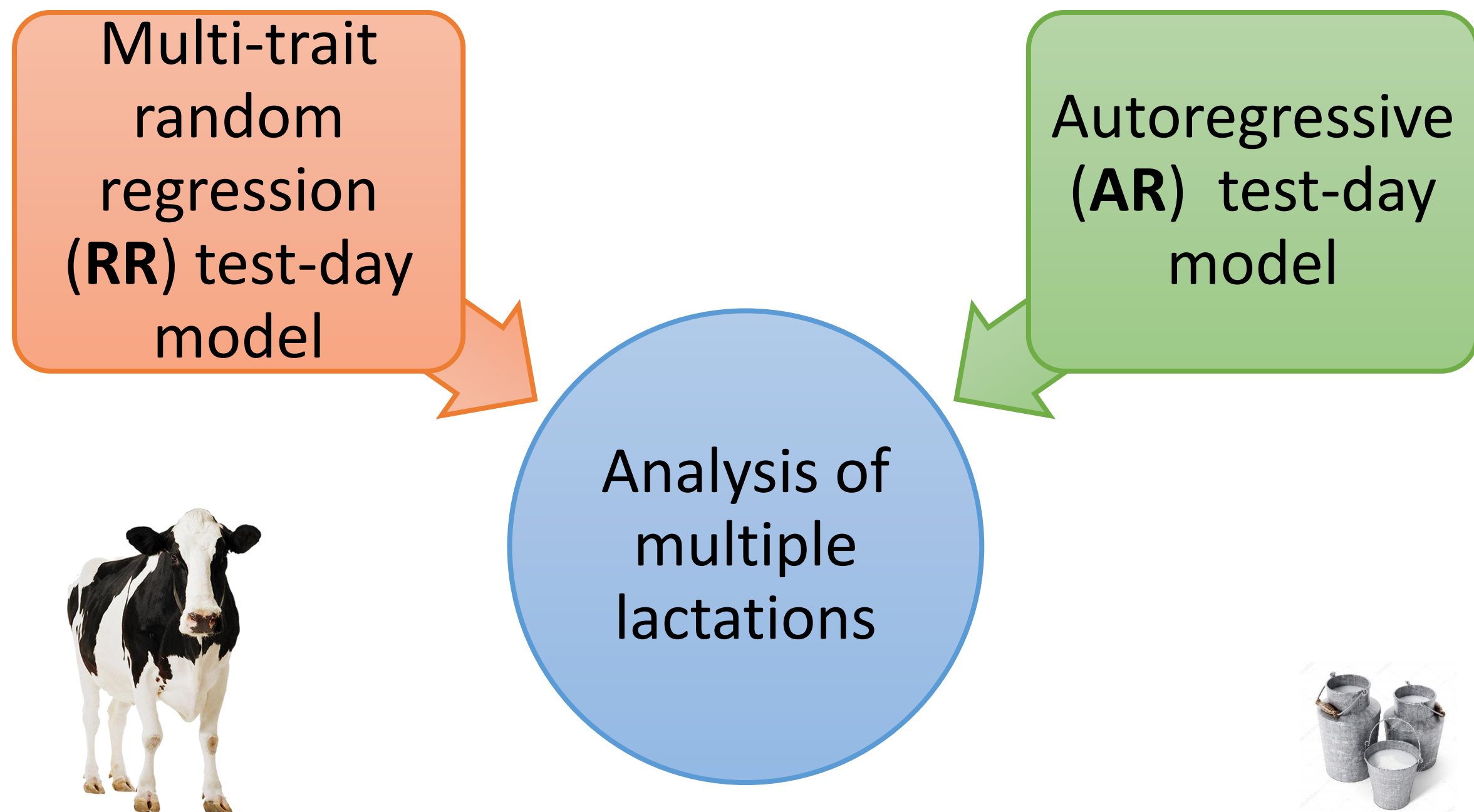
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Introduction



The objective of this study was to compare AR and RR models for multiple lactations test-day (TD) records of milk yield and somatic cell score in Brazilian Holstein cattle.

Results and discussion

Table 1. Variance components and heritabilities with respective standard-errors (SE) for milk yield (MY) and somatic cell score (SCS) estimated by the autoregressive (AR) and random regression (RR) models

Parameters	AR [†]		RR [‡]	
	MY ± SE	SCS ± SE	MY ± SE	SCS ± SE
σ_a^2	8.89 ± 0.268	0.63 ± 0.009	8.27 ± 0.559	0.49 ± 0.015
σ_{a1}^2	-	-	7.28 ± 0.411	0.41 ± 0.010
σ_{a2}^2	-	-	9.13 ± 0.808	0.58 ± 0.024
σ_{a3}^2	-	-	9.60 ± 0.602	0.61 ± 0.023
σ_p^2	≈0.00 ± ≈0.000	≈0.00 ± ≈0.000	-	-
σ_{t1}^2	18.47 ± 0.270	1.63 ± 0.022	21.35 ± 0.437	1.64 ± 0.022
σ_{t2}^2	22.39 ± 0.392	1.95 ± 0.017	24.41 ± 0.690	1.89 ± 0.020
σ_{t3}^2	29.57 ± 0.928	2.34 ± 0.027	31.59 ± 0.867	2.31 ± 0.025
σ_c^2	3.18 ± 0.101	0.18 ± 0.005	1.56 ± 0.053	0.09 ± 0.001
σ_{c1}^2	-	-	1.68 ± 0.054	0.12 ± 0.002
σ_{c2}^2	-	-	1.47 ± 0.056	0.07 ± 0.001
σ_{c3}^2	-	-	1.41 ± 0.075	0.05 ± 0.002
σ_{e1}^2	7.88 ± 0.209	1.22 ± 0.018	9.18 ± 0.114	1.39 ± 0.016
σ_{e2}^2	9.60 ± 0.236	1.22 ± 0.029	13.36 ± 0.250	1.45 ± 0.024
σ_{e3}^2	11.09 ± 0.246	1.26 ± 0.023	15.50 ± 0.239	1.50 ± 0.020
σ_{P1}^2	38.42 ± 0.579	3.66 ± 0.030	39.48 ± 0.513	3.56 ± 0.030
σ_{P2}^2	44.05 ± 0.801	3.98 ± 0.029	48.37 ± 0.891	3.99 ± 0.029
σ_{P3}^2	52.73 ± 1.210	4.41 ± 0.027	58.10 ± 1.335	4.47 ± 0.022
h^2	0.21 ± 0.003	0.16 ± 0.002	0.19 ± 0.012	0.13 ± 0.004
h_1^2	0.23 ± 0.004	0.17 ± 0.003	0.21 ± 0.012	0.11 ± 0.003
h_2^2	0.20 ± 0.003	0.16 ± 0.003	0.19 ± 0.015	0.14 ± 0.006
h_3^2	0.17 ± 0.003	0.14 ± 0.002	0.17 ± 0.008	0.14 ± 0.005

[†] σ_a^2 : additive genetic variance (kg² for MY and score units² for SCS); σ_p^2 : long-term environmental variance; σ_{t1}^2 : short-term environmental variance; σ_{t2}^2 : herd-test-day variance; σ_{t3}^2 : residual variance; σ_{c1}^2 : phenotypic variance; h^2 : Average heritability weighted by the number of records in each sample; h_1^2 : heritabilities; where $i=1, 2$ and 3 correspond to first, second and third lactations, respectively. [‡]values for σ_a^2 < 0.0001 ± < 0.00001. [†] σ_a^2 : Average additive genetic variance weighted by the number of records in each sample (kg² for MY and score units² for SCS); σ_{a1}^2 : additive genetic variance; σ_{a2}^2 : permanent environmental variance; σ_{a3}^2 : Average herd-test-day variance weighted by the number of records in each sample; σ_{c1}^2 : herd-test-day variance; h^2 : Average heritability weighted by the number of records in each sample; h_1^2 : heritabilities; σ_{t1}^2 : residual variance; σ_{t2}^2 : phenotypic variance; where $i=1, 2$ and 3 correspond to first, second and third lactations, respectively.

Conclusion

Both models performed well and may be used for genetic evaluations of production traits of the Brazilian Holstein cattle. Given the lower number of parameters to estimate the AR model is more parsimonious and would be a reasonable choice to be used in genetic evaluations.

Acknowledgments

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Material and methods

Data:

- ✓ First three lactations recorded between 1994 and 2016;
- ✓ 4,142,740 TD records;
- ✓ 2,322 herds;

Statistical models:

- ✓ AR model (using first order autoregressive covariance structure for non-genetic random effects):

$$y = X\beta + Za + Hc + Mp + Qt + e$$

- ✓ RR model (using 4th order Legendre polynomials for fixed and random regressions):

$$y = X\beta + Za + Hc + Mpe + e$$

AR model	RR model
<ul style="list-style-type: none"> ✓ Autocorrelations estimates: 	<ul style="list-style-type: none"> ✓ Correlations estimates:
<ul style="list-style-type: none"> Short term environment: <ul style="list-style-type: none"> • 0.68 to 0.76 for MY and, • 0.82 to 0.85 for SCS. Long term environment: <ul style="list-style-type: none"> • ≈0.00 for MY and SCS. 	<ul style="list-style-type: none"> Genetic: <ul style="list-style-type: none"> • 0.68 to 0.90 for MY and, • 0.71 to 0.92 for SCS. Permanent environment: <ul style="list-style-type: none"> • 0.15 to 0.70 for MY and, • 0.10 to 0.76 for SCS.
<ul style="list-style-type: none"> ✓ Annual genetic gains: 	<ul style="list-style-type: none"> ✓ Annual genetic gains:
<ul style="list-style-type: none"> Bulls: <ul style="list-style-type: none"> • 46.11 kg for MY and, • -0.019 score for SCS. Cows: <ul style="list-style-type: none"> • 49.50 kg for MY and, • -0.025 score for SCS. 	<ul style="list-style-type: none"> Bulls: <ul style="list-style-type: none"> • 47.70 kg for MY and, • -0.022 score for SCS. Cows: <ul style="list-style-type: none"> • 55.56 kg for MY and, • -0.028 score for SCS.

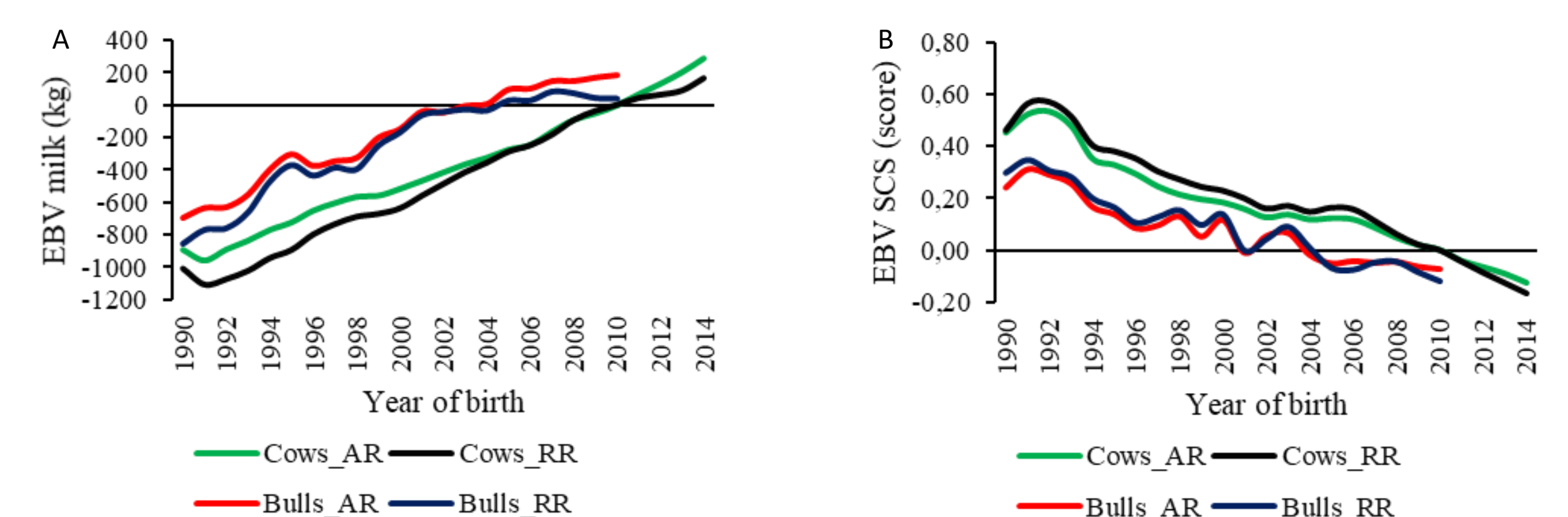


Figure 1. Genetic trends for milk yield (A) and somatic cell score (SCS - B) for bulls and cows born between 1990 and 2014 from evaluations using autoregressive (AR) and random regression (RR) models (base year = 2010).

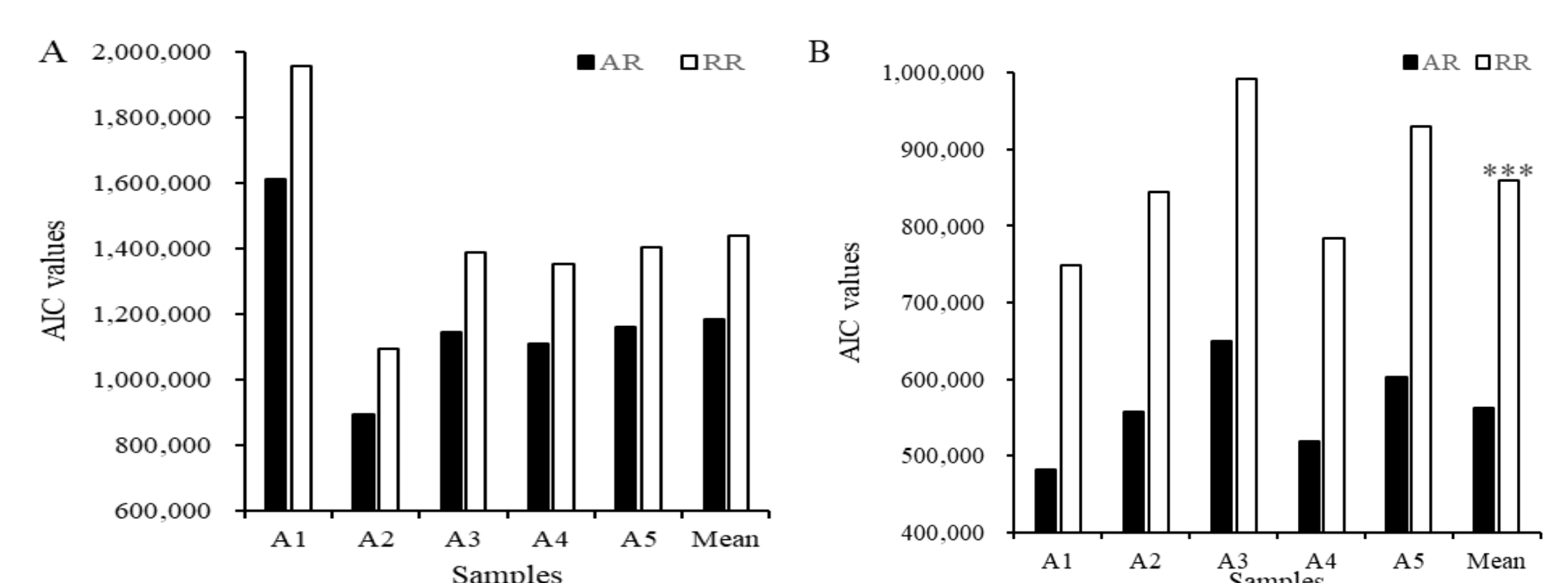


Figure 2. Akaike information criterion (AIC) values from five samples (A1-A5) used in the estimation of the variance components by the autoregressive (AR) and random regression (RR) models.