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Single and Multi Traits Animal Models for some Semen Traits on Friesian Bulls

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ABSTRACT

A total of 15153 ejection semen of 61 Friesian bulls, kept at International Livestock Management Training Center at Sakha Farm, belonging to Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt, during the period from 1992 to 2000 were used in the present study**.** Traits studied are volume ofsemen (Vol, ml.), concentrates (Con.Mill/mil.) and livability (Liva. %) of sperm. Single and multi traits animal models were used. The model included the fixed effects of month and year of collection and the random effects of animals, permanent environmental and errors. Means of Vol, Con and Liva.were 4.53 ml, 1820 mill/ml and 68.57%,respectively. Estimate of heritability from single trait andmultiple trait analysis were similar and being0.32±0.10, 0.14±0.09 and 0.18±0.09, for Vol., Con., and Liva., respectively.Genetic and phenotypic correlations amongsementraits are positive and ranged from 0.08 to 0.67 for genetic correlations and from 0.30 to 0.80 for phenotypic correlations. Estimates of sire transmitting ability (STA**)**from single and multi traits animal models are similar, while the accuracy of estimates are little higher for multi traits animal models and ranged from-2.88 to 3.54 ml, forVol., and from -930 to 511 mill/mil for con., and from – 23.14 to 12.15 % for liva.,

Keywords: Semen traits, Friesian, bulls

INTRODUCTION

Artificial insemination (AI) is the main tool used for genetic improvement of dairy cattle. Using AI, producers can introduce daughters from superior sires into their herds and improve traits of economic importance (Mathevon*et al*.1998). Also, artificial insemination, plays an important role in animal breeding, allowing the utilization of genetically superior sires. The objectives of AI are to use desirable genes widely, to control disease, and to increase economic profits (Sanghyon, 2003).

Semen traits (i.e, volume of semen, concentrates, mass and livability) are affected by some physiological factors (i.e., age of the bull), environmental factors (i.e,month and year of collection, collection frequency, nutrition and housing of bulls) and genetic factors. Estimates of heritability for semen traits ranged from 0.04 to 0.75 as reported by(Mathevon *et al*., 1998; Miroslay *et al*., 2000; El- Basuini, 2010; Shimma El-Komey, 2013 and Khattab *et al*.,2015). Genetic correlations among semen traits ranged from 0.58 to 1.00 as found by Barth andWaldner (2002), Druet *et al*. (2009), El- Basuini (2010), Shimma El- Komey (2013) and Khattab *et al*. (2015) working on different breeds of dairy bulls in different countries.

The objectives of the present study are (1) investigate non genetic factors affecting semen trait (volume, concentrates and livability of sperm), (2) estimates phenotypic and genetic parameters for these semen traits and (3) estimates sire transmitting ability (STA) for above semen traits by using Multi Trait Animal Model (MTAM) for Friesian bulls kept at International Center of Artificial Insemination and Embryo Transfer (ICAI) at Sakha Farm, Kafer El Sheikh Government.

MATERIALS AND METHODS

A total of 15153 ejection semensfrom 61 Friesian bulls kept at International Center of Artificial Insemination and Embryo Transfer (ICAI),Sakha Farm, belonging to Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt during the period from 1992 to 2000 were used in the present study. Semen for each bull was collected twice a week. Traits studied are volume of semen, concentrates and livability of sperm. The ejection volume was measured directly in mil to nearest 0.1 using graduated glass tube. A trop of fresh semen was diluted with sodium citrate solution (2.9%) on a slide and covered with a cover slip. Under the high power (400 X) the slide was examined on the microscope stage incubator at 37 $C^0$and the percentage of spermatozoa showing progressive forward motility was recorded. For live – dead count a smear of freshly ejaculated semen was made and stained by eosin negrosin mixture prepared as described by Hancock (1952). Concentration were by millions of spermatozoa/ml. The percentage of live sperm was calculated from a total number 100 spermatozoa counted in different microscope fields under magnification of (600 X) and using hand tally counter.

Semen traits were analyzed by Multiple Trait Derivate – Free Restricted Maximum Likelihood (MTDFREML), according to Boldman *et al*. (1995).Traits were analysis by using single and multi traits animal models (STAM and MTAM). Each model includes the fixed effects of month and year of collection and random effects of animal, permanent environmental and errors. Estimates of heritability, phenotypic and genetic correlations among semen traits studied and predicted sire transmitting ability are estimated according to Boldman *et al*. (1995).

RESULTS AND DISCUSSION

Means, standard deviation and coefficient of variability for semen traits studied are presented in Table 1. Mean of volume of semen was lower than those reported by many authors working on different breeds of dairy cattle. In this respect, Mathevon *et al*.(1998) with Holstein bulls, reported that volume of semen for young and mature bulls were 5.48 and 6.73 ml., respectively.Asad *et al.* (2004) with Friesian bulls, observed that volume of semen ranged from 12.16 to 14.26 ml. Karoui *et al.* (2011) with Holstein bulls found that average volume of semen was 5.40.while, the present mean of concentrates of sperm are higher than those reported by Mathevon *et al.*(1998)(1296 to 1389)andKaroui *et al.* (2011)(1267). Overall mean of live of sperm (68.57%) was higher than that reported byAsadpour *et al.* (2011) (46 to 55%) for Holstein bulls and Khattabetal. (2015)(65.96%) for Egyptian buffalo bulls.Coefficient of variability for the present semen traits ranged from 23.10 to 49.00 %, Table 1. Variation in semen parameters recorded in the present study may be due to individual variations, differences in age of bull, genetic makeup of the bulls, season of study and agro climatic conditions (Khattab *et al.* 2015).

Table 1. Means, standard deviation (SD) and coefficient of variation (CV%) for volume (vol, ml) , concentrates (mill./ml) and live sperm (liva %) for Friesian bulls.

Traits	Means	SD	CV%
Vol, ml	4.53	2.04	45.03
Con., mill/mil	1820	89049.00	
Liva, %	68.57	15.84	23.10

The differences between the present means of semen traits and those reported by different authors working on different breeds of dairy bulls in different countries could be due to differences in genetic, reproductive health, status of bulls, age of bulls, frequency of collection, pooled volume, nutrition, season and year of collection and management (Nazir, 1988; Soderquist *et al.* 1992; El- Basuini, 2010; Shimma El – Komey, 2013 and Khattab *et al.*, 2015).

Table 2. Estimates of heritability (h^2) for single (STAM) and multi traits animal model (MTAM), genetic correlations (r_g, below diagonal) and phenotypic correlations (r_p) above diagonal among different traits studied.

Traits	VOL	Con	Liva
Vol	0.32±0.1000.	30	0.40
Con	0.17±0.09	0.14+0.090.	80
Liva	0.08±0.02	0.67±0.10	0.18±0.09

The heritability estimates (h^2) for volume of semen, concentrates of sperm and livability of sperm from single and multi traits animal model were 0.32 ±0.10,0.14±0.09 and 0.18±0.09, respectively (Table 2). Estimates of h^2 and their standard errors from single and multi traits analysis were similar.According to moderate heritability estimates for volume and livability of sperm (Table 2), it could be concluded that genetic improvement for semen traits can be achieve through selection of bulls. A wide range of heritability has been reported in the literature. For volume of the ejaculate, estimates varied from 0.04 (Kaps *et al.,* 2000) to 0.75(Shimaa El – Komey, 2013). For concentration, estimates varied from 0.07 (Krislijan*et al.* (2003) to 0.36 (Mathevon *et al.*, 1998) and for livability, estimates ranged from 0.10 (Gredler *et al.* 2007) to 0.20 (Kealey *et al* 2006).Mathevon *et al.*(1998) concluded that the variation of heritability estimates for semen traits may be due to the different populations of bulls considered (e.g., with various intensities and criteria for selection, different breeds, or categories of animals), use of the average over multiple ejaculates versus individual ejaculates as observations, the types of models and methods of variance component estimation used and the limited accuracy of most estimate.

In addition, the present estimates of heritability for semen traits are lower than those reported by Shimma El – Komey (2013) with the same set of data using sire model, found that , heritability estimates for volume , concentrates and livability of sperm were 0.75, 0.70 and 0.75,respectively. Lower estimates of heritability by animal model may be due to including of some permanent environmental effects in the animal model and consequently a correction for this effect was considered in animal model, while, it was notconsidered in the sire model. In addition, estimates $h^2$from sire model was computed as four times of the covariance between paternal half sibs related to the total phenotypic variance.

Phenotypic and genetic correlations among semen traits are presented in Table 2. Genetic correlation between volume of semen and concentrates and livability of semen were positive and being 0.17± 0.09 and 0.08±0.02, respectively and between concentrates of sperm and livability was 0.67±0.10 (Table 2). The present results concluded that selection for volume of semen for Friesian bulls will increase concentrates and livability of sperm and this is the desirable goal of dairymen and will help in increased the fertility, which is considered as one of the most important economic traits in dairy cattle. Also, higher genetic correlation between concentrates and livability of sperm (0.67), indicated that concentrates and livability are correlated traits and selection of one trait will increase the other trait. Similar results are reported by many authors working on different breeds of dairy cattle in different countries. In this respect,Shimma El – Komey (2013) with the same set of data, found that r_g between volume of sperm and each of concentrates and livability of sperm were 0.03 and 0.19. Birgit *et al.* (2005) reported that $r_g$between volume and each of concentrates and livability of sperm were 0.31 and 0.06, respectively.

On Egyptian buffaloes, Khattab *et al.* (2015) found that r_g between volume and livability of sperm was 0.94.

On the other hand, negative genetic correlations between semen traits are reported by Kealey *et al.* (2006) working on Hereford bulls, found that r_g between volume and livability was -0.09. They concluded that this may be due to introduction of excess urine or seminal plasma as part of a typical electro ejaculation may affect the covariance of ejaculate volume with percentage of live and motile sperm. Also, Karoui *et al*. (2011) with 502 Holstein bull in Spain, using multi trait animal model, found that genetic correlation between volume of ejaculate and concentrates was negative (-0.13).

Phenotypic correlations between semen traits are positive and ranged from 0.30 to 0.80 (Table 2). Similar results are found by many authors working on different breeds of dairy cattle in different countries. In this respect,Druet *et al*. (2009) reported that phenotypic correlation between volume of semen and livability was 0.10. Shimma El– Komey (2013) with the same set of data, reported that phenotypic correlation between volume of sperm and each of concentrates and livability of sperm were 0.09 and 0.15, respectively.

On Egyptian buffalo bulls, Khattab *et al*. (2015) found that phenotypic correlation between volume of semen and livability of sperm was 0.31. The present results indicates that increase volume of semen will increase concentrates and livability of sperm and this is a goal of center of artificial insemination (AI) in Sakha farm, which is the big center of AI in Mediterranean Sea and provide the dairymen by Frozen semen.

On the other hand, negative phenotypic correlation between semen traits were reported by Birgit *et al*. (2005), Kealey *et al*. (2006) and ranged from -0.08 to - 0.17.

Table 3.Range of predicted sire transmitting ability (STA) and their accuracy for Volume (Vol, ml), concentrates (Con .) and livability (Liva, %) of sperm for Friesian bulls Obtained from single (STAM) and multi traits animal model (MTAM).

Traits	STAM				MTAM			
	Min.	Max.	Range	Accuracy	Min.	Max.	Range	Accuracy
Vol, ml	-2.88	3.55	6.64	0.71 to 0.98	-2.88	3.54	6.42	0.75 to 0.99
Con.	-930	511	1441	0.80 to 0.90	- 930	511	1441	1.00 to 1.00
Liva. %	-23.14	12.15	35.29	0.00 to 0.00	-23.18	12.14	35.32	0.00 to 0.20

Estimates of sire transmitting ability (STA), minimum, maximum, ranges and accuracy for semen traits as estimated from Single Trait Animal Model (STAM) and Multi Trait Animal Model (MTAM) are presented in Table 3. Means of STA ranged from -2.88 to 3.55 ml, from 930 to 511 for concentrates and from -23.14 to 12.15 % for livability, respectively. Estimates of STA from STAM and MTAM were similar, while the accuracy are little higher when used MTAM. Similar results are reported by Shimma El- Komey (2013) with the same set of data estimated STA by using sire model, found that mean of volume of semen, concentrates and livability ranged from -1.14 to 1.23 ml for volume of semen, from -442.42 x10-6 to 410.45 x 10-6 for concentrates and from -12.19 to 10.64 % for livability. The present results were similar to those reported by different authors working on different breeds of dairy cattle. El- Basuini (2010) with 109 Egyptian buffalo bulls, found that the STA for semen traits ranged from -0.448 to 0.449 ml for volume from -5.85 to 8.10 % for live spermatozoa. The present results showed large genetic differences between bulls for different semen traits. Sires have positive sire transmitting ability for volume of semen gives also positive STA for concentrates, and livability of sperm. Then selection of sires according to positive STA for volume of semen will increase concentration and livability of sperm.

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نموذج الحيوان لصفة واحدة وعدة صفات لبعض صفات السائل المنوى لطلائق الفريزيان

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استخدم فى هذة الدراسة عدد ١٥١٥٣ قذفة منوية جمعت من ٦١ طلوقة فريزيان تابعة للمركز الدولى للتلقيح الصناعى ونقل الاجنة بسخا – التابع لمهعد بحوث الانتاج الحيوانى – وزارة الزراعة – الدقى – القاهرة وذلك خلال الفترة من ١٩٩٢ الى ٢٠٠٠. الصفات اتى درست (حجم القذفة مل ، تركيز القذفة بالمليون قذفة لكل مل والنسبة المؤية لحيوية الحيوانات المنوية).حللت الصفات السابقة بنموذج الحيوان لصفة واحدة ولعدة صفات. اشتمل نموذج التحليل على التاثيرات الثابتة لكل من شهر وسنة الجمع والتاثيرات العشوائية لكل من الحيوان والتاثير البيئى الدائم والخطأ.قدرت المتوسطات ب ٤.٥٣ مل ، ١٨٢٠ مليون / مل ، ٦٨.٥٧ % لكل من حجم القذفة وتركيز وحيوية الحيوانات المنوية. لم يكن هناك فرق بين قيم المكافىء الوراثى المقدر من نموذج الحيوان لصفة واحدة ولعدة صفات وكانت قيم المكافىءالوراثى٠.٣٢ ، ٠.١٤ ، ٠.١٨ لكل من حجم القذفة وتركيز وحيوية الحيوانات المنوية على التوالى. تراوحت قيم الارتباط الوراثى ما بين ٠.٠٨ الى ٠.٦٧ والارتباط المطهرىمابين ٠.٣٠ الى ٠.٨٠.قدرت المقدرة العبورية مابين ٢.٨٨ـ إلى ٣.٥٤ مل لحجم القذفة ومابين٩٣٠ الى ٥١١ مليونمل لتركيز القذفة ومابين ٢٣.٤ـ الى ١٢.١٥ % لحيوية الحيوانات المنوية.وخلاصة البحث فانة يقترح دمج حجم السائل المنوي مع حركة ونسبة الحيوانات المنوية الحية .