

BUFFALOES AND BULLS GENETIC INDEX

This catalog, "Genetic Index of Buffaloes and Bulls", shows the results of the work carried out by the National Association of Buffalo Species Breeders (ANASB), an institution appointed by the State to create – in the interest of breeders and the community – Genetic Improvement Programs and to manage the Herd Book, for the purpose of genetic selection in the Italian Mediterranean breed buffalo.

The catalog shows the genetic indices of the tested bulls and of the buffaloes and heifers registered in the Herd Book present in the selected herds that participate in the ANASB genetic improvement program.

As illustrated in detail in this publication, the dataset for the processing of genetic indices is carried out on the entire ANASB database: the data for the genetic evaluation correspond to the analysis of the productions belonging to over a million certified lactations of 307.000 buffaloes and the analysis of approximately 124.000 animals subjected to morpho-functional evaluation. The data comes from all over the national territory.

In the catalog are published the indices of:

- All ANASB member breeders participating in the genetic improvement program.
- All bulls born since 1990 (for those born earlier, refer to the latest publication of its genetic index).
- All bulls indexed with the criteria established by the CTC of 11 December 2018 (minimum requirements: 10 lactating daughters in 3 farms, 5 daughters evaluated in 2 farms).
- All subjects alive on the date of extraction of the ANASB dataset.

ITALIAN MEDITERRANEAN BUFFALO INDEX – IBMI

The aggregate Selection Index for the Italian Mediterranean Buffalo (IBMI) aims to emphasize even more the dairy attitude of the subjects of the Italian Mediterranean Buffalo, enhancing at the same time the production levels (for example the Kg of milk) and the functional morphology (quality particularly requested by our members: having productive animals with morphological characteristics that favor their stay in the stable).

The updated weights, following the introduction of the Genetic Groups, of the individual genetic indices to build the IBMI are:

$$IBMI = 3.2 \times (1.55 \times EBV_{ARTP} + 1.45 \times EBV_{APPM} + 0.01 \times EBV_{LATTE} + 4.88 \times EBV_{GR\%} + 18.45 \times EBV_{PR\%}) + 100$$

Where EBV is the acronym for Estimated Breeding Value, which is the estimate of the genetic value of an individual for a given trait. IBMI maximizes the selection objective in which the importance of milk and yield is 45% for both, while it is 5% for the mammary system and 5% for the limbs and feet. With the use of the

IBMI, all the most balanced subjects or those who have characters that were not previously considered (such as morphology) are rewarded. For this purpose, the information relating to over 7.000 buffaloes with a tested father was extracted from the ANASB database and the genetic correlations reported in the following table 1 were calculated with these:

Table 1: Genetic correlations between IBMI's criteria and selection objectives

TRAITS	LIMBS &	MAMMARY	MILK	% FAT	% PROTEIN	YIELD
LIMBS & FEET	1,00	0,19	0,00	0,15	0,28	0,25
MAMMARY	0,19	1,00	0,29	- 0,08	0,03	-0,01
MILK	0,00	0,29	1,00	-0,55	-0,47	-0,54
% FAT	0,15	-0,08	-0,55	1,00	0,69	0,87
% PROTEIN	0,28	0,03	-0,47	0,69	1,00	0,96
YIELD	0,25	-0,01	-0,54	0,87	0,96	1,00

Observing table 1, it is clear that there is a negative genetic correlation between the two main objectives: Kg of milk and yield (-0.54). However, this correlation is not equal to 1 and therefore means that there is a space to improve both characters. The yield, as expected, is instead positively correlated with both the% of fat and the% of protein (selective criteria) but also with the limbs-feet, while it has an almost zero link with the mammary system. The knowledge of these relationships is essential to combine the different characters.

IBMI: GENETIC GROUPS

The two fundamental pillars on which any genetic improvement program is based are the data collected on farmed animals (e.g. milk production, % fat, % protein, morphological data) and information relating to their genealogy (e.g. personal data and ancestry). Through this information, the genetic indices, which represent the tools at the service of selection, can be estimated. If the starting information is incomplete, the results obtained may be over or underestimated, being inaccurate. As regards the personal information, in the case of the Mediterranean buffalo the percentage of use of artificial insemination (AI) is decidedly contained for many reasons linked to both physiological aspects, breeding techniques and organization. On the other hand, natural mating is still widely used, but this complicates the assignment of paternity which can only be done through a DNA test. We are therefore faced with a situation in which the production data is available for many animals, but a part of these does not have complete personal data. Paradoxically, only the "considered" best animals could have a complete registry certified by DNA tests but this, although important, puts the genetic evaluations themselves at risk because they are based on a selected and non-random sample. Furthermore, the possibility of using much more data, albeit with partial personal data, allows to observe all the variability of the characters of interest and therefore to obtain more precise estimates.

In any case, the absence of personal information has always been a matter at the center of the interest of those who develop genetic evaluation models, and methodological approaches have been available for decades that make it possible to "manage" the empty personal data. The approach par excellence is that of the use of so-called Genetic Groups, suggested over 30 years ago by Westell, Quaas and Van Vleck (1988), and which is based on the concept that subjects born in a certain period or from a certain territory are the result of specific selective choices and therefore "genetically different" from other subjects born in other periods or from other territories. If these differences are not taken into account, the genetic evaluation will be, as they say in the jargon, "flawed". Already used in dairy and meat cattle, the Genetic Groups take into account the selection that took place over the years and are assigned to animals with partial or missing genealogy, starting from groups that can be created with different rules (e.g. period of birth, sex, origin). Based on these considerations and in order to enhance the information collected and certified by the functional checks and morphological evaluation carried out in the Italian Mediterranean Buffalo, in the last Central Technic Committee held in Caserta on 17 September 2020, ANASB decided to include in the current model of genetic evaluation the use of Genetic Groups. This change concerns both the productive and morphological characters. Following various tests, the complete results of which will be the subject of a scientific publication, it was decided to assign a genetic group to subjects with partial or missing genealogy on the basis of the period of birth, as shown in table 2:

Table 2: Genetic Group definition in the Italian Mediterranean Buffalo

GENETIC GROUPS	DATE OF BIRTH
1	< 1986
2	1986-1991
3	1992-1997
4	1998-2003
5	2004-2009
6	2010-2015
7	> 2015

The impact of this modification on the genetic indices will depend on the "category" of the subject. In the case of AI bulls (73 authorized subjects), the effect is minimal, with a correlation between EBVs ranging between 0.98 and 0.99 (table 3). In the same table you can also see the maximum, minimum and average values for each character.

Table 3. AI Bulls: EBV comparison between March 2020 (before genetic groups) and October 2020 (after the introduction of genetic groups)

Bulls with at least 10 daughters in 3 herds		OCTOBER 2020			MARCH 2020		
EBV	Correlation	MAX	MIN	MEAN	MAX	MIN	MEAN
Milk	0,99	876,00	-390,00	147,37	829,00	-429,00	140,62
% Fat	0,99	0,97	-0,90	-0,01	0,89	-0,89	-0,01
% Protein	0,98	0,26	-0,28	0,00	0,25	-0,27	0,00
Kg Fat	0,98	54,00	-26,00	12,05	54,00	-31,00	11,41
Kg Protein	0,98	34,00	-15,00	6,93	34,00	-18,00	6,49
Yield	0,99	20,32	-19,88	-0,06	19,22	-19,76	-0,31
Limbs & Feet	0,99	5,88	-5,64	0,85	5,99	-6,31	0,45
Mammary System	0,99	4,53	-2,72	0,69	4,31	-2,79	0,57
IBMI	0,99	151	48	112	150	49	108

In the RANK 99 buffaloes' case, the results of the comparison between March 2020 and October 2020 can be seen in table 4.

Table 4. Rank 99 Buffaloes: EBV comparison between March 2020 (before genetic groups) and October 2020 (after the introduction of genetic groups)

RANK 99 buffaloes		OCTOBER 2020			MARCH 2020		
EBV	MAX	MAX	MIN	MEAN	MAX	MIN	MEAN
Milk	0,99	1396,00	-682,00	207,01	1354,0	-680,0	207,7
% Fat	0,99	1,41	-0,90	0,16	1,4	-0,9	0,2
% Protein	0,99	0,56	-0,30	0,08	0,6	-0,3	0,1
Kg Fat	0,98	74,00	-30,00	19,75	74,0	-30,0	20,2
Kg Protein	0,99	54,00	-22,00	11,34	55,0	-22,0	11,4
Yield	0,99	33,11	-20,25	4,10	32,8	-20,0	4,2
Limbs & Feet	0,95	5,02	-1,72	1,57	4,9	-2,1	1,3
Mammary System	0,98	4,37	-2,55	1,14	4,4	-2,8	1,1
IBMI	0,87	152	121	127	147	119	125

In this case we can observe how the correlations are very high for the productive characters and lower for morphology characters (consequently also for the IBMI). These results were widely expected and predictable because a change in the pedigree structure (consequence of the assignment of the various subjects to different groups and not to the same large medium group as previously) has a greater impact on traits with lower heritability, as is the case of morphological characters. In addition, especially the hoaxes with more children without a father are more affected by this type of change.

It should be noted that thanks to this new procedure, a greater number of subjects obtained an available and more accurate genetic index (8.401 more males and 64.701 females, of which 545 RANK 99). It is evident that even young subjects without their own data may have variations, mainly depending on the maternal component. In this way, the introduction of the Genetic Groups in the genetic evaluation model of the Italian Mediterranean Buffalo corrects an inconsistency that for many years has characterized the estimation of the genetic indices of this species and enhances all the available information, both in terms of characters. productive and morphological.

ANASB's goal is to collect complete information for everyone, but in the process of updating and improving information it is important to take advantage of all the technical and methodological tools that increase, even marginally, the accuracy of the final result.

GENETIC TRENDS AND DATABASE EXPANSION

Analyzing the genetic trends reported in Figures 1 and 2, we can observe how the selection carried out before the introduction of the aggregate index (December 2018), has markedly improved only the genetic level for the Kg of milk, neglecting the titles, thus obtaining a lower overall genetic potential. In fact, the analysis of genetic trends is of extreme importance, because it is on the basis of this analysis that one decides whether to change or not.

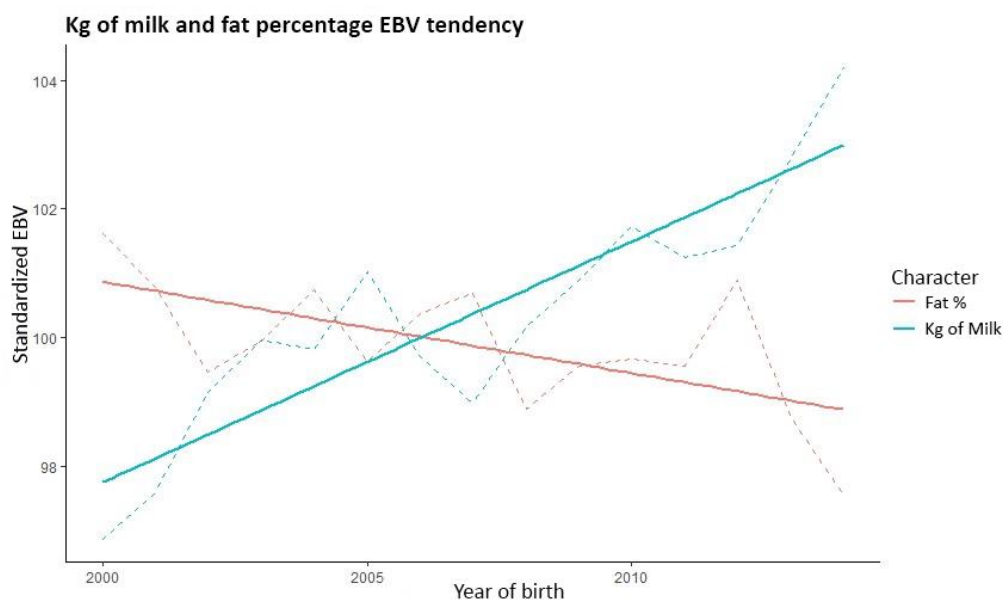


Figure 1: EBV evolution of Kg of milk and fat percentage

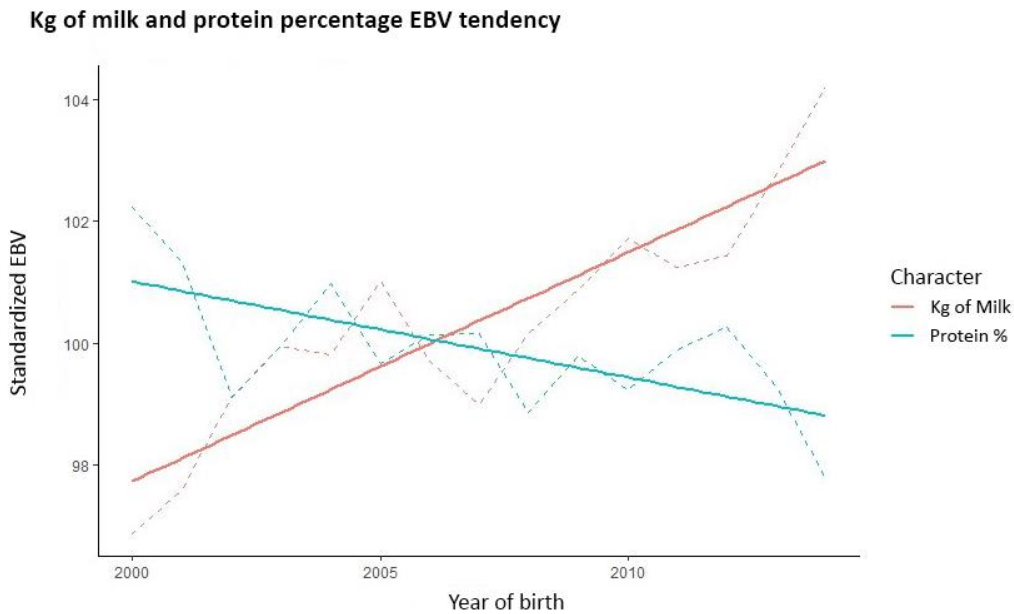


Figure 2: EBV evolution of Kg of milk and protein percentage

For these reasons, the adoption of a new methodological approach has served precisely to respond to a contingent unfavorable situation (constant worsening of the genetic level of milk titers) while at the same time expanding the improvement of other economically important characteristics (for example, mammary and locomotor system). In fact, IBMI has the goal of increasing the quantity of milk produced and at the same time the yield of mozzarella, improving the titles.

Thanks to a work carried out by the technical area of ANASB in collaboration with AIA, through the data collected from functional checks, it was possible to retrieve information relating to the number of milking's of all subjects subjected to morphological assessment. This made it possible to retrieve over 10.000 information, improving the quality and accuracy of the evaluation itself.

NEW GENETIC BASE

Knowing the genetics for a breeder is important because:

- the characteristics of a breed are determined by genetic properties that distinguish them from one another in a specific way;
- genetic characteristics are transmitted from one generation to another, and it is possible to work to modify them in order to obtain productive improvements that are lasting over time;
- these genetic characteristics have an impact on the company's economy, as they contribute to increasing its income.

What has just been reported is synonymous with selection, as only animals that have the desired genetic characteristics are chosen for reproduction. The genetic index represents the operational tool of selection, in the sense that through this tool I can choose the best subjects and mate them in such a way as to obtain a more "performing" progeny. The genetic index is therefore a numerical value that orders animals from best to worst for a certain characteristic (e.g. milk, fat, protein) or aggregate index (IBMI) and which is normally expressed as a difference with respect to a reference group, the so-called "genetic basis". It therefore represents the zero of the indices and allows you to quickly identify who improves and who does not. The genetic basis normally refers to a group of animals born in a certain year or period, identifying the average level of a population at that specific time. The genetic basis can be fixed (when updating only after a fixed period of time) or mobile (for example when updating every year) and ANASB has adopted the fixed genetic basis, updating it every 5 years. With the genetic evaluation of March 2020 (edition n° 37) the genetic basis has therefore been updated and is composed of buffaloes with lactation and known father born in 2015. All genetic indices are now expressed as a difference from the mean of the buffalo genetic indices with lactation born in 2015. The mean and relative standard deviation of the genetic indices, of the productions (calculated at 270 days of lactation) and of the scores of the buffaloes that make up the genetic basis can be observed in table 5.

Table 5. Genetic and phenotypic data of the genetic basis updated to the buffaloes born in 2015 (mean values ± standard deviation)

Genetic Data	Milk	Fat (%)	Protein (%)	Fat (Kg)	Protein (Kg)	Yield (gr/Kg)
	245,54±211,71	29,03±26,74	23,87±9,53	8,64±12,36	7,12±8,37	18,79±5,42
Phenotypic Data	Milk	Fat (%)	Protein (%)	Fat (Kg)	Protein (Kg)	Yield (gr/Kg)
	2465,99±525,85	7,88±1,29	4,66±0,30	192,59±46,45	114,46±23,83	254,51±20,44

YIELD GENETIC INDEX

Starting from this evaluation, in addition to the IBMI selection index and other genetic indices for individual traits, the genetic index for the YIELD trait is also available. The IBMI selection index has among its objectives the improvement of the yield in mozzarella, but until now the direct genetic index for the yield character was not published. The Yield genetic index is calculated together with the other productive genetic indices starting from a phenotype calculated according to the following formula:

$$^1\text{YIELD (g)} = 116,615 + 2,015 (\% \text{ protein} * \% \text{ fat}) + 2,928 (\% \text{ protein}^2)$$

¹ Research project: "Verification of the relationship between PKM and yield to the dairy in the evaluation of milk buffalo". Scientific Manager Rossella Di Palo (Campania Region - C.R.A.A. Consortium for applied research in agriculture). 2006-2009: Yield (g)= 116.615+2.015 (protein % * fat %) + 2.928 (protein %²)

The inheritability of the YIELD character is equal to 0,24. The goal is to bring know-how to the buffalo sector in order to obtain a genetic progress necessary for the needs of our members: the new methodological approaches will open scenarios to the world of the buffalo allowing the desired genetic progress.

HOW TO USE THE CATALOG AT THE BEST

The subjects with the highest index are those who come closest to the new selection objective, which is now more balanced in terms of production, quality and functionality.

Let's see with a practical example how to best use the ranking (table 6). Let's assume we have a buffalo with a very high genetic value for production; based on the structure of our population it is very likely that this animal will have negative values for titers (-0.05 for % protein and -0.12 for % fat). We want to mate this buffalo with a bull to produce new offspring. We choose a very strong milk bull (Milk Bull in Table 2). The expected result in terms of pedigree index (Result 1) is positive on the Kg but continues to be negative on the percentages. In addition, the limbs and feet also worsen.

We now choose a bull based on the IBMI (IBMI Bull) and deliberately choose it negative for the kg of milk (-308). The expected result in terms of pedigree index (Result 2) is this time positive on all traits, albeit using a negative milk bull. The new born will have a genetic potential for milk production higher than the average of the subjects currently present. It will still make more milk even if paradoxically a strongly negative bull was used. On the born subject, if female, a strong milk bull can be used again, thus allowing balanced growth.

Table 6. Results on using two different bulls on the progeny genetic potential

SUBJECT	KG MILK	% PROTEIN	KG PROTEIN	% FAT	KG FAT	LIMBS & FEET	MAMMARY SYSTEM
Buffalo	1031	-0,05	45	-0,12	75	3,44	0,48
Milk bull	760	-0,25	28	-0,77	38	-1,24	1,52
1 st result	896	-0,15	37	-0,45	57	1,10	1,0
IBMI bull	-308	0,21	-9	0,77	-8	0,37	2
2 nd result	362	0,08	18	0,33	34	2	1

Not only that, let's assume that the new born is a female with percentages at 270 days equal to those of the buffaloes born in 2016 (fat % = 8.11 and protein % = 4.64). If we add to these values the improvement/worsening in genetic terms and calculate the yield using the formula:

$$^1\text{YIELD (g)} = 116,615 + 2,015 (\% \text{ protein} * \% \text{ fat}) + 2,928 (\% \text{ protein}^2)$$

You get:

- with milk bull: 244.9 grams/liter;
- with IBMI bull: 262.1 grams/liter.

From this deliberately extreme example, 3 important considerations can be drawn:

1. **I have to choose the right bull for my breeding:** I cannot use a negative bull on a negative female but I can use it where I want to balance a situation that is too unbalanced;
2. **Is not correct to say that IBMI penalizes kg of milk:** even using a strongly negative bull I can obtain subjects with positive genetic potential;
3. **IBMI is a complete index for all breeders:** the goal that IBMI sets itself is precisely to act positively on all traits, favoring both animals and those who breed them.

RELATIONSHIP'S COEFFICIENT OF AI BULLS WITH THE POPULATION

To be able to choose it is essential that there is diversity. Among a large number of subjects that are all identical, there is no way to choose one subject better than another, so it cannot be improved. The mating of related animals to each other reduces their genetic diversity.

A correct and complete genealogy is essential in the context of genetic improvement also and above all because it allows us to estimate the consanguinity of an individual and his relationship with other individuals through mathematical and probabilistic calculations.

It is good to remember that consanguinity (probability between 0 and 100 that both genes present in an individual are identical by descent) refers to the single individual while when we talk about kinship, we refer to the percentage of genes in common between 2 subjects.

The two values are linked to each other and if I couple 2 relatives (Father/Daughter, Father/Grandson) the result will be a consanguineous individual.

In choosing a breeder it is therefore not essential to know its level of consanguinity but rather what will happen in one's stable when it will be used: it will therefore depend on the relationship between the bull and the buffaloes with which I will mate it.

It should also be remembered that the mating between two highly consanguineous individuals but not related to each other gives rise to unrelated offspring; on the contrary, the greater the degree of kinship between the parents, the higher the degree of consanguinity of the new born.

Choosing less related breeders already guarantees greater genetic variability in our breeding and, in the future, fewer inbreeding problems.

For these reasons, at the end of the IBMI index tables, both the kinship data between all tested and tested bulls and their kinship in the population are reported. Both information can be useful to guide some selective choices in a practical and quick way.