

Genetics and genomics to improve fertility in high producing dairy cows

R.F. Veerkamp*, B. Beerda

*Animal Breeding and Genomics Centre, ASG, Wageningen UR,
The Netherlands*

Abstract

Improving dairy cow fertility by means of genetic selection is likely to become increasingly important, since it is now well established that declining fertility cannot only be arrested by improved management. Profit margins per kg milk produced are decreasing, therefore farmers need to reduce cost and increase herd size. This restricts the labor input per cow and the disposable cost of getting a cow pregnant, whilst at the same time hormone treatments have become less acceptable. This makes it unlikely that additional management interventions will maintain fertility at acceptable levels in the near future. Genetic improvement seems the obvious solution. Effective selection tools are available in most Western countries using traditional breeding value estimation procedures. Also, in addition to gene assisted selection using individual genes or QTL, high throughput Single Nucleotide Polymorphism (SNP) technology allows genetic improvement of fertility based on information from the whole genome (tens of thousands SNP per animal), i.e. genomic selection. Simulation studies have shown that genomic selection improves the accuracy of selecting juvenile animals compared with traditional breeding methods and compared with selection using information from a few genes or QTL only. Research in the areas genomics and proteomics promise to make genetic selection even more effective. The genomic and proteomics technologies combined with the bioinformatics tools that support the interpretation of gene functioning and protein expression facilitate an exciting starting point for the development of new management strategies and tools for the improvement of reproductive performance.

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Keywords: Genetic selection; Fertility; High milk yield; Genomic selection; Dairy cows

1. Introduction

Dairy cow fertility has declined over the past decades [1]. Together with the continuing drive to reduce cost of milk production this sparks questions about the part genetic selection can play in improving fertility. In this overview, answers are explored by

means of addressing genetic variation in fertility related traits, the latter's association with milk yield, and the availability of management interventions to improve fertility. Breeding strategies have evolved from conventional ones, selection based on breeding values estimated with statistical models from large datasets collected on farm, to innovative strategies that incorporate genomic information. Aforementioned topics will be discussed, including recent developments in functional genomics and genomic selection. Thus, we aim to assess the validity of applying genetics to combat poor fertility in dairy cows and outline contemporary selection strategies.

* Corresponding author at: Animal Breeding and Genomics Centre, ASG, Wageningen UR, P.O. Box 65, NL-8200 AB Lelystad, The Netherlands. Tel.: +31 320 238261; fax: +31 320 238050.

E-mail address: Roel.Veerkamp@wur.nl (R.F. Veerkamp).

2. Reasons for applying genetics to improve fertility

2.1. Significant genetic variation for fertility

The existence of significant genetic variation in fertility is generally accepted [1–3]. Heritability for fertility traits commonly used in animal breeding (Table 1) is relatively low, as a consequence of the large unexplainable residual variation in statistical models trying to predict traits like calving interval and pregnancy rate at the individual cow level. The difficulty of predicting these traits is demonstrated by the low percentage of variance in fertility that is explained by, for example, measures of energy balance. A significant association exists between energy balance and days until first luteal activity as measured by milk progesterone, however, less than 4.8% of the variance may be explained by the measures of energy balance [4]. Hence, heritability estimates of 2–15% for fertility traits do not indicate the unimportance of genetics compared to management. The existence of strong genetic effects are evidenced by differences in mean calving interval of up to 30 days between daughters of different sires. Similarly, the difference in pregnancy rate between daughters of extreme Holstein sires is as high as 7%, which equates to roughly 29 days open per lactation [5]. During the last two decades the interval from calving to conception increased by 24 days in the US [6]. Illustrative of this trend, Holstein herds in south-eastern states reported increases in average days open of and over 40 days between 1982 and 1999, whilst conception rates decreased from about 50 to 34%. Unfavorable genetic changes in conception interval since 1980 accumulated to 1.0 genetic standard deviation and genetics has been estimated to account for one-third of the decline in pregnancy rate [6]. Hence, despite low heritability for commonly used fertility traits, substantial genetic effects have been reported, mainly as a consequence of ignoring

the genetics, and a predominant part of the explainable variation is genetically based. Therefore, appropriate bull selection seems a practical effective strategy to solve current fertility problems.

2.2. Associations between fertility and milk yield: conjoint improvement?

It may be assumed that genetic selection for improved female fertility is obstructed by the dairy industry's strive for high milk production levels. There is overwhelming evidence that increasing genetic merit for yield without considering genetic merit for fertility, reduces fertility [2,7]. The impact of this is such that, with single trait selection for yield and an increase of genetic merit of approximately 1000 kg milk, calving interval is expected to increase between 5 and 10 days. This expected genetic trend is also found in selection experiments [2]. The observed phenotypic trend may in fact be higher or lower than this depending on influences by management and nutrition. It is important to note that the association between milk production and fertility varies from herd to herd, both phenotypically [8] and genetically [9]. For example, the strength of negative associations between yield and fertility is equal to or lower in high production herds compared to low production herds [10–12]. This supports the growing evidence that there is no fixed direct inverse association between phenotypic yield and fertility, and that reduced fertility due to selection for yield is not necessarily the consequence of the increase in yield per se [5,13]. Different mechanisms may underlie the clear negative genetic correlation between yield and fertility, e.g. pleiotropic gene effects, linkage or complex physiological associations [7]. Also, genetic selection for yield may change the energy partitioning in lactating dairy cows causing a genetically induced negative energy balance and a lower body condition score [7,13], i.e. states associated with poor fertility. However, genetic associations between yield and fertility are such that conjoint improvement for milk yield and reproductive performance is possible [14–16] whilst maintaining 70–80% of the yearly increase in yield [17]. A practical example is given in the Finish Ayrshire cattle [2], where increasing the weight for fertility traits halted the negative genetic trend from selection for yield.

2.3. Constraints on the deployment of alternative management measures

The relative importance of genetic selection as compared to alternative management measures for improving fertility depends not only on the genetic

Table 1
Mean heritability for fertility traits estimated in 17 studies [2]

Fertility scores	Heritability (%)
Non-return after first insemination	1.9
Conception to first service	2.7
Number of services per conception	2.6
Interval traits	
Calving interval	3.4
Days open	2.4
Days to first service	5.0
Interval from first to last insemination	1.7

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