Animal Reproduction Science 124 (2011) 28–38

Contents lists available at ScienceDirect

Animal Reproduction Science

journal homepage: www.elsevier.com/locate/anireprosci

Time trends, environmental factors and genetic basis of semen traits collected in Holstein bulls under commercial conditions

Sofiene Karoui[a], Clara Díaz[a], Magdalena Serrano[a], Roger Cue[a,1], Idoia Celorrio[b], María J. Carabaño[a,*]

[a] Animal Breeding Department, National Institute for Agriculture and Food Research and Technology, Ctra. de La Coruña Km 7.5, 28040 Madrid, Spain
[b] ABEREKIN, S.A. Parque Tecnológico, Edificio 600, 48160 Derio, Spain

ARTICLE INFO

Article history:
Received 30 July 2010
Received in revised form 25 January 2011
Accepted 7 February 2011
Available online 13 February 2011

Keywords:
Semen quality
Breeding soundness evaluation
Bayesian analysis

ABSTRACT

The fact that results of artificial insemination (AI) are declining in highly selected dairy cattle populations has added a renewed interest to the evaluation of male fertility. Data from 42,348 ejaculates collected from 1990 to 2007 on 502 Holstein bulls were analysed in a Bayesian framework to provide estimates of the evolution of semen traits routinely collected in AI centres throughout the last decades of intense selection for production traits and estimate genetic parameters. The traits under consideration were volume (VOL), concentration (CONC), number of spermatozoa per ejaculate (NESPZ), mass motility score (MM), individual motility (IM), and post-thawing motility (PTM). The environmental factors studied were year-season and week of collection, which account for changes in environmental and technical conditions along time, age at collection, ejaculate order, time from previous collection (TPC) and time between collection and freezing (TCF) (only for PTM). Bull's inbreeding coefficient (Fi), bull's permanent environmental and additive genetic effects were also considered. The use of reduced models was evaluated using the Bayes factor. For all the systematic effects tested, strong or very strong evidence in favour of including the effect in the model was obtained, except for Fi for motility traits and TCF for PTM. No systematic time trends for environment or bull effects were observed, except for PTM, which showed an increasing environmental trend, associated with improvements in freezing–thawing protocols. Heritability estimates were moderate (0.16–0.22), except for IM, which presented a low value (0.07). Genetic correlations among motilities and between motilities and CONC were large and positive [0.38–0.87], VOL showed a negative correlation with CONC (−0.13) but with ample HPD95%. The magnitude of heritabilities would allow an efficient selection if required and grants the use of these traits as indicators of the sperm viability component of bulls breeding soundness.

1. Introduction

Bull fertility has been a concern for the dairy industry for decades. AI centres rely on the ability of their bulls to produce a sufficient amount of semen with a good fertilizing potential. Culling of high merit bulls due to impaired fertility may result in important economic losses for the whole dairy industry. More recently, the fact that results of AI are declining in highly selected dairy cattle populations (see, e.g., Lucy, 2001) has added a renewed interest to the evaluation of male fertility. Consequences of the intense selection for production traits on female fertility have been the subject of numerous studies. However, to the authors' knowledge, no results about trends for traits affecting the fertilizing capacity of the sperm or,

* Corresponding author. Tel.: +34 913476742; fax: +34 913478743.
E-mail address: mjc@inia.es (M.J. Carabaño).
[1] Present address: Department of Animal Science, McGill University, Macdonald Campus, 21111 Lakeshore Road Ste. Anne de Bellevue, QC, H9X 3V9, Canada.

0378-4320/$ – see front matter © 2011 Elsevier B.V. All rights reserved.
doi:10.1016/j.anireprosci.2011.02.008

more importantly, for male fertility in the last decades are available.

Bull breeding soundness evaluation is usually carried out based on semen traits routinely collected in the AI centres. These traits have been associated with bull fertility, but are affected by environmental factors that can bias evaluation of the bull's merit. Optimising the statistical model that allows a better appraisal of the bull's own merit in field conditions is important. Numerous studies have determined the effect of several environmental factors such as age of bull, ejaculate order, season, collection team or interval between collections on semen traits (Everett et al., 1978; Fuente et al., 1984; Taylor et al., 1985; Diarra et al., 1997; Mathevon et al., 1998; Brito et al., 2002a,b; Fuerst-Waltl et al., 2006; Hallap et al., 2006; Gredler et al., 2007; Druet et al., 2009; Koivisto et al., 2009; Fiaz et al., 2010; Mandal et al., 2010). However, many of those studies have been carried out in a relatively low number of animals and under experimental conditions. Moreover, additional effects might need to be considered. In this sense, the highly oscillating nature of commercial semen production requires identifying short term factors affecting production and quality around the collection day. In addition, the increasing rate of inbreeding in Holstein populations warrants its consideration for the statistical modelling.

The effectiveness of using semen traits to indirectly improve bull breeding soundness and the emphasis to be placed on each of them depends on the heritability, repeatability and correlations among them and between each seminal trait and the selection criteria. Estimates of heritability of semen traits in cattle are widely variable, ranging from low to moderate, depending on the trait, population studied, age of the bull and whether individual ejaculate measures or average production per bull are analysed. A significant relationship between bull fertility measured through results of AI and semen traits (more specifically sperm motility) has been found in several studies (see, e.g., Christensen et al., 1999, 2005; Januskauskas et al., 2000).

This study aimed to evaluate the statistical modelling including a short term contemporary group and inbreeding level, investigate time trends and to study genetic parameters for semen traits of Holstein bulls collected in commercial conditions in an AI centre from 1990 to 2007. Bayesian methods, which provide a flexible framework to make inferences about the parameters describing the data generation process and functions of them and a comprehensive set of tools to describe the uncertainty in the estimation of the quantities of interest and to compare alternative models for the analysis of noisy measures and unbalanced designs that characterize field data, were used in this study.

2. Materials and methods

2.1. Data

Data on five semen traits, volume of ejaculate (VOL), concentration (CON), mass motility score (MM), individual motility (IM) and post thawing progressive individual motility (PTM), which were routinely collected in a Spanish AI centre (Aberekin, S.A.) from 1990 through 2007, were provided by this AI centre. Number of spermatozoa per ejaculate (NESPZ) was then obtained from the product of VOL and CONC. Only records from Holstein bulls were analysed.

In this AI centre, semen is routinely collected using an artificial vagina in a nearly regular weekly basis. Ejaculate volume (milliliters) is measured directly from the collecting container. During the semen analysis, collected samples are kept in a 32 °C bath. Concentration is determined using an IMV ACCEULL spectrophotometer (IMV International Corporation, Maple Grove, MN, USA). Percent progressive motility, which has been named as individual motility, is estimated by examining unstained diluted semen using a 20× magnification and light microscopical observation equipped with a warm stage. Mass motility or motility score is subjectively assessed by a trained technician for undiluted unstained semen under microscope (10×) using a scale from 0 to 5 (best motility).

The ejaculates containing less than 300×10^6 spz/ml, 4 MM score and 75% of IM are discarded and not included in the pooled collections for freezing. The cut-off points are a 'rule of thumb' and not a strict guideline. Individual ejaculates are diluted with egg-yolk-tris extender containing glycerol and antibiotics (Bioxcell®, IMV Technologies). Final concentration of diluted samples is 120×10^6 spz/ml.

After gradually cooling to 5 °C (at a speed of 0.25–0.30 °C/min), the semen is packaged in 0.25 cc straws (30 million spz per straw) and frozen using a programmable *bio-freezer* (model 5300 3T, IMV Technologies). For post-thaw semen evaluation, two straws per ejaculate are thawed in a water bath of 36 °C and evaluated individually for the percentage of progressively motile spermatozoa, using a computerized Sperm Class Analyzer® (Microptic, S.L.) from year 2004.

Some changes in the routine collection and laboratory equipment have occurred along the period of collection of data. Up to year 1997, freezing was done using a traditional vapour method. From that date, a computerized programmable freezer has been used, as previously reported. The spectrophotometer used to measure CON was changed in years 1997 and 2006. The cooling system previous to freezing was improved in year 2003. The extender used to dilute the semen samples was changed from Triladyl® (minitüb) to the present one in year 2001. For all the equipment and protocols an improvement in repeatability and accuracy of measurements has been observed from year 2000, when the AI centre obtained the ISO certification.

For analyses, records received from the AI centre were edited according to the following criteria. All the records corresponding to ejaculates below the threshold of 1 ml per ejaculate or 300 million spz/ml or above the threshold of 20 ml and 4000 million spz/ml were discarded. Also the registries of bulls with age of collection less than 12 months and all the data of bulls with less than 5 observations were eliminated. Discarded records represented 4% of the initial data. Finally, 42,348 ejaculates corresponding to 502 bulls were analysed. A summary of the data statistics is presented in Table 1.