REVIEW ON GENOMIC TESTING OF DAIRY COWS, IMPORTANCE AND ADVANTAGES

Dănuț Nicolae ENEA[1], Gheorghe Emil MĂRGINEAN[1], Aurelia DEFTA (OSMAN)[1], Nicoleta DEFTA[1], Andrada Elena MOISE[1], Hippolyte MEKUIKO WATSOP[2], Livia VIDU[1]

[1]University of Agronomic Sciences and Veterinary Medicine of Bucharest,
59 Marasti Blvd, District 1, Bucharest, Romania
[2]University of Ngaoundere Cameroon, School of Veterinary Medicine and Science,
P.O Box 454 Ngaoundere, Camerron

Corresponding author email: liviavidu@gmail.com

Abstract

One of the main livestock productions is represented by the dairy sector. The progress made over time being significant, but constrained by a limiting factor, the interval between generations (5 years). An excellent tool that helps make progress by reducing the time period until performance is manifested is genomic testing. This provided the necessary means to constantly improve genetics in production, fitness and conformation of dairy cows. Through its implementation, important changes are occurring in this branch of animal husbandry. This paper aims to review the most important aspects regarding the genomic testing by analyzing a significant number of works on this topic Based on genomic testing, the farmer can take effective decisions about herd improvement, to verify parentage or to identify bacterial strains associated with particular disease outbreaks.

Key words: dairy cows, genomic testing, milk production.

INTRODUCTION

There is a high demand for animal products at the moment and dairy sector is one of the main suppliers. This sector is growing fast, world milk production is expected to increase by 177 million tons by 2025 (FAO, 2016). At this moment, this production is composed of: 81% cow, 15% buffalo, and 4% for goat, sheep and camels combined (OECD | FAO, 2023). Milk is a complex food consisting of proteins, fats, lactose, vitamins, and minerals (Nicklas et al., 2009; Vidu et al., 2010; Čuboň et al., 2012; Keresteš, 2016; Mihai et al., 2023). Dairy proteins have been suggested to help reduce adipose tissue (visceral fat) and body weight (Mirmiran, 2005; Teegarden, 2005; Zemel, 2005; Vergnaud, 2008). These effects have been observed in both healthy individuals and those who are overweight (Rosell, 2006; Faghih, 2011; Josse, 2011; Abargouei, 2012; Sanders, 2012) or have diabetes (Liu, 2006; Shahar, 2007). In addition to casein, whey proteins appear to be particularly effective (Pal, 2010; Sousa, 2012) with effects mediated by mechanisms such as increased satiety and reduced appetite (Sousa, 2012). In accordance

with global trends, milk and dairy products are frequently consumed food products, in Romania (Defta et al., 2023). Our country having some traditional products made from milk (Șuler et al., 2021).

To produce the amount of milk needed for human consumption, dairy farmers are constantly striving to do more. However, the situation is more complex than it appears at first glance. Total milk production can be increased by either increasing the number of cows or improving individual production through genetic progress. The most convenient option appears to be the first one, as it provides results in a relatively short amount of time. However, it has the undesirable effects, increasing gas emissions (emission = emission factor × number of cattle) (Wójcik-Gront, 2020), respectively the demand for more feed to sustain them. Farmers often rely on increasing genetic progress, the disadvantage being time, as cows have long intervals between generations, more than 5 years in dairy cattle (Jonas and de Koning, 2015). Genomic testing has been introduced to facilitate the reduction of the generation interval in dairy cows. In 2008, the first genomic evaluation of

dairy cows was conducted by the USDA (United States Department of Agriculture), however, the service only became officially available a year later for the Holstein, Jersey and Brown breeds (Wiggans, 2011). Since then, genomic testing has been in use in many countries in order to determinate the genetic value (Loberg and Dürr, 2009). In the Netherlands, the Illumina chip was developed on the basis of SNPs (De Ross et al., 2009), and the following year, BovineSNP50 (Interbull, 2010). Canada collaborated with the USA in the development of the genomic evaluation system, based on BovineSNP50 (Wiggans et al., 2009a), the programme was officially launched in 2009 (Van Doormaal et al., 2009). In the same year, a genomic evaluation system was implemented in Germany. (Reinhardt et al., 2009). New Zealand has also adopted the BovineSNP50 chip and subsequently promoted its use for obtaining bulls that have been genomically tested. In 2012, in Lincoln, UK was developed *GeneSeek Genomic Profiler* (GGP), for dairy cattle (Wiggans et al., 2012). France has been using a marker-assisted selection programme since 2001, in 2008 started to use a small number of SNPs for evaluation, but in an unofficial setting (Ducrocq et al., 2009). The fact that many states embraced genomic testing has been extremely beneficial, a large reference population is needed to have a high predictive value (Goddard and Hayes, 2008; Hayes et al., 2009a). Accurate prediction based on genomic testing was possible in large populations such as Holsteins, but not in smaller populations such as Danish Jerseys.

Tissue samples, blood or hair follicles must be taken from the animals to be tested in order to perform genomic testing.
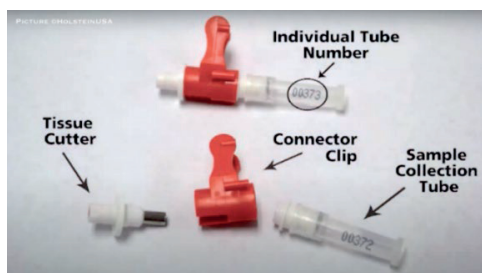

Figure 1. Tissue sampling unit and its component parts
(Source: https://www.holsteinusa.com/)

As can be seen in the previous Figure 1, the sampling unit is not at all complicated, with only three component parts. It is attached to a pair of pliers similar to those used for earwigs and a single puncture is made in the ear to collect a sample of ear tissue.

The information provided by genomic testing also enables:
- ranking of the animals according to their productive/reproductive performance;
- verification of the genealogy;
- avoidance of inbreeding;
- establish of nominated pairs;
- the opportunity to use the highest quality sexed semen on the most valuable females identified through genomic testing.

MATERIALS AND METHODS

In order to carry out the present paper 41 bibliographic sources were consulted, all from specialized literature. The studies utilised for this review have been accessed from databases such as Google Academics, Journal of Dairy Science, Frontiers, Science Direct, Springer.

In this paper, the research methods used were the observation, analysis, graphical interpretation of data regarding the advantages obtained by farmers in case of genomic testing of the herd and how the genomic testing favors genetic progress.

RESULTS AND DISCUSSIONS

In the breeding of dairy cattle, selection programmes are of overwhelming interest. While improving the quality and quantity of milk, researchers have also studied the possibility of reducing the interval between generations. A study on this topic was also carried out by Jonas and de Koning in 2015. It is a well known fact that sires play a crucial role in the genetic enhancement of a population. They are having more offspring that a cow, especially if they are used in artificial insemination (AI), situation when their impact on population is even stronger (Gerrits et al., 2005; Funk, 2006).

The main disadvantage that is staying in front of genetic progress in dairy cows sector, as we mention before is the length of the interval between generations. To make an accurate

estimate, time is needed for phenotypes to manifest and be evaluated (Schefers & Weigel, 2012). In addition to the extended duration, .

farmers also face the expenses of maintaining a large herd over an extended period (Figure 2).
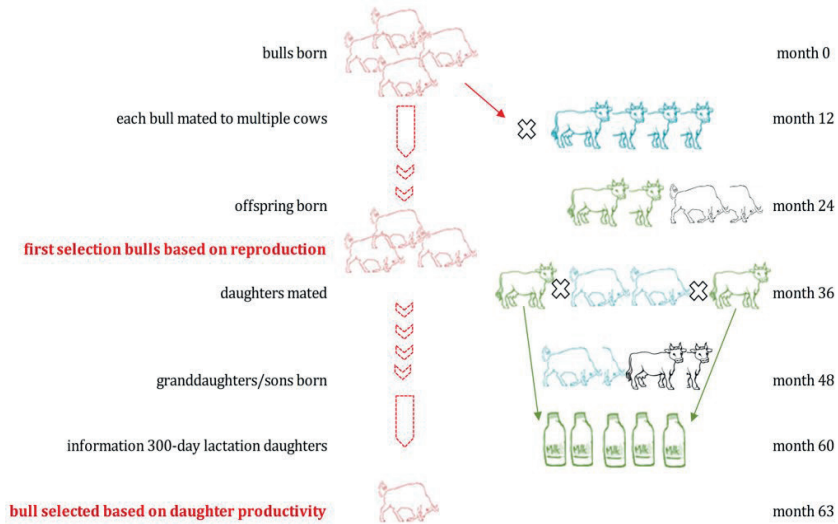

Figure 2. Selection candidates in traditional breeding at dairy cattle (Source: Jonas & de Koning, 2015)
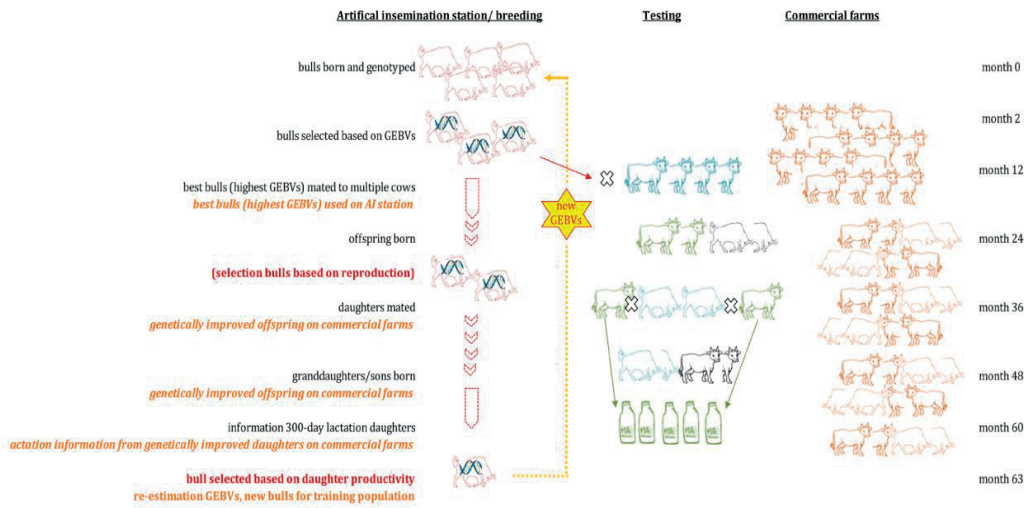

Figure 3. Genomic Selection in dairy cattle (Source: Jonas & de Koning, 2015)

As demonstrated in the previous figure, the bulls - selection candidate (born at month 0) are mated around the age of 12 months with multiples cows. After that, another 48 months must pass for daughters to record the first information regarding the milk yield (to reach puberty, to be mate and to finish the first lactation). Three months later, we obtain the estimated breeding value (EBV) of the bulls, thus obtaining a sire tested on the offsprings.

After performing genomic tests, the effects of each marker are estimated and summarised into genomic estimated breeding values (GEBV). These values can be used to rank the animals and to make a selection. The main advantage is that GEBVs are available from the month 0, in

a training population. The bulls selected based on GEBV (with the highest values) are mated in order to multiple cows, in commercial farms. This action, correlated with artificial insemination favours genetic progress. As can be observed in Figure 3, the genomic selection reduces the generation interval from 5.5 years to less than 2 years, a significant reduction, if the selection is realised according to the figure.
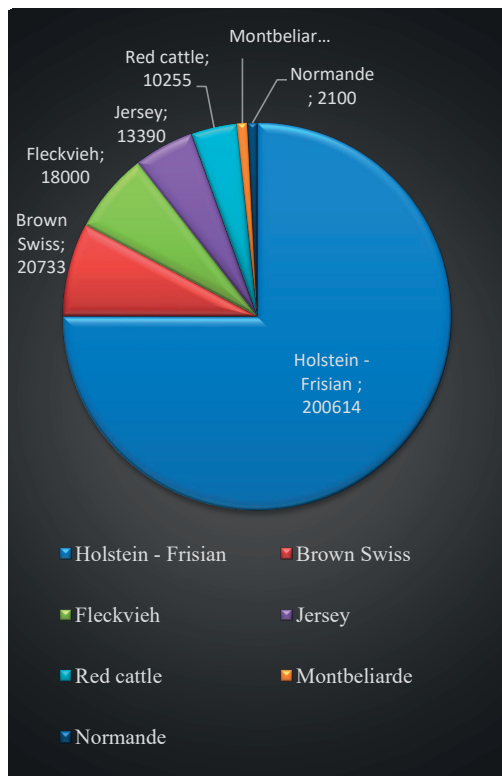

Figure 4. Numbers of bulls active in genomic selection breeding programs (Source: Thomasen, 2013)

According to Figure 4, the largest number of bulls active in genomic selection are Holstein - Frisian, followed by Brown Swiss and Fleckvieh.

To enhance genetic progress, genomic testing is useful not only in reducing the interval between generations but also by increasing reliability. The formula of genetic progress is:

$$\Delta_g = \frac{i \times r \times \sigma_g}{L}$$

Δ_g – genetic progress;

i – selection intensity;
r – reliability (accuracy of selection);
σ_g – genetic standard deviation;
L – generation interval.

Through genomic testing, companies such as Neogen Genomics are confirming the parentage. If we do not have this crucial information, we will miss the opportunity to enhance the accuracy of herd's breeding values and we will not be able to accelerate the genetic gain. If the exact parentage of an animal is unknown, data on its individual values can only be obtained by recording the performance of animals by measurements throughout its lifetime.

According to Neogen Genomics, the reliability varies as follows:
  ➢ a calf with parentage known is having a *parentage average* (PA) of reliability 27% (per trait different);
  ➢ a calf with unknow sire has a PA <21% reliability;
  ➢ a calf with incorrect parentage has a PA of 0% reliability;
  ➢ PA + own production records is approximative 50%;
  ➢ an animal genomic tested without genotyped parentage has < 70% reliability;
  ➢ an animal genomic tested with correct parentage has > 70% reliability;
  ➢ a daughter proven bull with thousands of offsprings has a reliability > 90-99%.

In order to increase the reliability in genomic testing are combined also information regarding the siblings, progenity.

The benefits of using genomic testing do not stop there; the same company, Neogen, also provides information on fat production, protein production, somatic cell score, pregnancy rate. As can be observed in the previous table, the key traits are providing a lot of data, only based on them the farmer can easily take a decision regarding if an animal is eligible for selection. Among the essential information (milk yield, fat yield, protein yield), mention before we can notice that data regarding the profit that an animal is estimated to make it, along with a prediction of its capability to survive and the most important reproduction traits.

Table 1. Health traits resulted from genomic test (Source: https://www.neogen.com/en-gb/dairy-genomics)

No.	Trait	Description
1	Cow Livability (LIV)	animals that leave the heard due to death
2	Displaced Abomasum (DAB)	the expected resistance of an animal's offspring to displaced abomasum
3	Hypocalcemia (MFV)	the expected resistance of an animal's offspring to hypocalcemia
4	Ketosis (KET)	the expected resistance of an animal's offspring to ketosis
5	Mastitis (MAS)	the expected resistance of an animal's offspring to clinical mastitis
6	Metritis (MET)	the expected resistance of an animal's offspring to metritis
7	Retained Placenta (RPL)	the expected resistance of an animal's offspring to retained placenta

Table 2. Health traits resulted from genomic test (Source: https://www.neogen.com/en-gb/dairy-genomics/)

No.	Trait	Description
1	Sire Calving Ease (SCE)	the ability of calves of a particular sire to have an unassisted birth
2	Heifer Conception Rate (HCR)	the percentage of inseminated heifers that become pregnant at each service
3	Cow Conception Rate (CCR)	the percentage of cows that become pregnant at each service
4	Daughter Stillbirth	the ability of a cow, or daughters of a bull, to have a live calf that survives past 48 h
5	Sire Stillbirth	the ability of calves from a particular sire to be born live and survive past 48 h
6	Gestation Length (GL)	measures the difference in length of gestation

From Tables 1 and 2, it is evident that genomic testing provides to the farmers a wide range of valuable information. However, the dairy breeder also receives data on conformation traits. This includes stature, feet and legs, rump, udder attachment, udder cleft etc. Additional information, such as A2 beta casein or Bovine Viral Diarrhea Virus, can be provided. A2 beta casein is a protein less common than A1, there are some studies that consider it more beneficial to the human body than A1 so in consequence this milk is having a higher price and more selected by the processors. A2 beta casein is a co-dominant trait, meaning both variants are fully expressed. Nevertheless, a herd can be selected for A2 milk rapidly, even if the cows are all A1/A1 and we will use sires only A2/A2:

- in the first generation all animals will be A1/A2;
- in the second generation approximately 50% of the animals would be A2/A2;
- in the third generation
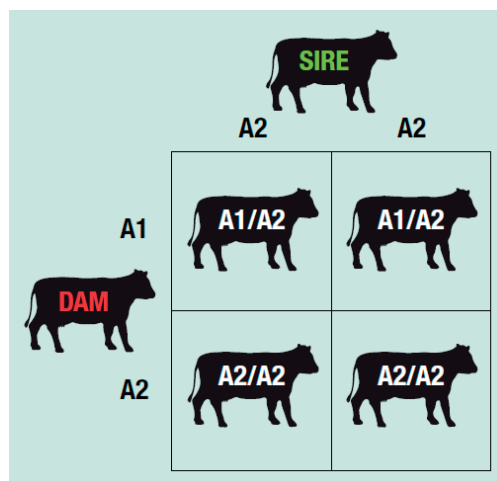- approximately 75% of the animals would be A2/A2 (Figure 5).

Figure 5. Selection for A2 milk

Bovine Viral Diarrhea Virus (BVDV) represents one of the most significant diseases dairy farmers face, that can cause reproductive disorders and increase mortality. So, the detection of persistently infected animals should be carried out as early as possible in order to eliminate them from the herd, which can be achieved by genomic testing.

Appears, of course, the question if the young genomic bulls are not inferior compared to the proven bulls. In order to answer to this question, de Roos and his collaborators made an study in 2011, entitled "*Effects of genomic selection on genetic improvement, inbreeding, and merit of young versus proven bulls*". The study shows that genomic selection will increase the rate of genetic gain and will not adversely affect the rate of inbreeding per generation. More precisely, using young bulls

without their own performance or progeny, as parents doubled the rate of genetic progress, while the percentage of inbreeding per generation remained the same as for a traditional BLUP scheme (de Roos et al., 2011).

A similar study was conducted by Pryce et al., 2010, they analysed various selection models incorporating genomic selection, in order to determine population response through genetic progress. the conclusions recorded by them are the following:

- a higher response rate was recorded in all tested breeding schemes compared to conventional schemes;
- where GEBV were available from foreign countries, nucleus schemes and "worldwide" schemes registered the highest responses to selection;
- when juvenile females were used greater responses in reproductive technologies were achieved;
- the greatest gain in genomic selection (in dairy cows sector) is achieved by reducing the generation interval;
- in some genomic selection schemes, the inbreeding level decreased by 50%;
- the cost of efficiencies using genomic selection schemes are considerably higher than progeny-testing schemes.

One year before, in 2009, Koning et al., made an economical evaluation of genomic breeding programs. They concluded that by replacing conventional testing with genome – wide selection economic efficiency and an annual increased genetic gain is possible. In the study various breeding scenarios for German Holstein population were realised and showed that a doubling of discounted profit is possible by using genomic selection compared to traditional selection scheme.

Research on the benefits of genomic evaluations extends beyond the current scope, with studies exploring their potential future contributions. Recent studies, such as the one undertaken by McWhorter et. al., in 2023, have addressed the selection of heat stress-resistant dairy cows, specifically Jersey and Holstein, based on GEBV. The study showed that genomic predictions can be a useful tool for selecting high - yielding animals in high - temperature and high - humidity environments.

CONCLUSIONS

Summarizing the data of all the articles consulted for the present review, the following conclusions were summarized:

1. The bulls selected based on GEBV favours genetic progress;
2. Genomic selection results in a noteworthy decrease in the generation interval;
3. The confirmation of parentage is possible through genomic testing, fact that improves the accuracy of selection for a given trait;
4. The farmer can receive data regarding production, reproduction and health of animals, so that management decisions can be made more easily;
5. The genomic selection will not affect the inbreeding level, on the contrary, there are studies that prove the opposite and will increase the genetic progress;
6. Breeding programmes that utilise genomic selection are more cost-effective than traditional breeding programmes;
7. Studies on the benefits of genomic testing continue to be conducted, with new opportunities for its use being discovered.

REFERENCES

Abargouei, A.S., Janghorbani, M., Salehi-Marzijarani, M., & Esmaillzadeh, A. (2012). Effect of dairy consumption on weight and body composition in adults: a systematic review and meta-analysis of randomized controlled clinical trials. *International journal of obesity, 36*(12), 1485-1493.

Čuboň, J., Haščík, P., & Kačániová, M. (2012). *Evaluation of raw materials and foodstuffs of animal origin*. Nitra, Slovak Republic: Slovak University of Agriculture in Nitra, 381.

De Roos, A.P.W., Schrooten, C., Veerkamp, R.F., & Van Arendonk, J.A.M. (2011). Effects of genomic selection on genetic improvement, inbreeding, and merit of young versus proven bulls. *Journal of Dairy Science, 94*(3), 1559-1567.

De Roos, A., Schrooten, C., Mullaart, E., Van der Beek, S., De Jong, G., & Voskamp, W. (2009). Genomic selection at CRV. *Interbull Bulletin*, (39), 47-47.

Defta, N., Vidu, L., Mihai, R., Dragomir, N., Posan, P., & Oprea, I. (2023). Study on the dynamics of cattle livestock, milk production and fresh dairy products in Romania between 2016-2020. *Scientific Papers. Series D. Animal Science, LXVI*(2), 465-470.

Ducrocq, V., Fritz, S., Guillaume, F., & Boichard, D. (2009). French report on the use of genomic evaluation. *Interbull workshop on genomic selection*, 39, 17-22.

Faghih, S. H., Abadi, A. R., Hedayati, M., & Kimiagar, S. M. (2011). Comparison of the effects of cows' milk, fortified soy milk, and calcium supplement on weight and fat loss in premenopausal overweight and obese women. *Nutrition, metabolism and cardiovascular diseases, 21*(7), 499-503.

Funk, D. A. (2006). Major advances in globalization and consolidation of the artificial insemination industry. *J. Dairy Sci., 89,* 1362–1368. doi: 10.3168/jds.S0022- 0302(06)72203-2.

Gerrits, R.J., Lunney, J.K., Johnson, L. A., Pursel, V.G., Kraeling, R.R., Rohrer, G.A., et al. (2005). Perspectives for artificial insemination and genomics to improve global swine populations. *Theriogenology, 63,* 283–299.

Hayes, B.J., & Goddard, M.E. (2008). Prediction of breeding values using marker-derived relationship matrices. *Journal of animal science, 86*(9), 2089-2092.

Hayes, B.J., Bowman, P.J., Chamberlain, A.C., Verbyla, K., & Goddard, M.E. (2009). Accuracy of genomic breeding values in multi-breed dairy cattle populations. *Genetics Selection Evolution, 41,* 1-9.

Jonas, E., & Koning, D. J. D. (2015). Genomic selection needs to be carefully assessed to meet specific requirements in livestock breeding programs. *Frontiers in genetics, 6,* 49.

Josse, A.R., Atkinson, S.A., Tarnopolsky, M.A., & Phillips, S.M. (2011). Increased consumption of dairy foods and protein during diet-and exercise-induced weight loss promotes fat mass loss and lean mass gain in overweight and obese premenopausal women. *The Journal of nutrition, 141*(9), 1626-1634.

König, S., Simianer, H., & Willam, A. (2009). Economic evaluation of genomic breeding programs. *Journal of dairy science, 92*(1), 382-391.

Liu, S., Choi, H.K., Ford, E., Song, Y., Klevak, A., Buring, J. E., & Manson, J. E. (2006). A prospective study of dairy intake and the risk of type 2 diabetes in women. *Diabetes care, 29*(7), 1579-1584.

Loberg, A., & Dürr, J. (2009). Interbull survey on the use of genomic information. *Interbull Bulletin*, (39), 3-3.

McWhorter, T. M., Sargolzaei, M., Sattler, C. G., Utt, M. D., Tsuruta, S., Misztal, I., & Lourenco, D. (2023). Single-step genomic predictions for heat tolerance of production yields in US Holsteins and Jerseys. *Journal of Dairy Science, 106*(11), 7861-7879.

Mihai, B., Posan, P., Marginean, G.E., Alexandru, M., & Vidu, L. (2023). Study on the trends of milk production and dairy products at european and national level. *Scientific Papers. Series D. Animal Science, LXVI(1)*, 309-316.

Mirmiran, P., Esmaillzadeh, A., & Azizi, F. (2005). Dairy consumption and body mass index: an inverse relationship. *International Journal of Obesity, 29*(1), 115-121.

Nicklas, T. A., O'Neil, C. E., & Fulgoni, V. L. (2009). The role of dairy in meeting the recommendations for shortfall nutrients in the American diet. *The Journal of the American College of Nutrition*, 28(1), 73-81. http://doi.org/10.1080/07315724.2009.10719807

OECD/FAO (2023), OECD-FAO Agricultural Outlook 2023-2032, *OECD Publishing*, Paris, https://doi.org/10.1787/08801ab7-en.

Pal, S., Ellis, V., & Dhaliwal, S. (2010). Effects of whey protein isolate on body composition, lipids, insulin and glucose in overweight and obese individuals. *British journal of nutrition, 104*(5), 716-723.

Pryce, J. E., Goddard, M. E., Raadsma, H. W., & Hayes, B. J. (2010). Deterministic models of breeding scheme designs that incorporate genomic selection. *Journal of Dairy Science, 93*(11), 5455-5466.

Reinhardt, F., Liu, Z., Seefried, F., & Thaller, G. (2009). Implementation of genomic evaluation in German Holsteins. *Interbull Bulletin*, (40), 219-219.

Rosell, M., Håkansson, N. N., & Wolk, A. (2006). Association between dairy food consumption and weight change over 9 y in 19 352 perimenopausal women. *The American journal of clinical nutrition, 84*(6), 1481-1488.

Sanders, T. A. (2012). Role of dairy foods in weight management. *The American Journal of Clinical Nutrition, 96*(4), 687-688.

Schefers, J. M., & Weigel, K. A. (2012). Genomic selection in dairy cattle: integration of DNA testing into breeding programs. *Anim. Front., 2,* 4–9. doi: 10.2527/af.2011-0032.

Shahar, D. R., Abel, R., Elhayany, A., Vardi, H., & Fraser, D. (2007). Does dairy calcium intake enhance weight loss among overweight diabetic patients?. *Diabetes care, 30*(3), 485-489.

Sousa, G.T., Lira, F.S., Rosa, J.C., de Oliveira, E.P., Oyama, L.M., Santos, R.V., & Pimentel, G. D. (2012). Dietary whey protein lessens several risk factors for metabolic diseases: a review. *Lipids in health and disease, 11,* 1-9.

Suler, A., Posan, P., Tudorache, M., Bahaciu, G., Nistor, L., Custura, I., & Maftei, M. (2021). Microbiological examination of telemea cheese in consumption network. *Scientific Papers. Series D. Animal Science, LXIV(1)*, 479-486.

Teegarden, D. (2005). The Influence of Dairy Product Consumption on Body Composition. *The Journal of nutrition, 135*(12), 2749-2752.

Van Doormaal, B. J., Kistemaker, G. J., Sullivan, P. G., Sargolzaei, M., & Schenkel, F. S. (2009). Canadian implementation of genomic evaluations. *Interbull Bulletin*, (40), 214-214.

Vergnaud, A.C., Péneau, S., Chat-Yung, S., Kesse, E., Czernichow, S., Galan, P., ... & Bertrais, S. (2008). Dairy consumption and 6-y changes in body weight and waist circumference in middle-aged French adults. *The American journal of clinical nutrition, 88*(5), 1248-1255.

Vidu, L., Georgescu, G., Van, I., Udroiu, A., Popa, R. A., & Popa, D. C. (2010). Studies on physicochemical and nutritional attributes of row milk for cheese buffalo. *Scientific Papers. Series D. Animal Science*, 53(1), 213-216.

Wiggans, G.R., Cooper, T.A., Van Tassell, C.P., Sonstegard, T.S., & Simpson, E.B. (2013). Characteristics and use of the Illumina Bovine LD and Gene Seek Genomic Profiler low-density bead

chips for genomic evaluation. *Journal of dairy science, 96*(2), 1258-1263.

Wiggans, G.R., VanRaden, P.M., & Cooper, T.A. (2011). The genomic evaluation system in the United States: Past, present, future. *Journal of dairy science, 94*(6), 3202-3211.

Wójcik-Gront, E. (2020). Analysis of sources and trends in agricultural GHG emissions from annex I countries. *Atmosphere, 11*(4), 392.

Zemel, M.B., Richards, J., Mathis, S., Milstead, A., Gebhardt, L., & Silva, E. (2005). Dairy augmentation of total and central fat loss in obese subjects. *International journal of obesity, 29*(4), 391-397.

*** https://www.fao.org › cc3020en_milk

*** https://interbull.org

*** https://www.neogen.com/en-gb/dairy-genomics/