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Sire X Herd and Sire X Herd-Year Interactions on Genetic Evaluation of Buffaloes

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1. Introduction

According to FAO, (2012), World's Total Milk Production is 703,996,079 tonnes per year considering Cow milk (585,234,624 tonnes per year), Buffalo milk (92,140,146 tonnes per year), Goat milk (15,510,411 tonnes per year), Sheep milk (9,272,693 tonnes per year), Camel milk (1,840,201 tonnes per year). This gives us an average milk consumtion of 108 kg per person per year (FAO, 2012).

In 2010, the largest milk producers in the world were USA (87,461,300), India (50,300,000), China (36,022,650), Russian Federation (31,895,100), Brazil (31,667,600), Germany (29,628,900), France (23,301,200), New Zealand (17,010,500), UK (13,960,000) and Turkey (12,480,100) tonnes (DAIRYCO, 2012).

The USA was the largest cow's milk producer in the world in 2010 accounting for 14.6% of world production. World cow's milk production in 2010 stood at nearly 600 million tonnes, with the top ten producing countries accounting for 55.7% of production. The USA is the largest cow's milk producer in the world accounting for 14.6% of world production, producing over 87 million tonnes in 2010, an increase of 1.8% when compared to 2009 (DAIRYCO, 2012).

India is the second largest cow's milk producer, accounting for 8.4% of world production and producing over 50 million tonnes in 2010. The UK is the 9th largest producer in the world producing nearly 14 million tonnes in 2010 and accounting for 2.3% of world cow's milk production (DAIRYCO, 2012).

According to the Brazilian Institute of Geography and Statistics - IBGE (2011), the buffalo herd in 2009 was 1,135,191 heads. Since these animals were distributed by the five regions of Brazil, in the following amounts and proportions: North: 714.852 (62,97%); Northeast:

125.603 (11,06%); South: 121.251 (10,68%), Southeast: 105.615 (9,3%); e Midwest: 67.870 (5,98%).

Compared to dairy cattle herds, the information on buffaloes is considered small. Informations cited below refer to livestock grazing, conducted in Brazil. Studies make an assessment of information generated from the control of the major Murrah buffalo cows herds.

Almost all the buffalo farms in Brazil adopts the extensive regime, characterized by deficient in of control livestock, health and nutrition (Tonhati, 1997). These animals are distributed among the five regions of Brazil, consequently the response to selection is different, considering the weather conditions and objectives of the farmers.

In Brazil the largest amount of bufallo is found on the Marajó Island, but it is in the Southeast that we will find the best quality in dairy products and in the south the best meat production. The first Buffalo breeders Association from the world was criated in Brazil. Despite this and despite of efforts from several breeders and researchers, few are the properties that do proper zootechnical bookkeeping of their herd thus hindering the research and the improvement of the species.

However, the buffalo culture is showing great expansion in Brazil, as shown by Ramos (2003), who observed an yearly 10% growth, therefore, there is an expectation to the development of well structured breeding programs. This large growth is due to the capacity of these animals in being rustical, good food converters when explored for milk and meat, long-living and being able to occupy spaces not inhabited by other animal species economically exploited by man. Based on this information, Ramos (2003) proposed a genetic improvement program of the species to be conducted together with Brazilian Association of Buffalo Breeders.

Buffalo has milk yield per lactation ranging from 500 to 4000 kg, depending on breed and management used. The age of the buffaloes at birth ranged from 24 to 266 months. In Brazil, Tonhati et al. (2000) found this feature to an average of 1259.47 ± 523.09 kg of milk per lactation in cattle exploited in the state of Sao Paulo. The lactation length can vary from 260 to 327 days, being greatly influenced by management type (Pereira et al., 2007).

In literature, we observed the average heritability and comparing several studies, we conclude that there is sufficient genetic variation among individuals in the populations so that they can apply to the methods of selection. However, there has also been observed that, due to different populations, seasons and regions, the coefficient values of heritability for milk production are quite varied, indicating a possible effect of the interaction from genotype x environment.

The environment for the selection of animals, as well as the interaction effect is of interest for animal breeding and has been widely discussed in literature. According to Reis & Lôbo (1991) the environment conditions the results of the improvement process. According to Hammond (1947), selection should be made in superior environment so that the animal

could show its full potential, on the other hand, Lush (1964) argues that the selection of future breeders should be done in similar environmental conditions to which their progeny will be submitted.

Falconer (1952) suggests that, depending on the environment, the gene cluster responsible for the expression of a particular feature may not be the same. Thus, including the genotype-environment interaction in genetic evaluation models would end up in better results.

In recent years an increase in the production of buffalo milk has been observed, but also an increasing in the number of zoothecnic, health and nutrition controlling. As well as an increased number of daughters of sires in distinct regions of Brazil, providing greater possibility of studies, especially studies involving the genotype environment interaction.

Most procedures for genetic evaluation in dairy cattle, assumes homogeneous genetic and residual variances between herds. Thus, if the variances increases with the increase in average production and are assumed homogeneous, they could induce to bias in genetic evaluation; and so animals could be wrongly classified. For this reason, several studies made in Brazil (Costa et al., 2002a; Costa et al., 2002b; Melo et al., 2005; Freitas, 2003; Cobuci et al., 2006, Araujo et al. 2008) have been performed to identify a better model in milk production using different breeds and species.

Facing this problem, and it's evident importance, the objectives of this study were:

- to evaluate the effect of the inclusion of the sire x herd or sire x herd-year interaction over the milk production in lactating buffalo records, and;
- to determine the most appropriate model in genetic evaluation of animals.

2. Revision about study

Milk production in Brazil in 2010 was of acquired raw or cooled milk (thousand liters), 20,966,731, of which 99.51% of raw milk production was industrialized or cooled by the establishment (Brazilian Institute of Geography and Statistics - IBGE, 2011). In the fourth quarter of 2010, there were 5.557 billion liters of milk formula. Comparing the fourth quarter of 2009 there was an increase in the industrialization of 2.0% and 7.4% from the third quarter of 2010.

The purchase of buffalo milk in Brazil showed an ascending character in the last 13 years, the biggest change in 2005 (12.3%), and lowest in 2002 (0.0%). These values are due to unfavorable weather conditions and increased production costs in some regions of Brazil (Brazilian Institute of Geography and Statistics - IBGE, 2011).

From all of the milk acquired in Brazil 26.0% comes from the state of Minas Gerais and 14.3%, of Rio Grande do Sul The Southeast Region with 40.3% of production, followed by the South with 33.4% Midwest 14.7%, 6.0% North with the production, and the Northeast with 5.6%. When comparing to the previous year's production, the North, Midwest and Southeast regions showed a decline of milk yield, respectively 13.6%, 6.7% and 0.7% (Brazilian Institute of Geography and Statistics - IBGE, 2011).

It has been observed that the highest daily production of buffalo milk was recorded in April, and lowest in January (Macedo et al., 2001). The reproductive seasonability of buffalo is conditioned by the decrease in daytime light (Pereira et al. 2007). It was observed that the highest birth frequency occurr in the period from February to April.

Ramos (2003) points out that the genetic progresses have also been gained for the milk production in several dairy herds in Brazil. Marques (1991) noted that crossings have also been adopted as a way to promote improved performance. This author found heritability estimatives for various productive and reproductive traits, among which may be cited values range from 0.249 to interpartos, 0.39 for service period, 0.304 for milk and 0.412 for weaning weight.

Boldman & Freeman (1990) using milk producing records of cows in the U.S., from 1976 to 1984, in an animal model that ignored the relationship between animals, to estimate genetic and residual variances at different levels of production, ignoring the covariance between levels found an increase of genetic and residual variance and of permanent environment with the level of production. They also noted that the estimates of heritability and repeatability were lower at low level but similar in levels of medium and high production.

2.1. Variances heterogeneity

Lofgren et al. (1985) estimated heritability for milk yield in three levels of standard deviation for Holstein and Jersey cows. The increase in the variance of sire and herd standard deviation was proportionally greater than the growth of the residual variance, producing higher heritability in herds with a high standard deviation. Heritabilities increased with the standard deviation of herd, approximately 17% (0.18 to 0.21) for Holstein, and 46% (0.25 to 0.37) for Jersey animals.

The variability among herds, or the variability between levels of stratification adopted in the data, especially in dairy cattle, has been disregarded, causing the concentration of animals in these selected herds, with greater expression of phenotypic variability (Hill et al., 1983).

The alternative proposals that may solve the problem of heterogeneous variances are: grouping the data based on some criteria and subsequent analysis of multiple traits, as did Hill et al. (1983), has in principle the proposal by Falconer (1952), considering the expression of genotype in different environments as different traits.

According to the idea of Falconer (1952), if the genetic correlation is high, the performance in both environments represent approximately the same characteristica, determined by the same genes group, and if there are no special circumstances affecting the heritability or the selection intensity, there will be little difference in the environment in which the selection will be performed. If the genetic correlation is low, the characteristics will be considered different, and high or low performance will require different sets of genes. So, it would be advantageous to conduct the selection in the environment where the animals should live. As long as heritability or selection intensity in other environment, be considerably higher.

Van Vleck (1986) noted that the fraction of animals selected from an environment determines selection intensity as a factor in direct response and correlated in various environments. A high heritability leads to a more accurate assessment of the low heritability of the same number of daughters, or equal accuracy with few daughters. The effects of different residual standard deviations when heritability is the same in different environments can also be calculated. According to the author, the genetic correlation between the expressions of a genotype in different environments can also be considered if the correlation is too different from the unity.

Garrick & Van Vleck (1987) exposed that the consequences, for evaluation, of incorrectly assumed homogeneity are demonstrated by progeny testing and by an artificial breeding program that test cows and bulls of heterogeneous populations. Selection assuming homogeneity can be very efficient as heritability and then the accuracy of the selection is greater in the most feasible environment. Therefore, there is appreciable reduction in the results when the heritability is greater in less variable environments.

These authors observed in their progeny test results, that the effect of incorrect variance components in the equation of mixed models is greater when the most variable environment has lower heritability. When heritability increases with residual variance, there is little loss in selection efficiency of selection assuming homogeneity. Furthermore, there is a negligible effect to take a correlation between the same genetic performance in different environments when in fact little interaction is present.

They also consider that it is worth investigating the reduction in efficiency of the selection assuming the heterogeneity for applications in individual breeding. The study with bulls also showed that the bulls sampling is represented in the variety of different livestock environments.

The accuracy in the estimation of genetic parameters depends on the influence of a large set of factors. Freitas (2000) gave more emphasis on the estimation method used, but also stated that the variance heterogeneity is a problem which, if not treated properly, may result in biased prediction of genetic value. According to this author, the quality of data collected in the field also contributes to decrease the accuracy of genetic evaluations. This problem is more serious in small data sets, because in this case, the estimation of some variance components and covariance is fully committed. In a genetic evaluation program, the economic relevance of the characteristics to be evaluated is as important as the quality of solutions.

In a study of milk production in buffaloes it was observed that herds with bigger variability interact with more animals, and if the variability between herds is not considered, the sire selection of the performance of their daughters, may be due not only to its potential, but also to the environment in which their progeny express the phenotype (Cardoso, 2005).

The similarity of the treatment used in females can reduce the environmental variability, if they receive the same amount of food or may increase if the cows in a herd start to receive more differentiated diets as adults. These factors may be responsible for changes in variance

components from one level to another, in one year or one year to another (de Veer & van Vleck, 1987).

According to Winkelman & Shaeffer (1988), when the heterogeneity is caused by environmental factors, the genetic evaluation of the animal should be higher due to its environment than their genetic composition. Among the environmental factors that cause variance heterogeneity are herd-period, region, year of birth and management (Ibáñez et al., 1996).

Researches have shown that, in a selection of the best animals in a high quality management environment, there is a tendency to select genotypes with high response value. In contrast, in the selection of the better individuals in an environment of low quality, there is a tendency to select, genotypes with low responsiveness to environmental improvement. Based on this information, it emphasizes the tendency of the responses of animals to associate negatively with phenotypic means in environments of low quality and positively to the averages in high quality environments. In environments of intermediate quality, there is a clear trend of association between phenotype and the average response of animals (Reis & Lôbo, 1991).

Hammami et al. (2009) to overcome the lack of detailed information obtained from routine milk recording data, genotype×environment interaction measure can be based on experiments. These authors confirmed that genotype×environment interaction was essentially when high differences between production environments and/or genotypes (genetically distant genotypes) were observed. Environmental effects were aggregated in most studies and identification of the components of the environment was largely unresolved, with only a few studies based on more definite-descriptors of environment.

Hill et al., (1983) herds were stratified by milk production , according to the average, the variance and variation coefficient in high and low levels, to estimate milk, fat and protein heritability, and fat and protein percentage. Heritabilities to the productions caracteristics were higher in higher production levels with greater heritability differences between the variance levels above mentioned. Results for milk components were similar, except in herds with low variation coefficient, where the heritability estimates were slightly higher.

Moita et al. (2010) observed that when selecting animals without considering the variance heterogeneity tends to favor those belonging to high variance herds, to the detriment of lower phenotypic variability. They also noted that the stratification of the buffalo herds on high and low standard deviation corrected for variance heterogeneity.

In evaluating the effects of variance heterogeneity the use of different criteria is recommended to compare the results, considering that such effects may not be evident depending on the methodology used. Thus, it is indicated that the effect of variance heterogeneitys is considered to reduce the risk, because they have equal or superior results to those obtained by the evaluation that assumes homogeneity of variance (Carvalheiro, et al. 2002).

Araújo, et al. (2008b) concluded that there is variance heterogeneity among herds that exploit the milk production in Murrah buffaloes and also that the nature of this variance heterogeneity is a result of environmental factors. So the sires are being selected because of the variable environment in which their progeny are created, than to its own genetic merits.

In a study evaluating variance heterogeneity, Balieiro et al. (2004) found out that the genetic variance components were higher, in the stratified data, than the ones obtained in the univariate analysis, and residual variance components were lower, resulting in higher heritability estimates for the analysis of multiple traits. Such joint analysis allowed higher redemptions of portions of additive genetic variances, which would be directed to the residual component in the analysis of unique feature.

Araújo, et al. (2008b) observed in their study evaluating herds of Murrah buffaloes that constant variances among herds in genetic evaluation of animals, disregarding the level of production or the estimated variance among herds, according to results obtained in the overall analysis there may be a misclassification of animal genetic merit. With the increasing of variances, the production of daughters of sires, raised in herds with greater variability and in consequence less productive, as in the case of this study, would influence more the essessment of the breeders than the daughters raised in herds with less variability.

Torres´work (1998) characterized the pseudo-interaction described by Dickerson (1962), which occurs when the genetic correlations are high, therefore, the ranking of the animals would not be altered, but the magnitude of the variability of the components, as well as the heritability evaluation, would vary from the phenotypic standard-deviation to selection programs.

Normally, genetic variance heterogeneity, additive or residual, within the herd is due to matings and to preferencial treatments given to specific reproducers (Norman,1974). One alternative to restrict the effect of the preferential treatment between herds is the inclusion of sire-herd interaction in the statistic model, in the form of environmental-correlation. However, it recalls that the heterogeneity of the variance can be responsible for part of the variability component attributed to interaction (Norman,1974).

When there is variance heterogeneity and the same is ignored, the progeny of the daughters of a given sire will be weighted in proportion to the standard deviations of the herds in which they were raised. The result is that the progeny of the daughters in herds with higher variabilities will influence the evaluation of the breeders more than progeny of the daughters originated from herds with lesser variability (Vinson, 1987). Also, there is the risk of erroneous sorting from animals through their genetic values and, therefore, the genetic progress can be affected (Araújo, et al. 2008b).

In the evaluation of females, to ignore the effect of variance heterogeneity would tend to favor females that had their production in herds with high variance, the opposite occurs with females in herds with low variance (Araújo, et al. 2008b). Of practical importance, would be the likely trend existing in the evaluations of high-producing cows, chosen as parents of future breeders in artificial insemination. In the long run, we can say that any

trend in the evaluations of the females would accumulate along the time, because daughters and mothers tend to express productions in the same herd (Torres, 1999).

Costa et al., (2000) used records for milk and fat production to study the variance heterogeneity between sites, which were classified into two groups (low and high) based on phenotypic standard deviation of milk production per herd-year. They noted that the variance components of sire and residual for milk and fat in environments of low standard deviations were lower than in environments with high phenotypic standard deviation.

The variance heterogeneity has a greater effect on the genetic evaluation of females, because these are evaluated within herds, and their predicted genetic values would be greatly affected by the variance within herd, which tends to be uniform over time (Torres, 1999).

Assuming homogeneity variances has little effect in the evaluations of breeders, if these are used in herds of different production levels, and heritability increases with the increasing of residual variances (Garrick & Van Vleck, 1987; Vinson, 1987; Winkelman & Schaeffer, 1988). However, when heritabilities are smaller in the environment in which the residual variances are greater reductions in the efficiency of selection of bulls may happen for falsely considering that the variances are homogeneous.

Carvalheiro, et al. (2002) observed in their study evaluating the variance heterogeneities that calves and cows have their breeding genetic values most affected by the variance heterogeneity of the bulls.

In a simulation study, Garrick & Van Vleck (1987) observed a reduction in genetic gain of up to 3.4% when the effect of variance heterogeneity was ignored in progeny testing schemes resulting in the selection of environments with low heritability, as they are more variable. When the heritability increased with the increase of variability, the reduction was only 0.1%.

Variance heterogeneity between herds results in the reduction of the selection and implies in unequal genetic progress between environments classified by the standard deviation of the herd. So to ignore the variance heterogeneity has consequences in the selection and in the genetic gain, reducing the effectiveness of a breeding program (Van Vleck, 1987; Vinson, 1987).

According to Visscher et al. (1991) The initial adjustment for variance within herd-year-season phenotypic variance was more effective in reducing the variance heterogeneity, and seems to be the most practical way to variance heterogeneity for genetic evaluation per animal model.

According to Vinson (1987), the proportion of selected animals from more variated environments increases with the intensity of imposed selection. Hill (1984) in a normal data distribution, showed that the standard-deviation of more variable populations is 50% higher than the least variable, and the proportion of selected animals is 0,01, indicating that 95% from the selected individuals are provenient of more variable populations.

The genetic correlations for milk and fat production between the two groups of environments in a study of variance heterogeneity between places, were close to 1.0. The authors concluded that genetic evaluations in Brazil should consider the variance

heterogeneitys to increase the accuracy of evaluations and the selection efficiency for the milk and fat production in Holstein (Costa et al., 2000).

Carvalheiro, et al. (2002) observed that effects of heterogeneity of residual variance on genetic evaluations are associated with the selection pressure and heterogeneity levels. If corrections are not made, herds that practice intense selection and that present accentuated levels of residual variance heterogeneity can have their animals incorrectly classified and, consequently, less responsive to selection.

The effect of heterogeneity, if any, in the genetic evaluation should be best determined by examining the position of animals on the magnitude of the relative difference in the genetic values in levels of variances in herds (Dong & Mao, 1990).

Van der Werf et al. (1994) observed that the correction for variance heterogeneity within herds did not remove all biases of the average in parents, but the improvement in bias and accuracy of genetic value can be expected. They also observed an increase of phenotypical standard-deviation of milk production in herds over the years, probably due to increased production. They found that the variation coefficient within herd-year was 31%, indicating that the method of genetic evaluation could be improved with corrections for heterogeneity variance. Correction methods of heterogeneity probably would correct all the biases in EBV (Expected breeding value), especially if these biases were due to preferential treatment.

2.2. Genotype by environment interaction

The differences between livestock in the variability of production, usually results from differences in climatic factors, regional or local, and types of management, including such factors as intensity of power, supply voltage according to the production, success of diseases control programs and quality procedures for the creation of young breeders (Vinson, 1987).

According to Van Vleck (1987), if the genetic and residual variances and covariances were known in each environment, represented by a set of herds, then selection based on the results obtained from analysis of multiple traits in mixed models, would produce an assessment quality that could be used to select optimally bulls or cows to produce in herds or in specific environments.

According to Stanton et al. (1991), there are two situations in which differences in responses to selection would be verified in different environments, characterizing the genotype x environment interaction. The first situation occurs when the genetic correlation between the phenotypic expression in two environments would be substantially less than 1.0, indicating that different genetic bases would be acting in different environments.

The genetic correlations derive informations about the genotype x environment interaction and can be used to quantify the loss of information when using production records from a different environment from where the animals selected will be used.

Another case cited by Stanton et al. (1991) that characterizes the genotype x environment interaction would result from the variance heterogeneities, as in the case of evaluations of

simple features, in which sires have the same classification in each environment, but differences in response to selection of the daughters and the genetic values from the bulls would be lower in an environment with less variability.

Houri Neto (1996) evaluated genotype x environment interaction between Brazil and USA. through 332,617 lactations obtained from the State of New York (USA) and 115,547 productions observed in Minas Gerais, Espírito Santo, São Paulo, Santa Catarina and Rio Grande do Sul, in the period 1979 to 1991. Genetic correlations of milk productions obtained between the two countries ranged from 0.46 to 0.68. This result indicates that sires evaluated in the USA did not show the same performance in Brazil.

Paula, et al. (2009) studying the effect of genotype by environment interaction for production of Holstein noted different bull genetic values when environment was modified, what characterizes genotype x environment interaction and proves that the genotype x environment interaction alters the classification from the animals and can lead to the inappropriate choice of bulls in certain regions, damaging the genetic improvement of livestock.

Cienfuegos-Rivas et al., (1999), when comparing the performance of daughters of Hollstein bulls in Mexico and in the northeast from the USA found different and lesser answer from the daughters of bulls selected in USA and raised in mexican environment, suggesting that the better answers are predicted to Mexico, when using information from daughters raised in american environment of low standard deviation of herd-year milk production.

These authors concluded that the genotype x environment interaction, evidenced both by the variance heterogeneity, and the genetic correlation coefficients, not only prevents genetic gain, but contributes severely to the reduced and different net economic benefit from the biotechnology of artificial insemination in the countries of Latin America, using American semen.

Cardoso (2005) in a study evaluating the genotype x environment interaction for milk production in buffaloes observed that there is variance heterogeneity among herds that exploit the production of buffalo milk, predominantly Murrah, and still that the nature of variance heterogeneity is resulting from environmental factors. He also noted that the admission of constant variances among herds in genetic evaluation of animals leads to a misclassification of the genetic merit of the best animals.

2.3. Study of variances

Ratings of genetic (co) variances between groups of herds indicated that the correlations between the three major types of variances were above 0.80. These correlations were high, indicating little benefit in the calculations for evidence of bulls if a non singular matrix of genetic variances and covariances was used instead of a singular matrix (Winkelman & Schaeffer 1988).

Higher values for genetic and residual variances, as the average production or the standard deviation within environments increases, have been presented in several papers (Boldman

& Freeman, 1990; & Dong Mao, 1990, Torres, 1998; Araújo , 2000, Araújo et al., 2002). Most of these studies show high heritability estimates, as the variability of production within the environment increases (Hill et al., 1983, Lofgren et al., 1985; de Veer & Van Vleck, 1987; & Dong Mao, 1990; Meuwissen & van der Werf, 1993; Araujo, 2000).

Dong & Mao (1990) observed that the increase in the percentage of residual variance in the group of herds with values considered low to medium production were equal to or greater than the percentage increase in the group of herds with medium to high values of production. However, the rate of increase of the residual variance in the group of herds with values considered low to high was not great as that observed in the sire variance.

Dorneles, et. al. (2009) observed an increase in estimates of heritability partially associated with the reduction of permanent environmental variance, which promoted the reduction in total variance and, consequently, increasing the proportional contribution of additive genetic variance. This growing trend is similar to those reported by Melo (2003) and Cobuci et al. (2005), for Holstein, using the Wilmink function to model the genetic variance and permanent environment. Decreasing trend was observed, in Brazil, by Costa et al. (2005), for Gyr, by Freitas (2003), for Gyr-Holstein, and Dionello et al. (2006), for the Jersey breed.

2.4. Sire by herd interaction

Mayer (1987) observed that the variance components due to the effect of bull-environment interaction on the effect of environment, have been found with values as high as the variance between sires for milk, fat and protein production. A variety of factors may have contributed to greater similarity between the daughters of the same sire in different herds or identified in subclasses in herd-year-season. One of them is a difference in variation between herds, which can be reduced by transforming the data.

Mohammad et al. (1981) observed that the variance components of sire-herd interaction accounted for 10% of the phenotypic variance in milk yield and these presented a negative effect. Araújo (2000) found that the use of herd-sire interaction was not effective as a way to set the variance heterogeneities.

The increasing in the number of daughters for breeding using artificial insemination, include several herd-year-season and several stable matings, and could also reduce the interaction influence next to errors caused by other factors and thus be used in the selection of bulls (Kelleher et al., 1966).

The study of the production of daughters of a certain sire that does not consider the variance heterogeneities will be adjusted by the ratio of standard deviation of the herds to where they were created. The production of the daughters of breeders raised in more variable herds will influence more in the evaluation of sires than in the production of daughters derived from herds less variable (Vinson, 1987).

Winkelman & Schaeffer (1988), with the aim to estimate variance components of sire and residual to Canadian herds, noted that the accuracy of the estimated variance components within herds, could influence the effectiveness of assessment for variance heterogeneity, since small sample sizes could lead to large sampling errors on the estimates.

This variance behavior led to higher heritability estimates during the initial phase of lactation, with a maximum value of 0.30 at the third test-day. Probably, this pattern is due to the fact that only more persistent cows remain producing until the tenth month of lactation which would decrease genetic variability (Tonhati et al. 2008).

Stratifying records intrarebanho-year variance proved to be the most effective way to estimate the variance components and heritability (Dong & Mao, 1990). When the data were divided by production levels, the residual variance components of sire in high production were less than twice than those of low production (Dong & Mao, 1990).

The knowledge of residual genetical variances covariances in each herd or on the environment represented by a set of livestock, represents for selection based on results obtained by multiple characteristics analysis in mixed models, the production of a quality evaluation that could be used to properly select bulls and cows,to produce in herds or in specific environments (Van Vleck,1987).

Bueno et al. (2005) working with Brown Swiss cows found that the inclusion of the effects from the interaction of sire x herd or sire x herd-year in genetic evaluation models changed very little the estimates of the components of addictive and residual genetic (co) variance and consequently, heritabilities.

2.5. Methods

Information obtained from the measurements of production of buffalo milk in Brazil were used to estimate variance components and foresaid genetic parameters and breeding values. For this, the month of delivery of buffaloes were grouped in two seasons, season 1, from April to September, which corresponds to the months of lower rainfall, and season 2, corresponding to the months from October to March, in which there is more rainfall precipitation, except for a herd located in the Northeast, where the opposite was considered.

Subsequently, the effects of herd and year were grouped into subclasses, and required at least four observations per herd-year subclass. So that it was possible to investigate the effect of interaction of sire x herd or sire x herd-year on milk production it was required that each sire had at least two daughters distributed in more than one herd.

After the necessary deletions were made, the data file consisted of 1774 lactations, from 754 Murrah buffaloes, daughters of 39 sires, which, calved in the period 1987 to 2005, and were distributed in 13 herds. The duration of lactation was maintained from 64 to 305 days and age at birth ranged from 24 to 185 months. The connectedness of the data was performed to assess breeding-herd according to the daughters.

Estimates of variance components and genetic parameters and breeding values were obtained using MTDFREML (Multiple Trait Derivative Free Restricted Maximum Likelihood), described by Boldman et al. (1995), using an animal model.

The pedigree file that caused the numerators parenthood matrix (NRM) coefficients, used in all analysis, contained 864 different animals, 1776 non-zero elements in the NRM and no endogamous animal, consequently, the mean coefficient of inbreeding was equal zero.

The existence of genotype x environment interaction has been tested by the estimation of variance components, comparing models including or not the effect of genotype x environment interaction (Banos & Shook, 1990, Bueno, et al. 2005). Another way to detect the presence of genotype x environment interaction would be the comparison between the classifications of animals, according to breeding values.

Some studies have shown that if sire x herd interaction is included in the model of genetic evaluation, the influence of observations from a few herds will be more limited in the evaluation of breeding and may not significantly affect the evaluation of animals with progeny in many herds. However, ignoring it would increase the estimates of addictive genetic variance, which would underestimate the breeding values of sires and its accuracy.

In the present study the analysis were conducted using six models of simple traits, in which, were considered as fixed effects season of calving and herd-calving year and cow age as a covariate (linear and quadratic effects). The random effects of the six models are described below: 1 - additive model (additive effect and error), 2 - repeatability model (model 1 plus permanent environmental effect), 3 - additive model with the sire x herd interaction (model 1 more sire x herd interaction) 4 - additive model with interaction of sire x herd-year (including a model interaction of sire x herd-year), 5 - repeatability model with the sire x herd interaction (model 2 including the interaction of sire x herd), 6 - repeatability model with the interaction of sire x herd-year (model 2 including the interaction of sire x herd-year).

The importance of including the sire x herd interaction and sire x herd-year and permanent environment effect model in genetic evaluation of animals was performed using the likelihood test of models sequentially reduced (Rao, 1973). The test statistic of the likelihood estimate (LR) was compared with the value obtained through the distribution of chi-square ($\chi 2$), with 1 degree of freedom. The estimate was obtained by the expression

$$\mathbf{LR_{ij}} = -2\log_e\left(\mathbf{L_j} / \mathbf{L_i}\right),$$

$$\mathbf{LR_{ij}} = 2\log_e\left(\mathbf{L_i}\right) - 2\log_e\left(\mathbf{L_j}\right),$$

$$\mathbf{LR_{ij}} = 2\left[\log_e\left(\mathbf{L_i}\right) - \log_e\left(\mathbf{L_j}\right)\right],$$

Where

LRij= test statistic is the likelihood ratio for models sequentially reduced;
Li= is the maximum likelihood for the complete model i, and
Lj= is the maximum likelihood for the reduced model j.

The null hypothesis test implies that the functions of likelihood of full and reduced models did not differ among themselves, ie.,

$$\mathbf{H_0}: -2\log_e\left(\mathbf{L_i}\right) = -2\log_e\left(\mathbf{L_j}\right),$$

The decision rule used was:

If LRij > χ^2_{tab} , the test was significant and the full model provided the highest likelihood function over the reduced model;

If LRij < χ^2_{tab} , the test was not significant and the full model did not provide the greatest value of likelihood function over the reduced model.

The breeding values of animals for milk production have been organized into files, in order to assess possible changes in the magnitude of the predictions of breeding values and ranking of sires based on such predictions, when the sire x herd interaction and sire x herd-year was included in the model by means of the Pearson and Spearman correlations.

3. Result and discussion

The highest yield per lactation in buffaloes, observed in this study was observed around the 108º month of age. The observed average milk production up to 305 days, referring to 1774 lactations from 754 buffaloes in the period 1987 to 2005, was 1736.66 kg, with a standard deviation of 705.85 and a variation coefficient of 40.64%. Smaller values were found by Fraga et al. (2006), with an average production of 820 kg per lactation, in Cuba, for Tonhati et al. (2000), 1259.47 kg in Brazil; by Patel & Tripathi (1998) that in Surti buffaloes, found an average of 1442.6 kg.

However, higher values were found by Baghdasar & Juma (1998), 5419.95 kg, Iraq, for Rosati and Van Vleck (1998), 2286.8 kilograms, Italy and Moioli et al. (2006), 2184 kg in Italy. However, Khan (1998) study the Nili-Ravi buffaloes in Pakistan found values ranging from 1835 to 2543 Kg.

It is essential to monitor cumulative genetic progresses in selection programs not only to quantify the occurrence of genetic changes but mainly to evaluate benefits and to perform adjustments when necessary. Thus, it is necessary to know the genetic trend of the population studied (Euclides Filho et al. 1997).

The effects of variance heterogeneity on response to the selection depends on the magnitude of differences in genetic variance for milk production and their relations with the phenotypic variances. In the study in models of simple features it was found that the inclusion of the permanent environment (model 2 versus model 1, P = 0.052), the interaction reproductive years herd-(4 versus model a model, P = 0.047) in additive model were significant. The inclusion of sire x herd interaction in the repeatability model (model 5 versus. model 2, P = 0.219) was not significant, whereas the inclusion of the interaction of sire x herd-year (model 6 versus. model 2, P = 0.025) was significant (Table 1).

The study of these interactions lead us to consider how much the environment has influence in the effect of the features, which would be the best way to perform the study. The presence of genotype x environment interaction (G*A) is characterized by a different response of the genotypes to environmental variations, which can cause changes in the ordonance of the performance of the genotypes in different environments (Falconer & Mackay, 1996).

Silva (2002) working with buffaloes, also found no significant effect of inclusion of sire x herd interaction in the model of repeatability. However, Araújo (2000), working with Holstein cattle, and Sirol et al. (2005), with cattle breed Brown Swiss, found a significant effect in the inclusion of sire x herd interaction in the model of repeatability.

Models	-2log$_e$ L	LR	Significance level
(1)Additive	22,658.5037	-	-
(2)A + P	22,654.7100	3.793797	0.052099609
(3)A+RR	22,655.3691	3.134660	0.081110901
(4)A+RRA	22,654.5854	3.918380	0.046616186
(5)A+P+RR	22,654.7099	3.04E-05	0.219078768
(6)A+P+RRA	22,650.3313	4.378671	0.026356906

[1] A + P= additive + permanent environment, A+RxR= additive + interaction sire x herd; A+RxRA = additive + sire x herd-year interaction, A+P+RxR= additive + permanent environment + sire x herd interaction; A+P+RxRA=additive + permanent environment + sire x herd-year interaction.

Table 1. Values of -2 times the natural logarithm of the likelihood function (-2 loge L) and the likelihood ratio test (LRij) to sequentially reduced models, obtained for milk production in buffaloes, in the analysis of simple traits

Breeders produced in these herds are then distributed to be used in various environments. The knowledge of the importance of this interaction allows, in some cases, to set the environmental conditions in which the animals will be selected (Correia et al. 2007). Based on the fact that genotype x environment interaction can affect the genetic populations of beef cattle by inappropriate use of breeding is very important to consider this interaction in genetic evaluation. It is important to know in which of the additive or repeatability models its inclusion would have a significant effect, that in this study was observed in the additive model.

Correa, et. al. (2007) observed that the genotype environment interaction is significant when the differences in genetic and environmental levels are significant. The existence of this type of interaction implies in the optimal combination between genotypes and environments in order to maximize the production. This interaction can be influenced in situations where the selection herds are located in the best regions, using management practices well above average.

Estimates of additive genetic variance components for milk production were higher in models 1, 3 and 4 when compared to models that consider the effect of permanent environment 2, 5 and 6, respectively. Thus, it appears that the inclusion of permanent environmental effect caused a reduction in additive genetic variance.

Silva (2002) working with some of these data found higher values for additive genetic variance 66601.81, 66187.01 and 64989.44, respectively, for additive models + permanent environment, additive + permanent environment + sire x herd interaction, and additive + permanent environment + sire x herd-year interaction. He also noted that the inclusion of sire x herd caused a reduction in additive genetic variance. While Sirol et al. (2005), was

working with data on milk production in Brown Swiss breed, found that estimates of residual (co) variance and additive genetic (co) variance did not change when the models were adjusted for the effects of sire x herd interaction.

Models	Variance Components				
	σ_a^2	$\sigma_{c^1}^2$	$\sigma_{c^2}^2$	$\sigma_{c^3}^2$	σ_e^2
(1)Additive	135,186.081	-	-	-	165,086.573
(2)A + P	57,414.559	63,919.5	-	-	164,142.767
(3)A+RR	132,176.705	-	7,870.55		163,389.444
(4)A+RRA	135,545.905	-	-	9,988.00	156,675.128
(5)A+P+RR	57,502.2693	63,911.2	0.038309	-	164,144.258
(6)A+P+RRA	53,060.472	67,674.9	-	10,651.6	155,285.904

[1] A + P= additive + permanent environment, A+RxR= additive + interaction sire x herd; A+RxRA = additive + sire x herd-year interaction, A+P+RxR= additive + permanent environment + sire x herd interaction; A+P+RxRA=additive + permanent environment + sire x herd-year interaction.

Table 2. Estimates of additive genetic variance components (σ_a^2), permanent environmental ($\sigma_{c^1}^2$), the sire x herd interaction ($\sigma_{c^2}^2$), interaction of sire x herd-year ($\sigma_{c^3}^2$) and residual (σ_e^2) for milk production in buffaloes in an analysis of simple trait

The reduction in the estimated variance component of the permanent environmental effect was 0.013%, when the term of sire x herd interaction was included in the repeatability model (model 5 versus. 2). However, the term includes the sire x herd-year interaction increased by 5.87% (model 6 versus. 2), this result shows the importance of including the sire x herd-year interaction and confirms the results of the likelihood ratio test applied in this study (Table 2).

Silva (2002) in working models 2, 5 and 6, in buffaloes, found lower values for the variance component for permanent environmental effect, 37942.52, 37905.22 and 37983.33, respectively. The inclusion of sire x herd interaction caused a decrease of 0.98% in the component, whereas, by including the sire x herd-year interaction, an increase of 0.107%.

Estimates of residual variance components were smaller in models that included the sire x herd-year interaction (about 5% in model 1 versus. 4, and 6 versus 2). While the inclusion of sire x herd interaction caused a reduction of 1.03% in the estimate of residual variance component, the additive model and in the repeatability model the change was only 0,000009%. These results indicate that the inclusion of interaction of sire x herd-year is more important than the sire x herd interaction in models of buffaloes genetic evaluation.

The heritability estimate obtained for the characteristic of milk production decreased from 0.45 to 0.20 when we included the effect of permanent environment of additive model. So when the effect of permanent environment is not included, the expected genetic gains are inflated. By adding the sire x herd interaction or sire x herd-year interaction in model, the heritability estimates did not show large variations between the models studied (Table 3). Similar results were obtained by Araújo (2000), when working with Holstein cows and Silva (2002), when working with buffaloes.

Tonhati et al. (2004) found low values in the heritability estimative in four correcting types for buffalo production, showing that the genetic gain through selection were low. Genetic correlations between productions were high,therefore, to select through production periods permitted that breeders were selected among the remaining ones.

Dionello et al, (2006) in his research using milk production in Jersey cows noted that the values obtained by heritability estimates suggested the repeatabilty model as adjustment alternative for the milk production on controlling day, however, the repeatability estimate does not support the hyphotesis that the production during lactation should be considered with the same characteristics.

The heritability estimates were 0.22 for total milk yield and 0.19 for 305 days. For test-day yields, the heritability estimates ranged from 0.12 to 0.30, with the highest values being observed up to the third test month, followed by a decline until the end of lactation. The present results show that test-day milk yield, mainly during the first six months of lactation, could be adopted as a selection criterion to increase total milk yield (Tonhati et al. 2008).

Models	Milk Production				
	h^2	C^1	C^2	C^3	E
(1)Additive	0.45 (0.031)	-	-	-	0.55 (0.031)
(2)A + P	0.20 (0.091)	0.22 (0.085)	-	-	0.57 (0.030)
(3)A+RR	0.44 (0.033)	-	0.026 (0.019)	-	0.54 (0.031)
(4)A+RRA	0.45 (0.030)	-	-	0.033 (0.018)	0.52 (0.033)
(5)A+P+RR	0.20 (0.094)	0.22 (0.086)	0.13E-06	-	0.57 (0.030)
(6)A+P+RRA	0.19 (0.090)	0.24 (0.084)	-	0.037 (0.019)	0.54 (0.033)

[1] A + P= additive + permanent environment, A+RxR= additive + interaction sire x herd; A+RxRA = additive + sire x herd-year interaction, A+P+RxR= additive + permanent environment + sire x herd interaction; A+P+RxRA=additive + permanent environment + sire x herd-year interaction.

Table 3. Heritability estimated (h^2) and phenotypic variance proportion about permanent environment effect (C^1), sire x herd interaction effect (C^2), sire x herd-year interaction effect (C^3) and environment proportion for total variance (e), for buffaloes milk production, in an analysis of simple trait.

The heritability estimates for milk production in buffaloes, found by Khan (1998), in Pakistan (0.18), and Raheja (1998), India (0.19) were close to those found in Models 2, 5 and 6 of this work. Higher estimates in Brazil, were found by Tonhati & Vasconcelos (1998), 0.25; Tonhati et al. (2000), 0.28, and Silva (2002), 0.31. Values below the estimated in this study were obtained Rosati & Van Vleck (1998), 0.14, and Kalsi Dhilon & (1984), 0.13.

The proportion of phenotypic variance due to permanent environmental effects (C1) was 0.22 for model 2 and 5, and 0.24 for model 6. While Silva (2002) found values slightly below

(0.18) for the same models in buffalo. Rosati & Van Vleck (1998) found similar values (0.24) to the present study.

The proportion that represents of sire x herd interaction decreased with the inclusion of permanent environmental effect in the model, 0.027 (model 3) and 0.000013 (model 5), fact not observed with the inclusion of sire x herd-year interaction, 0.033 (section 4) and 0.037 (model 6) (Table 3). Silva (2002) found lower values for the models that consider the effects of permanent environment and of sire x herd interaction or sire x herd-year interaction, respectively 0.0000026 (model 5) and 0.02 (model 6), buffalo. Sirol et al. (2005), was working with cattle breed Brown Swiss also found that the proportion of total variation explained by sire x herd were near zero for milk production.

The range between the predicted breeding values for animals was very different between models 1 and 2. However, this difference is smaller when comparing models 1, 3 and 4 or 2, 5 and 6.

Models	Breeding values				
	Average	SD	Amplitude	Minimum	Maximum
(1)Additive	-6.70903	254.2341	2,009.420	-813.4204	1196
(2)A + P	-6.21746	135.7058	995.0106	-439.9113	555.0993
(3)A+RR	-4.71076	243.4701	1,953.337	-777.3368	1,176
(4)A+RRA	-6.26055	253.4086	2,007.501	-804.5006	1,203
(5)A+P+RR	-6.21974	135.8125	995.7977	-440.2247	555.5730
(6)A+P+RRA	-5.69773	126.1884	918.6691	-408.5506	510.1185

[1] A + P= additive + permanent environment, A+RxR= additive + interaction sire x herd; A+RxRA = additive + sire x herd-year interaction, A+P+RxR= additive + permanent environment + sire x herd interaction; A+P+RxRA=additive + permanent environment + sire x herd-year interaction.

Table 4. Average breeding values for all animals, standard deviations, maximum, minimum and maximum amplitudes in buffalo milk production in an analysis of simple trait

The Pearson correlation coefficient was equal to unity between the two models (additive over environment) and 5 (more additive plus permanent environmental sire x herd interaction) and close to 1 between models 5 and 6 (more additive plus permanent environmental interaction sire x herd-year). The same happened to the Spearman correlation. This implies that there is no difference between models 2 and 5. Despite the correlation between the 5 and 6 models to be high, statistically significant differences when using of sire x herd-year interaction (Table 1). Thus, despite the likelihood ratio test was significant (P <0.03), no significant change in the expected magnitude of the predicted values when the model is or is not adjusted for the effect of sire x herd interaction or sire x herd-year interaction (Table 5).

Falcão, et al. (2006) found low values of genetic correlation and demonstrate the effect of genotype x environment interaction, showing that the best sires may not be the same in different environments. Therefore, the choice of the breeder, the genotype × environment interaction should be considered.

Models	1	2	3	4	5	6
1	1	0.95076	0.99621	0.99873	0.95088	0.94719
2	0.94735	1	0.93433	0.94568	1.00000	0.99847
3	0.99527	0.92927	1	0.99725	0.93447	0.93263
4	0.99826	0.94184	0.99646	1	0.94581	0.94453
5	0.94748	1	0.92942	0.94197	1	0.99847
6	0.94301	0.99778	0.92731	0.94068	0.99777	1

Table 5. Pearson's correlation coefficient above the diagonal and Spearman below the diagonal, between breeding values for milk production, in analysis of simple trait

Similar results were obtained by Silva et al. (2002). Sirol et al. (2005) also found correlations from Pearson and Spearman for animals from the Swiss-Brown race, obtained by different models next to 1. The same was observed by Mohammad et al. (1982), that found Pearson and Spearman correlation above 0,99 for models that included and that ignored the interaction sire x herd effect and concluded that to ignore the interaction effect would not cause major alterations in the classification in Holstein cattle.

(1)Additive		(2)A + P		(3)A+RR		(4)A+RRA		(5)A+P+RR		(6)A+P+RRA	
AI	BV	AI	BV	AI	BV	AI	BV	AI	BV	AI	BV
145	1,196.199175	417	555.099273	145	1,176.458158	145	1,202.885413	417	555.573032	417	510.118508
417	1,096.918037	145	534.741842	417	1,021.933134	417	1,083.087238	145	535.263843	145	500.446971
648	932.169385	830	443.041801	535	925.531012	648	946.064351	830	443.419160	830	406.857072
535	916.531689	648	417.798173	648	904.522785	535	940.492253	648	418.269010	648	389.193901
158	866.897851	535	407.532504	158	880.667644	158	874.750424	535	407.951156	535	388.678508
830	829.170969	633	399.643734	830	783.759571	830	815.939882	633	400.032722	158	373.762665
763	804.776426	158	396.902144	372	757.467738	763	797.078757	158	397.264084	633	368.644302
633	789.345535	780	387.983107	763	756.916825	633	783.553783	780	388.305834	780	361.965814
707	729.145247	88	377.104287	633	735.288004	707	755.150389	778	377.345364	88	347.851767
372	704.552849	778	377.029700	707	714.328625	372	716.738100	88	377.246737	778	343.801016
780	692.384619	763	355.236708	599	687.152329	780	694.440688	763	355.629186	533	324.039457
533	681.656841	533	352.189245	780	674.324676	599	684.550793	533	352.536469	708	320.667190
778	670.211976	708	342.453984	533	655.734153	156	675.159165	708	342.801505	763	318.772181
156	666.651135	498	340.036913	156	635.988657	533	674.976642	498	340.275739	707	313.277979
708	654.593767	781	330.849318	778	635.410788	708	659.764026	781	331.076036	498	312.627546
638	650.632615	829	330.147344	708	635.173974	778	651.799147	829	330.387198	781	307.745756
599	647.109638	494	324.896616	638	615.855574	135	629.955574	494	325.188312	494	301.316618
135	615.840639	707	324.539277	135	600.695858	638	624.301576	707	324.866834	829	300.288924
494	594.167074	92	315.587774	412	583.553355	412	592.398731	92	315.884408	92	290.646106
276	589.146008	413	303.638671	276	573.741561	494	590.895416	413	303.826051	156	285.113078

[1] A + P= additive + permanent environment, A+RxR= additive + interaction sire x herd; A+RxRA = additive + sire x herd-year interaction, A+P+RxR= additive + permanent environment + sire x herd interaction; A+P+RxRA=additive + permanent environment + sire x herd-year interaction.

Table 6. Breeding values for 20 the best animals, animal identification (AI); breeding values(BV), in models 1, 2, 3, 4, 5 e 6

There were no great changes in the ranking of animals based on predicted breeding values when using different models. In comparing the top 20 animals one sees that 65% were common in all models (Table 6). This result was confirmed by the Spearman correlation estimates was equal to unity between models 2 and 5 and close to unity between models 2 and 6. Similar behavior was observed for the Pearson correlation.

Comparing the templates 2 and 5, it is observed that the top 20 animals were common, and that 95% were common between the models 1 and 4, 2 and 6, 3 and 4, and 5 and 6. The lowest percentage of animals was observed in common between the models 2 and 3, 3 and 5, 3 and 6, and 4 and 5. What shows us that even considering the six models studied, 95% of the best animals were common to most models which shows that the environmental variance influenced animal performance when added to the model the effect of environment.

4. Conclusion

This study concluded that the inclusion of sire x herd interaction and sire x herd-year interaction, had no significant effect. Although the heritability estimates have been low, estimates of phenotypic and genetic correlations between all the characteristics show the possibility of developing a selection scheme to improve the characteristics of milk production in buffaloes. More studies are needed to select the best animals for they can be used in various environments.

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