Genetic Parameters For The Somatic Cells Count In The Milk Of Buffaloes Using Ordinary Test Day Models

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ABSTRACT: The buffaloes dairy milk production (BDMP) has increased in the last 20 years, mainly for the manufacturing of mozzarella cheese, which is recognized by its high nutritional quality. However, this quality can be affected by several factors i. e. high somatic cells count (SCC) provokes changes in the milk's constituents. As in bovine dairy milk, the SCC is used as diagnostic tool for milk quality; because it enables the diagnosis of sub-clinic mastitis and also allows the selection of individuals genetically resistant to that disease. Based on it, we collected information about SCC and BDMP along the lactation in Murrah breed buffaloes, during the period between 1997 and 2005. Curves were designed to estimate genetic parameters. These parameters were estimated by ordinary test-day models. There were observed variations in the estimated heritability for both characteristics .The lowest score for somatic cells count (SSCC) was seen at first month (0.01) and the highest at sixth months (0.29 The genetic correlation between these traits varied from -1 at the 1 and 9th months to 0.31 and 0.30 in the2 and 4th month of lactation. Phenotypic correlations were all negative (-0.07 in the second month and up to -0.35 in the eighth month of lactation). These results showed that environmental factors are more important than genetics in explain SCC, for this reason, selection for genetic resistance to mastitis in buffalos based in SCC should not be done. In the other hand, negative phenotypic correlations demonstrated that as the SCC increased, the milk production decreased.

Key words: Buffaloes dairy milk production, Sub-clinic mastitis, Somatic cells count (SCC), Murrah.

INTRODUCTION: In the last years, genetic analyses known like "Test-day" have been introducing that use the same individual's repeated information during the lactation, allowing the accomplishment of analyses that describe the path of the milk yield and their constituent and somatic cells count in the different phases of the lactation (Rodriguez-Zas et al., 2000; Jensen, 2001; Haile-Mariam, 2001a and Mrode and Swanson, 2002). The models "test-day" can be applied in the genetic study of SCC that is used as indirect characteristic

for selection for genetic mastitis resistance, as it was studied in bovine by Rodriguez-Zas et al. (2000), Schaeffer et al. (2000), Haile-Mariam et al. (2001 b), Mrode and Swanson (2002). The heritabilities estimates using "test-day" models varies along the lactation, Emanuelson and Philipsson (1984) estimated heritabilities varying from 0.26 to 0.40; Gadini et al. (1996) from 0.007 to 0.09 and Mrode and Swanson (2002) from 0.04 to 0.17.In the last years, several countries have been opting to evaluate their animals using "test-day" models instead of models that use the mean of SCC in the lactation, because results are more accurate. The objective of this study was estimate genetic parameters for the SCC by test day models and correlations with the (BDMP), besides verifying the possibility of the use SCC as selection criterion in genetic evaluations in buffaloes Murrah.

MATERIAL AND METHODS - It was analyzed 4,757 complete lactations of Murrah buffaloes, belonging to 12 farms of São Paulo state-Brazil, recorded from 1985 to 2005. Lactations were truncated to the 270 days of lactation. The contemporaries' group (CG) was defined as farm-year-month of control; the respective restrictions were applied for each GC, i. e., four observations at least to guarantee data's linkage. The pedigree file had 11,760 animals in the relationship matrix. SCC was transformed in scores (SSCC) according to the scale of Shoock (1982) and they were estimated the (co) variance's components for SSCC using "test day models" of finite dimension, dividing the lactation in 9 controls, as different characteristics, using uni and bi-characteristics analyses. The (co) variance's components were estimated by the restricted maximum likelihood method (REML), using MTDFREML software (Boldman et al., 1993). The model utilized was:$Y = X\beta + Za + Wp + e$; Where Y was a vector containing the observation (SSCC), and X, Z and W are incidence matrix related Y at ß, a and p whom the vectors the fixed effects (contemporary group and age of the cow), and random and permanent environment, respectively, and e was the residual variance term.

RESULTS AND CONCLUSIONS - The SSCC mean's at the first month of lactation was 4.1±1.5; and decreased at the second month to 3.37±1.34, then increased again to reach the value of 4.21± 1.48 at 9 month these results showed an inversely proportional curve to the curve of production milk, similar results were found by Reneau (1986) and Harmon (1994). The results of this study were similar to results found by ikonen et al., (2004) in dairy cattle, being the values 4.02±1.21, and different to means reported by Moroni et al., (2005) which found a mean of 2.49 in healthy buffaloes females up to 3.62 in animals with intramamary infection. The herdability coefficients were from 0.0 at the eighth month up to 0.29 at the sixth month of lactation (Table 1). Gadini et al. (1996), Mrode and Swanson (2002), Negussie et al., (2006), Emanuelson and Philipsson (1984) reported similar results, being the values ranged from 0.007 to 0.09, from 0.04 to 0.17, from 0.05 to 0.11 and from 0.26 to 0.40, respectively. The estimates of genetic correlations between test day for SSCC are show in the table 2. It can be observed that they are positive and high, in the same way as the phenotypic correlations, were positive. Negussie et al., (2006) in dairy cattle reported similar results. In the table 2, genetic and phenotypic correlations between different test day for SSCC and BDMP are presented. In general, estimates of genetic and phenotypic correlations are negative. Similar results were reported by Ikonen et al., (2004) in Ayrshire cattle, being the values for genetic and phenotypic correlations -0.07 and -0.13, respectively.

Baro et al., 1994 also found similar results with Spanish Churra ewes, being the values for genetic and phenotypic correlations -0.37 and -0.05, respectively. For SSC, these results showed that environmental factors were more important than genetics factors. Therefore selection for mastitis genetic resistance in buffalos based in SCC should not be done. In the other hand, negative phenotypic correlations demonstrated that as milk production decreased the SSCC increased. It is recommended development new analyses including other methodologies with the purpose of obtaining results more accurate

Table 1. Estimated of genetic (above diagonal) and phenotypic correlations (below diagonal), between different Test Day for SSCC (SSCCTD1 - SSCCTD9) and heritabilities for SSCC (diagonal).

	SSCC TD1	SSCC TD2	SSCC TD3	SSCC TD4	SSCC TD5	SSCC TD6	SSCC TD7	SSCC TD8	SSCC TD9
SSCCTD1	0,15	0,93	1	0,93	1	1	1	1	1
SSCCTD2	0,25	0,11	0,91	1	1	1	1	1	1
SSCCTD3	0,28	0,37	0,05	1	1	0,97	1	1	1
SSCCTD4	0,17	0,40	0,40	0,1	0,95	1	1	1	1
SSCCTD5	0,38	0,35	0,37	0,50	0,01	1	1	1	1
SSCCTD6	0,47	0,38	0,32	0,44	0,51	0,29	1	1	1
SSCCTD7	0,43	0,33	0,29	0,44	0,51	0,51	0,14	1	1
SSCCTD8	0,53	0,32	0,31	0,38	0,49	0,51	0,59	0	1
SSCCTD9	1,00	0,21	0,29	0,20	0,37	0,47	0,44	0,55	0,11

Table 2. (Co) genetic variances, (co) environmental variances, (co) variances phenotypic, genetic correlations (ra), environmental correlations (re), and phenotypic correlations (rp), between different Test Day for SSCC and BDMP.

	COVa	COVe	COVp	ra	re	rp
SSCCTD1/ PLTD1	-0,36223	-0,07053	-0,85171	-1	-0,33	-0,27
SSCCTD2 /PLTD2	0,11939	-0,08423	-0,17897	0,31	-0,07	-0,07
SSCCTD3 /PLTD3	-0,11007	-0,22041	-0,48474	-0,44	-0,2	-0,20
SSCCTD4 /PLTD4	0,15454	-0,26068	-0,61012	0,3	-0,23	-0,23
SSCCTD5 /PLTD5	-0,15057	-0,19133	-0,4957	-0,81	-0,16	-0,19
SSCCTD6 /PLTD6	-0,03386	-0,30237	-0,59247	-0,06	-0,28	-0,26
SSCCTD7 /PLTD7	-0,09527	-0,32042	-0,71109	-0,33	-0,29	-0,33
SSCCTD8 /PLTD8	-0,08322	0,40119	-0,79847	-0,78	-0,35	-0,35
SSCCTD9 /PLTD9	-0,07776	-0,28497	-0,70696	-1	-0,34	-0,28

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