# Genetic parameters for milk yield of *Bubalus bubalis* using unadjusted and adjusted milk production for days in milk.[1,2]

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**ABSTRACT:** The objectives of this study were to estimate genetic parameters for unadjusted and adjusted milk production for 270 and 305 days of lactation and, subsequently, to verify the coincidence of rank of 2%, 5%, 20% and 40% best sires selected based on both models. Complete lactations from 90 or 150 days of lactation to 270 or 350 days of lactation were considered in the analyses. Milk production was adjusted for lactation length by multiplicative correction factors, or by including lactation length as a covariable in the model. Heritabilities, genetic correlations and breeding values were estimated for each trait, and variance and covariance components were estimated by restricted maximum likelihood methodology. Heritability estimates varied from 0.16 to 0.27. Genetic correlations between unadjusted and adjusted milk production for lactation length were higher than 0.64. Heritabilities for adjusted milk production were higher than heritabilities for unadjusted milk production for lactation length. In situations with high selection intensity, probably, modifications will happen in the rank of bulls and/or in the bulls chosen for mating if records are adjusted or unadjusted for 305 days.

**Key words:** Genetic parameters, Lactation length, Milk production, Spearman correlations.

**INTRODUCTION -** In general, different adjustment procedures such as linear regression (Magdalena, et al., 1992; Khan et al., 2000 and Bajwa et al., 2002) and a method combining the daily milk yield average and the last test day milk yield (Khan et al., 2000 and Bajwa et al., 2002), can be used to correct milk yield for lactation length. Multiplicative correction factors, for different classes of days in milk, were developed for milking buffaloes (Tonhati et al., 2004). Genetic parameter estimates obtained for milk yield adjusted for days in milk were different from those for not adjusted (Khan et. al., 2000 and Bajwa et. al., 2002). Madalena et al. (1992) working with a crossbreed dairy cattle, found that adjusting milk yield for days in milk or excluding short lactation records reduced additive genetic variance estimates. However, Khan et al. (2000) and Bajwa et al. (2002) indicated that adjusting milk yield for lactation length could increase heritability estimates. The objectives of this study were to estimate genetic parameters for unadjusted and adjusted milk produc-

tion for 270 and 305 days of lactation and, subsequently, to verify the coincidence of rank of 2%, 5%, 20% and 40% best sires selected based on both models.

**MATERIAL AND METHODS -** Murrah buffaloes milk yield records were obtained from monthly test day from 1987 to 2006 in 10 herds in the state of São Paulo. Animals were raised on pastures. Data comprised 4,408 complete lactation records from 1,879 animals with an overall mean of 1,617 liters by lactation. Complete lactations from 90 or 150 days in milk to 270 or 350 days in milk were considered in the analyses. Milk production was adjusted for lactation length by multiplicative correction factors (Tonhati et. al., 2004), or by including lactation length as a covariable in the model (linear effect). Records of abnormal lactations or records for cows older than 144 months at calving were excluded. The studied traits were: milk production unadjusted for lactation length, considering a complete lactation from 150 to 270 days ($_{150}UM_{270}$), from 150 to 305 days ($_{150}UM_{305}$), from 90 to 305 days ($_{90}UM_{305}$) and from 90 to 270 days in milk ($_{150}UM_{270}$); milk production adjusted for lactation length by multiplicative correction factors considering a complete lactation from 150 to 270 days ($_{150}FM_{270}$), from 150 to 305 days ($_{150}FM_{305}$), from 90 to 305 days ($_{90}FM_{305}$) and from 90 to 270 days in milk ($_{90}FM_{270}$); milk production including lactation length as a covariable in the model, considering complete lactation from 150 to 270 days ($_{150}CM_{270}$), from 150 to 305 days ($_{150}CM_{305}$), from 90 to 305 days ($_{90}CM_{305}$) and from 90 to 270 days in milk ($_{90}CM_{270}$). The model for analysis included fixed effects of contemporary group (herd - year and calving season), age of cow at calving (linear and quadratic effects) as covariable and as random the genetic and permanent environmental effects of cow. For $_{150}CM_{270}$, $_{150}CM_{305}$, $_{90}CM_{305}$ and $_{90}CM_{270}$, lactation length was included in the model as covariable (linear and quadratic effects). Contemporary groups with less than 5 lactations were eliminated. Variance and covariance components were estimated by the restricted maximum likelihood method (REML), using MTDFREML (Boldman et al., 1993). Heritabilities were obtained by one-trait analyses and genetic correlations were obtained by two-trait analyses. There were 11,749 animals in the relationship matrix and 261 sires. The breeding values of the sires were predicted for each trait by one-trait analyses. Spearman correlations were estimated among predicted breeding values for all traits and the coincidence of rank of 2, 5, 20 and 40% best sires were verified.

**RESULTS AND CONCLUSIONS -** Variance components and heritability estimates obtained by one-trait analyses are presented in Table 1.
Heritability estimates for all traits were from low to moderate. Heritability estimates for milk yield adjusted for days in milk were higher than for unadjusted milk production. Similar results were described by Khan et. al. (2000) and Bajwa et. al. (2002) for milking buffaloes. The highest difference between heritability estimates for unadjusted and adjusted milk yield was when short lactations were included in the analyses. Heritability estimates were higher when the records were adjusted by multiplicative correction factors than by including lactation length as covariable in the model. Estimates of genetic correlations between milk yield unadjusted and adjusted for days in milk were higher than 0.64 and are presented in Table 2. Genetic correlation estimate of unit was obtained between milk yield analyzed including days in milk in the model as covariable and not adjusting milk yield for days in milk. Spearman correlations among predicted breeding values for all traits and the

**Table 1.** Estimates of additive direct ($\hat{\sigma}_a^2$), permanent environment ($\hat{\sigma}_c^2$), residual ($\hat{\sigma}_e^2$), phenotypic ($\hat{\sigma}_p^2$) variance heritability coefficients ($\hbar^2 \pm se$), obtained by one-trait analyses.

| Trait[1] | $\sigma_a^2$ | $\sigma_c^2$ | $\sigma_e^2$ | $\sigma_p^2$ | $h^2$ |
|---|---|---|---|---|---|
| $_{150}UM_{270}$ | 33,782 | 45,567 | 104,666 | 184,015 | 0.18±0.04 |
| $_{150}CM_{270}$ | 32,463 | 35,329 | 77,951 | 145,743 | 0.22±0.04 |
| $_{150}FM_{270}$ | 40,350 | 37,859 | 90,253 | 168,462 | 0.24±0.04 |
| $_{90}UM_{270}$ | 32,362 | 50,616 | 119,266 | 202,244 | 0.16±0.04 |
| $_{90}CM_{270}$ | 31,474 | 34,752 | 78,149 | 144,375 | 0.22±0.04 |
| $_{90}FM_{270}$ | 48,391 | 37,108 | 94,223 | 179,722 | 0.27±0.04 |
| $_{150}UM_{305}$ | 38,021 | 49,904 | 119,397 | 207,322 | 0.18±0.04 |
| $_{150}CM_{305}$ | 34,369 | 36,326 | 78,908 | 149,603 | 0.23±0.04 |
| $_{150}FM_{305}$ | 48,723 | 44,868 | 106,611 | 200,202 | 0.24±0.04 |
| $_{90}UM_{305}$ | 36,502 | 55,116 | 135,079 | 226,697 | 0.16±0.04 |
| $_{90}CM_{305}$ | 32,743 | 35,366 | 77,934 | 146,043 | 0.22±0.04 |
| $_{90}FM_{305}$ | 55,397 | 45,039 | 109,658 | 210,094 | 0.26±0.04 |

[1]$_{150}UM_{270}$, $_{150}UM_{305}$, $_{90}UM_{305}$, $_{90}UM_{270}$: unadjusted milk production for lactation length for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation. $_{150}FM_{270}$, $_{150}FM_{305}$, $_{90}FM_{305}$, $_{90}FM_{270}$: adjusted milk production for lactation length by multiplicative correction factors for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation. $_{150}CM_{270}$, $_{150}CM_{305}$, $_{90}CM_{305}$, $_{90}CM_{270}$: adjusted milk production for lactation length by including lactation length as a covariable in the model for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation.

**Table 2.** Estimates of genetic correlations between unadjusted and adjusted milk production for days in milk, obtained by two-trait analyses.

| Trait[1] | $_{150}F_{270}$ | $_{90}F_{270}$ | $_{150}F_{305}$ | $_{90}F_{270}$ | $_{150}C_{270}$ | $_{90}C_{270}$ | $_{150}C_{305}$ | $_{90}C_{270}$ |
|---|---|---|---|---|---|---|---|---|
| $_{150}M_{270}$ | 0.98 | | | | 1.00 | | | |
| $_{90}M_{270}$ | | 0.64 | | | | 1.00 | | |
| $_{150}M_{305}$ | | | 0.97 | | | | 1.00 | |
| $_{90}M_{270}$ | | | | 0.77 | | | | 1.00 |

[1]$_{150}UM_{270}$, $_{150}UM_{305}$, $_{90}UM_{305}$, $_{90}UM_{270}$: unadjusted milk production for lactation length for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation. $_{150}FM_{270}$, $_{150}FM_{305}$, $_{90}FM_{305}$, $_{90}FM_{270}$: adjusted milk production for lactation length by multiplicative correction factors for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation. $_{150}CM_{270}$, $_{150}CM_{305}$, $_{90}CM_{305}$, $_{90}CM_{270}$: adjusted milk production for lactation length by including lactation length as a covariable in the model for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation.

Table 3.     Spearman correlations between predicted breeding values for milk yield unadjusted and adjusted for days in milk and the coincidence of rank (in percentage) of 2, 5, 20, 40 and 100% best sires (between parenthesis).

| Trait[1] | 2% | 5% | 20% | 40% | 100% |
|---|---|---|---|---|---|
| $_{150}FM_{270}$ | 0.90 (83%) | 0.94 (92%) | 0.89 (87%) | 0.91 (87%) | 0.95 |
| $_{150}CM_{270}$ | 1.00 (83%) | 0.83 (85%) | 0.87 (83%) | 0.87 (83%) | 1.00 |
| $_{90}FM_{270}$ | 1.00 (66%) | 0.68 (77%) | 0.76 (81%) | 0.83 (81%) | 0.89 |
| $_{90}CM_{270}$ | 1.00 (50%) | 0.53 (77%) | 0.81 (79%) | 0.79 (79%) | 0.90 |
| $_{150}FM_{305}$ | 0.40 (66%) | 0.74 (92%) | 0.86 (85%) | 0.84 (85%) | 0.92 |
| $_{150}CM_{305}$ | 0.40 (67%) | 0.75 (85%) | 0.84 (81%) | 0.83 (81%) | 0.91 |
| $_{90}FM_{305}$ | 0.40 (66%) | 0.40 (62%) | 0.68 (77%) | 0.79 (77%) | 0.87 |
| $_{90}CM_{305}$ | 0.80 (67%) | 0.50 (69%) | 0.74 (77%) | 0.75 (77%) | 0.89 |

[1]$_{150}FM_{270}$, $_{150}FM_{305}$, $_{90}FM_{305}$, $_{90}FM_{270}$: adjusted milk production for lactation length by multiplicative correction factors for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 90 to 270 days of lactation. $_{150}CM_{270}$, $_{150}CM_{305}$, $_{90}CM_{305}$, $_{90}CM_{270}$: adjusted milk production for lactation length by including lactation length as a covariable in the model for complete lactation from 150 to 270, from 150 to 305, from 90 to 305 and from 150 to 305 days of lactation.

coincidence of rank of the sires chosen for mating are presented in Table 3. In situations with high selection intensity, probably, modifications will happen in the rank of sires and/or in the sires chosen for mating if records are adjusted or unadjusted for 305 days. However, sires chosen for mating will be different only if short lactations are included in the analyses and the records are adjusted for 270 days of lactation.

These results indicated that milk production adjusted for days in milk by multiplicative correction factors or by including lactation length as a covariable in the model will show higher response to selection than selection for milk yield unadjusted.

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