GenoCells: individual somatic cell count of dairy cows by genotyping tank milk

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Abstract

The somatic cell count (SCC) monitoring is essential to monitor health of cows in production and to optimize milk price. GenoCells® is a revolutionary technology to determine with a high accuracy the SCC of each cow directly from the DNA analysis of a sample of tank milk. This technology is based on the correspondence between animal genotypes (= genetic identity) and presence of their DNA via their somatic cells in the mixing milk sample. Therefore, the tank milk genotype allows obtaining the SCC for each cow.

The SCC results from this disruptive genomic method are as accurate as traditional flux cytometry method.

GenoCells® is more practical than a classic milk control operation because only one tank milk sample is necessary. This method can be performed several once in a year and in less expensive by 20% compared to the classic method. The farmer can also get access to the genomic indexes to make selection schemes.

With this method, a quick decision regarding SCC can be performed and lead to a better economic impact. GenoCells® represents also a disruptive method to manage the SCC of the herd worldwide.

Keywords: cells, dna, milk tank, individual SCC.

Introduction

Monitor cells in farm is a big challenge for farmers both to optimize milk price and to have healthy cows. The current monitoring schema of cells by milk recording organization (MRO) presents some limits: low frequency and few flexibility notably in milking automation system where milk sampling is very restrictive. Blard *et al.* (2012) proposed a method to identify cows with subclinical mastitis by the analysis of tank milk. This method uses a linear model to determine the contribution of each cows to the DNA found in tank milk and only needs that all the cows are genotyped beforehand and that the milk yield of each cow contributing to tank be known. Few tests had been done in real conditions, so in 2017, Seenovia (formerly Clasel) initiated tests on four farms of different sizes and with different density chips to validate this approach in commercial farms. Following the first tests that were conclusive, the service GenoCells®

has been launch the 1rst of January, 2018. The main results of the tests done in farm are presented in a first part and the service as it was deployed on the Seenovia area is described in a second part.

Validation in farms

Material and methods

Before proposing this new service to breeders, a trial was conducted in four dairy farms to validate the method in real conditions. The smallest herd had 47 cows in lactation and the biggest 127. In total, 48 bulk samples were taken on the 4 farms between December 2015 and June 2017. The sampling was done on one or two milkings with usual operators. For each cow, SCC was determined by both the traditional method (analysis of individual sample by Fossomatic FC 6000 or FT+ and the new method GenoCells®.

Results

For all the farms, the determination of the cell counts is sufficiently accurate to be used in routine. Figure 1 presents the results of a farm of 53 dairy cows. The coefficient of determination was of 0.99 between Foss SCC and GenoCells SCC. By zooming on the 0-400 000 cells area, the coefficient of determination was of 0.97 (Figure 2).

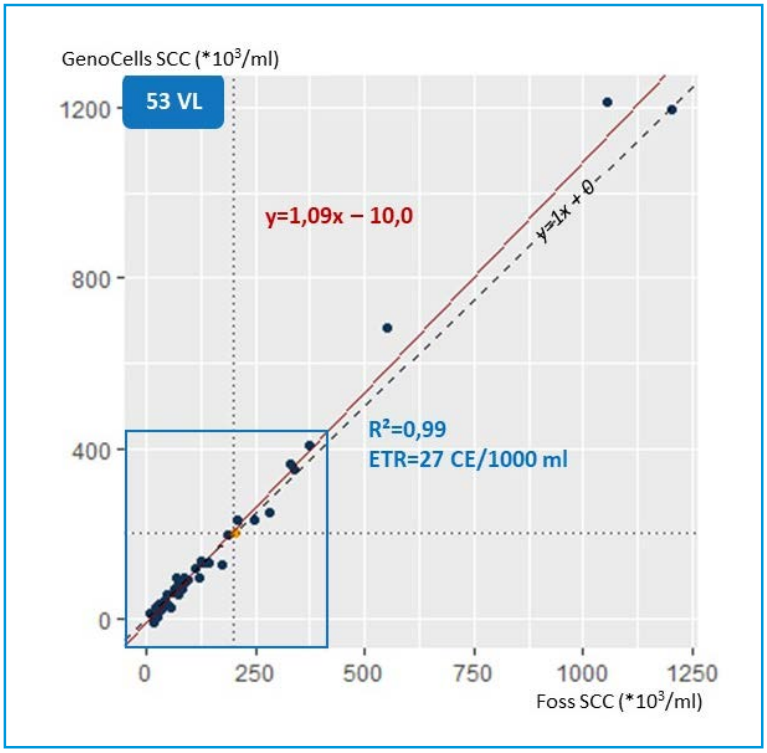

Figure 1. Results obtained with 53 dairy cows.

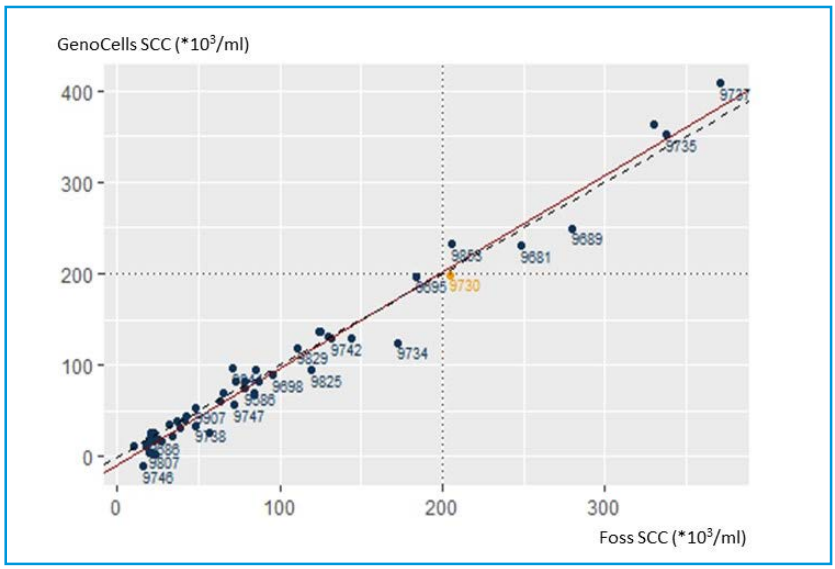

Figure 2. Zoom on the figure 1.

Deployment of the service

The results obtained during the testing phase lead to deploy GenoCells® from the 1rst of January 2018. In practice, four steps can be distinguish: sampling in farm (cows and bulk milk), laboratory analysis, calculation and result restitution (SCC and index).

Sampling in farm

The use of GenoCells® requires that all cows of the farm be genotyped. If the cow has never been genotyped, a cartilage sample is taken otherwise the genotype is retrieved from the breeding company.

To obtain individual SCC a milk sample is directly taken into the tank and the farmer has to indicate via a web interface what volume of milk has been brought to the tank by each cows. To simplify the declaration, milk yields are automatically recovered for connected milking parlors (automatic milking system, electronic milk meter). For conventional milking parlors, a first estimate of the milk yield of each cow is made from the data indicated by the farmer (bulk volume, number of milking, number of cows) and curve lactation models. The farmer can then individually correct the values if he finds significant differences. In addition to the milk yield declaration the farmer indicates via the web interface that a sample has been done and the sample is collected under 12H by a firm specialized in the logistic of fresh products. Let's keep in mind that the analisis could be done directly ont the milk payment sample.

Laboratory analysis

Genotyping process is performed using the Infinium Beadchip HTS Bovine from Illumina (USA). The first day of genotyping corresponds to the DNA amplification step. The second day corresponds to the DNA fragmentation and hybridization steps. The third day corresponds to the scanning and analysis steps.

The first day of genotyping, bulk milk samples are analysed by Fossomatic FC or FT+ to determine the total cells of bulk sampling.

Calculation and results

Once the genotype of tank milk is known, statistical analysis allows determining the cellular responsibility of each cow in the tank. This result is used to calculate individual cell counters by using the following formula: (% DNA of each cow / % milk of each cow in the bulk)*Bulk cell count

To sum up

Each week, around 800 samples are genotyped. The average interval between bulk sampling and restitution of the results is of 4 to 6 days according to the day of milk sampling.

In addition of SCC results, the farmers have access to genomic indexation results.

Conclusion and perspectives

With GenoCells, it is possible to monitor the cells:

- At herd level via the cellular responsibility
- At individual level by SCC.

The first approach is very interesting in the case of big herds (>200-300 dairy cows) by underlying only cows with high cellular responsibility. The second one interests farmers with few dairy cows.

List of References

Blard, G., Z. Zhang, W. Coppieters and M. Georges 2012. Identifying cows with subclinical mastitis by bulk single nucleotide polymorphism genotyping of tank milk. J. Dairy Sci. 95: 4109-4113.

Perrin, F. and Marg-Haufe B., 2019, A revolution in milk sample analysis, TECAN Journal 1/19, 12-13.