

Abstract of Mariusz Meller's doctoral dissertation entitled:

„An analysis of the selected functional traits in genomic evaluated half-sisters and sisters from bovine maternal lineages”

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The world has seen enormous production and genetic progress in dairy cattle breeding for three decades. Skilful implementation of genomic analysis and embryo transfer can maximize the benefits that come from improving functional and production traits. The functional traits, such as fertility, somatic cell count, conformation and health, have an indirect impact on the level of production. These traits are significantly involved in the profitability and production of dairy cattle.

The objective of the studies was to determine a relationship between the levels of functional and production traits and the values of chosen selection subindices for genomic analyses cows in Poland and the USA. The applicative objective was to demonstrate the validity of breeding maternal lineages based on national and American genomic analyses of young females, with the following wording of the objective: to demonstrate a potential for more efficient breeding of maternal lineages and expression of selected production and functional traits.

The studies were carried out in 2019-2021 on Dobrzyniewo and Mrozowo farms, owned by Dobrzyniewo Horse Farm (Stadnina Koni w Dobrzyniewie Sp. z o.o.), with 598 females representing 7 maternal lineages (326 cows and 272 heifers), Polish Holstein-Frisian cattle, black and white variety with the genomic estimated breeding values in Poland and the USA. Milk yield and milk composition, including SCS, and basic reproduction parameters were analysed for a maximum of three completed lactations. Dairy strength and conformation were also evaluated during 1st lactation between days 15 and 300 after calving. The reasons for culling were also investigated. The data for the above-mentioned analyses were sourced from the SYMLEK database. Moreover, a thorough analysis of the genomic breeding values for the production and functional traits was carried out for the individual animals within the maternal lineages and between the lineages (a comparison of Poland and the USA).

Based on the studies and the results, it was concluded that all maternal lineages showed high production potential, and the milk yield values were positive and analogous between the compared countries. The actual milk yield in the study period for the maternal lineages with lower daily milk production coincided with lower estimated breeding values for the same period. However, the cows with higher milk yields demonstrated higher productivity yet the respective ranking was not unequivocal, which would suggest an interaction between the genotype and the environment. Regarding the estimated breeding values in the USA, it was discovered that coinciding with the increase in milk yield breeding values, the genomic analysis contributed to an improvement of the genetic tendency for Heifer Conception Rate (HCR) and Profitable Lifetime Index (PLi) expressed in months, which is a very beneficial tendency, concerning the unfavourable trend for the discussed functional traits in HF cattle population that has been seen for many years.

The author's studies demonstrated that the calving interval for the evaluated maternal lineages reached the desired values, but the estimated tendency confirmed that the increase in production resulted in longer calving interval due to a longer calving–conception interval, with a similar number of days open.

Furthermore, the estimated fertility values for cows (CRk vs. CCR, for Polish and American estimates, respectively) helped to demonstrate that according to the national genomic evaluation, only the cows from lineage No. 5 had estimated CRk values below 100. As far as the American genomic analysis is concerned, all investigated maternal lineages showed negative estimated values. It illustrates that the breeding associations in the USA have implemented the above-mentioned trait in the breeding program much earlier, and the American HF cattle population demonstrates more beneficial values of the discussed trait.

The estimated conception values were similar for the two countries and corresponded to the real numbers. For the cows included in lineage No. 2, 4 and 3, successful insemination consumed from 1,59 to 2,08 semen units during the first three lactations. It was the lowest semen consumption among the investigated maternal lineages; however, these cows demonstrated the best calving–conception interval and calving interval values and had the best estimated breeding values for CRk and CCR. The cows in lineage No. 5 had the lowest estimated and actual CRk and CCR values among the investigated maternal lineages and demonstrated the worst calving–conception interval values, consuming the highest number of semen units (2,68)

per successful insemination. There was a correlation between the above-mentioned traits and milk somatic cell score (SCS). The animals from lineages No. 4 and 2 produced milk with the lowest SCS and had the shortest calving–conception interval, 80,6 and 85,3 days respectively. The cows from lineage No. 7 had the highest SCS values (299 450 cells/mL) and demonstrated one of the longest calving–conception intervals of 120,4 days.

The estimated breeding values for milk somatic cell score (LKS vs. SCS, for Polish and American estimates, respectively) were similar for the two countries.

Furthermore, it was found that the anatomical characteristics of the udder impacted udder health. The estimated breeding values for the investigated materials in Poland and the USA were generally analogous, and the real numbers corresponded to the estimated values, which was confirmed by analysing the extreme maternal lineages. The anatomical udder defects were the reason for 7,0% of culling rates. However, during the study period, the main causes of culling were reproductive issues (21,6%), foot and leg problems (17,0%), metabolic conditions (12,3%), and mastitis (10,5%).

The studies indicate a need for further improvements in functional traits and the selection of excellent animals through genomic analysis since this helps achieve more efficient breeding of a maternal lineage, which was demonstrated in the author's studies. Within the investigated population, the highest percentage of animals born following ET was found in lineage No. 4 (57,14%) and 6 (44,78%). The identification of excellent animals with genomic tests and intensive implementation of embryo production resulted in maximizing breeding progress within these lineages. Of the animals in lineage No. 7, only 18,18% were produced with the above-mentioned reproduction technology; however, among the heifers, none of them was born with ET. This maternal lineage demonstrated the lowest estimated breeding values both in Poland and the USA, which had an impact on breeding decisions.

Of all investigated lineages, the maternal lineage No. 4 (Barbie) showed the most efficient estimated breeding values for many traits both in Poland and the USA. The above-mentioned relationship translated into a completely different profile of the given study group than the other lineages as far as fertility, conformation and udder health are concerned both for cows and heifers. Transferred genetics for the functional traits from the mother onto a daughter substantiates the need for maintaining maternal lineages.

Furthermore, the actual values recorded during dairy strength assessments confirmed the estimated breeding values in a real-life scenario. Selection and breeding efforts discussed in the PhD thesis indicate a potential for efficient breeding of the maternal lineage and warrant maintaining the identity and distinct features of individual maternal lineages.