
The importance of recording of AI data for the genetic systems. The context of AI from service to genetic progress

J. Philipsson¹ & H. Jorjani²

¹*Dept. of Animal Breeding and Genetics, SLU,
P.O. Box 7023, SE-750 07 Uppsala, Sweden*

²*Interbull Centre, SLU,
P.O. Box 7023, SE-750 07 Uppsala, Sweden*

The application of Artificial Insemination (AI) in cattle breeding in the 1940's was primarily done in order to eradicate diseases transmitted through the use of bulls for natural services. AI became an important tool to improve the fertility in dairy cows. However, it was soon realised that AI also was a mean for more wide-spread use of good bulls, thereby contributing to genetic improvement of the cattle stock. The technology status and lack of knowledge at that time on efficient methods for genetic evaluation and selection meant though that genetic improvement in production was marginal, whereas traditional selection for conformation was enhanced. Also fertility of bulls was improved as selection pressure was put on bull's libido and semen quality to get an efficient AI service.

The great importance AI plays in modern breeding programs of today, rely heavily on the following three building blocks:

1. The invention and full use of frozen semen
2. The recording and technical development of data handling through consistently more capable computers
3. Increased knowledge on the genetics of fertility and development of efficient methods for genetic evaluation of fertility

In the following the implications of these developments will be discussed in the context of efficient use of AI data and its opportunities and challenges.

Introduction

AI as a breeding tool changed the breeding program structures globally

The wide-spread use of frozen semen, whereby individual bulls could be used for up to several hundreds of thousands of inseminations, completely changed the structure of breeding programs both nationally and globally. The opportunities to store semen meant that a number of smaller countries collected the semen of individual bulls necessary for use also as a proven bull in a few months time as a young bull, and then the bulls were slaughtered. After progeny test results were obtained semen of only the best bulls were used, while the semen of all the others was thrown away. It was a cost effective breeding program, provided the population was limited. When opportunities opened for export of semen of genetically superior bulls the scene looked different. Both for health control reasons and access to semen of the very best bulls for many farmers the progeny tested bulls had to be kept alive until the progeny tests were known. This so-called lay-off system meant that all young bulls were used to get reasonably accurate progeny tests after which they were layed off until some of them were selected according to their daughter performance for wide-spread use.

Internationally the opportunities for extensive use of individual bulls at a rather cheap price meant that many bulls were used in the same countries all over the world. The “holsteinisation” of the black and white Friesian cattle is the most striking example of globalised use of semen contributing to a total change of a whole breed in just a couple of generations. However, this development took place much faster than the development of genetic tools did to make the most wise selection decisions for breeding programs to be sustainable.

Today the major dairy breeds of the world are kept in more than one country and are served by AI studs marketing their semen not only nationally but also internationally on a highly competitive market. Such a development can only be sustainable if breeding programs include a broad range of economically important traits under various environmental conditions. The knowledge gained in recent decades on the genetics of a number of auxiliary traits important for the functionality of cows has provided new opportunities. These assume though that you have accurate registration of all breeding records to get correct pedigree information, and that you have the ability to compare bulls for all traits across AI studs and nations.

Computerized AI records – basis for genetic studies and fertility improvement

In early days of AI activities they were handled by special AI organizations with technicians responsible for reporting of all inseminations for both administrative reasons and for the needs to follow up the fertility records of individual bulls. Simple measures, such as percentage of Non-Return Rate (NRR) within certain intervals after the insemination, were effectively used to monitor the fertility of AI bulls. Two important developments have followed and which have had dramatic impact on the opportunities for an effective AI service as a basis for not only a continuous improvement of fertility but also for providing the information necessary to automatically construct pedigree records of all recorded animals.

The first development referred to is the integration of AI records with milk-recording information and from other sources of information such as disease records, conformation classifications, slaughter data etc. (Figure 1). The greatest advantage of such an integration of

AI data with the other sources of information is that it can automatically provide the pedigree information needed for genetic studies of all traits recorded, i.e. production, conformation, calving traits, fertility etc. and the genetic evaluations of these traits. Organizations involved in dairy cattle production including AI and milk-recording

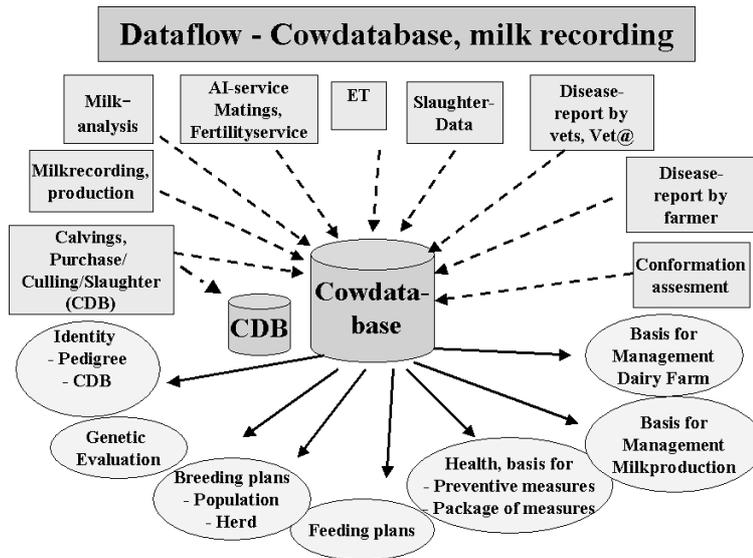


Figure 1. Example of an integrated cow data base including AI records (from Philipsson et al., 2005).

merged in Sweden already in the 1960's enabling both computerization and a successive integration of data from all sources. This development was early followed in the other Scandinavian countries and made genetic studies of cow fertility and its relationships to other traits possible already 2-3 decades ago. Today such integrated cow information systems are available in many countries.

The role of an integrated data base for research and genetic evaluations can be illustrated as in Figure 2 showing the principal relationship between recording schemes delivering relevant animal data and the continuous feed-back from research for improvement of such practical applications as genetic evaluations and use of the results for selection.

The value of an integrated data base containing the information as envisaged above depends on the amount of data and the correctness of the information. In the Swedish case 87% of all dairy cows are recorded and about the same number of animals is

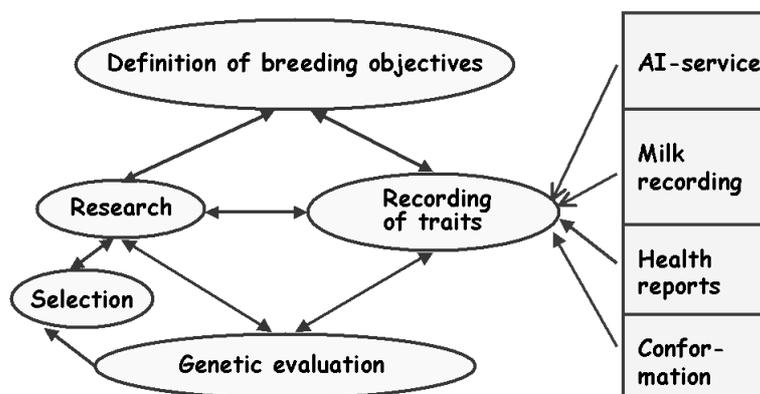


Figure 2. Interactive parts of a breeding programme.

used with AI. Thus, very good opportunities are given for research as well as for efficient application of results for e.g. management at herd and company levels and for genetic evaluations.

The second development refers to the restructuring of the AI organizations leading to fewer inseminations by employed technicians in favour of more do-it-yourself inseminations by the herdsmen. This development easily leads to less accurate or incomplete recording of inseminations, which may seriously hurt the opportunities to monitor individual bull's fertility as well as the completeness of pedigree recording in the herds.

Fertility – a complex of interacting traits...

The interaction of a number of traits at the endocrinology and morphology levels constitute the cow fertility as measured in a pregnancy following successful heat detection and insemination. The complex of fertility traits as can be measured in various ways can be divided into the following three categories:

1. Ability of the virgin heifer to show estrus with visible heat signs
2. Ability of the cow to resume the reproductive cycle post-partum and show visible heat symptoms
3. Ability to become pregnant following insemination

Fertility in virgin heifers and lactating cows must be considered as different traits as it is a difference to show good fertility when the cow is under lactation stress compared when she is not having that stress. Genetic correlations between heifer and cow fertility measures are usually around 0.6-0.7 (Roxström *et al.*, 2001).

Practical measures of fertility used for herd management as well as for genetic evaluation purposes are based on records reported by AI technicians or herdsmen that practice do-it-yourself. Most commonly used is the interval from calving to first insemination (CFI) for the second category, and no. of inseminations (NINS) or NNR as measures of pregnancy rate. Days open (DO) and calving interval (CI) are combinations of these measures, but are restricted to only cows conceiving and which therefore are somewhat selected.

New measures of estrus and heat symptoms include records of pedometers as the activity of cows increase when they are in heat. A more sophisticated method is based on regular measures of progesterone in the milk during a critical period post-partum, whereby the time of ovulation can be more accurately recorded, but at a higher cost (Pettersson, 2007).

Some of these measures may not be as easily recorded when certain interventions are practiced such as heat synchronization, having a bull free among heifers in loose-housing systems or on pasture.

... which show low heritability... but large genetic variation among progeny groups!

It is a well-known fact that fertility traits generally show low heritability. In one of the most extensive studies in recent years heritability measures were generally in the range 2-4% (Roxström *et al.*, 2001). This level of heritability has been confirmed in a number of studies comprising different countries and breeds. For international genetic evaluation of female fertility traits more than 150 heritability values are submitted for different breeds and traits, of which 80% have a value of 4% or less (Interbull, 2008). Previously it was thought also that the additive genetic variation in cow fertility was small due to both the low heritability values and the fact that non-additive genetic effects usually are important for the variation in fertility. Thanks

to the availability of AI records integrated with milk recording statistics since the early 1970-ies in Sweden it was possible to show empirically that there was a large variation in fertility measures between large progeny groups within both the Swedish Friesian and the Swedish Red cattle breeds (Philipsson, 1981). In fact it was shown that the additive genetic standard deviation for female fertility (measured as coefficient of variation) amounted to about 7%, compared to the usual 8-10% for milk production. This meant that there was a difference of 15-20% in pregnancy rate among progeny groups.

It is now undisputable that cow fertility is unfavourably correlated with milk production. This was shown already by Janson and Andreasson (1981) on Swedish data and later on confirmed in many studies. In Sweden the correlations are generally of the order 0.3-0.4, which clearly means that fertility will decline as a result of selection for production if not selection pressure is also put on fertility. Similar results have been observed for other countries and breeds and the negative correlations are of the order 0.2-0.5 (VanRaden, 2006; Jorjani, *et al.*, 2007). There is also another relationship of practical importance: cows that in classifications are considered angular or “sharp” have a genetically inferior fertility than other cows according to a study involving data from Sweden, Denmark and USA by Rogers *et al.* (1999). This means that selection according to traditional conformation classifications has led to a further deterioration of cow fertility. Such deterioration is costly. In most dairy populations fertility problems are already the most common reason of culling cows (e.g. Pryce *et al.*, 1997) indicating the necessity to apply methods for direct selection for female fertility.

The availability of fertility records, primarily based on AI records, and accurate pedigree information enabled a genetic evaluation system to be put in place in Sweden already in the mid-seventies. It was gradually improved when the BLUP procedure became available and as a result of the research conducted by Janson (1980) and Roxström (2001). The necessity to consider female fertility as an important sub-trait in the Total Merit Index (TMI), as previously developed by Philipsson *et al.*, (1975) was well demonstrated by Philipsson and Lindhé (2003). An unchanged or slightly improved fertility was shown for the SRB breed along a strong increase in production, whereas a steady decrease of the fertility was noted in the Black and White cattle due to its “holsteinization” and lack of selection for female fertility when choosing bull sires.

Today many countries apply genetic evaluations for their major dairy cattle breeds. In the last two years this development has led to the implementation of international genetic evaluations for fertility by Interbull. In the last routine evaluation (April 2008) data from six breeds originating from 20 countries, comprising up to 5 traits from each country were included in the analyses of in total 50 populations.

As a result of these international evaluations AI bulls can be compared across countries not only for production, conformation, calving traits, mastitis resistance and longevity but now also for a number of female fertility traits. As a side effect it is now also possible to monitor the genetic trends in different traits by breed on a global scale. As an example Figure 3 shows the genetic trend for a number of fertility traits of the Red Dairy Cattle breeds dominated by the Scandinavian red breeds. It is

Unfavourable correlations with production

National and international genetic evaluations for female fertility

The global genetic trend for fertility differs between breeds

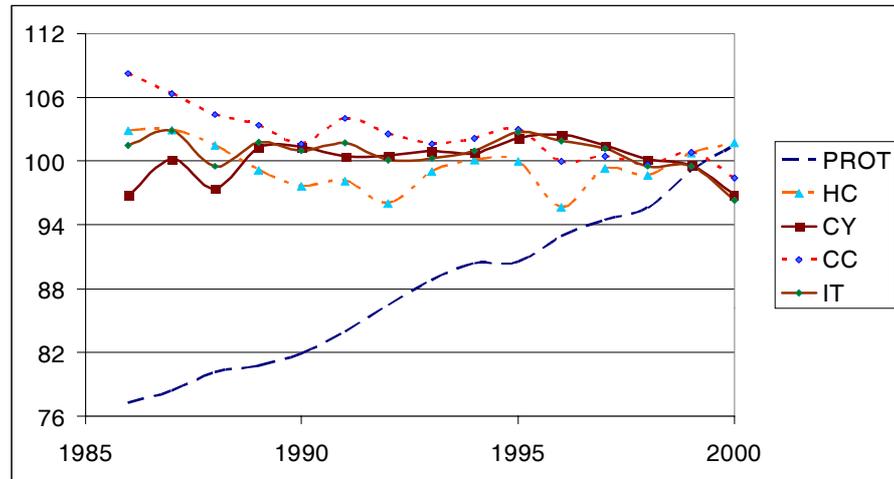


Figure 3. Genetic trends for production and fertility traits of bulls of Red Dairy Cattle populations. (PROT=Protein, HC=heifer conception, CY=Cow re-cycling ability, CC=Cow conception, IT=Interval traits).

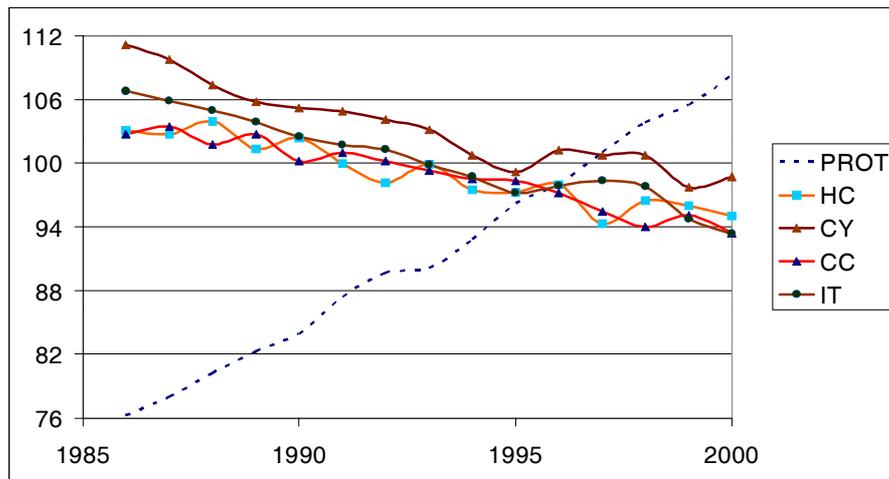


Figure 4. Genetic trends for production and fertility traits of bulls of Holstein populations. (PROT=Protein, HC=heifer conception, CY=Cow re-cycling ability, CC=Cow conception, IT=Interval traits).

obvious from this figure that fertility traits, measured as heifer's conception (HC), cow's re-cycling ability (CY), cow's conception (CC), and interval traits (IT, days open/calving interval), have been kept rather unchanged over a long period of time. At the same time a strong increase in protein yield (PROT) has taken place.

The trend for the same traits in the Holstein populations (Figure 4) gives a clear indication that fertility has seriously declined during the same period. This is the result of lacking information on breeding values for female fertility when bull sires

have been selected all over the world in this breed. Thus, the decline is a function of the unfavourable correlations with production and with some conformation traits traditionally being selected for.

It is obvious from what has been presented that cow fertility is an important trait that needs to be considered in national breeding programs as well as globally. The negative genetic trend detected for the Holstein breed globally needs to be seriously discussed and acted upon internationally. Such trends should be regularly monitored at both national and global level for all breeds in order to re-evaluate the relative weights of traits in the breeding objectives.

The opportunity to estimate reliable breeding values for female fertility of AI bulls depend heavily on the complete and accurate recording of all breeding events and calving dates. Specific considerations must be devoted to the recordings by herdsmen when they are themselves inseminating the cows. Also handling records from natural services and of synchronized heats may be worth studying in more detail in order to make best use of these and to make sure they are not messing up other information, e.g. expected calving dates, calving intervals etc. Of utmost importance is anyway that the AI service holds such a quality and price that it is the first choice of any farmer, and that these are provided with such information that they understand the needs for correct and complete records for both on-farm statistics to be used for management purposes and for the calculation of both the bull's own fertility and for estimation of breeding values for female fertility.

Female fertility in dairy cattle is made up of a complex of traits that can be indirectly measured from AI and milk-recording statistics. The heritability is low for all fertility traits but the genetic variation is still substantial as demonstrated by large differences among progeny groups in daughter fertility. There is a clearly unfavourable genetic correlation between fertility and production, indicating the needs for direct selection for improved fertility. The application of genetic evaluation systems for female fertility depends on the opportunities for accurate and complete recording of all breeding and calving dates and that all AI records are integrated with all other trait records. Additional methods for heat detection may improve future evaluation systems. The recently applied international genetic evaluations for fertility by Interbull provide new opportunities for selection of AI bulls across countries. Genetic trends in female fertility should be monitored in all breeds at both national and global level.

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Future challenges

Conclusions

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