BIOLOGISKA YRKESHÖGSKOLAN
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Correlations between bull's estimated breeding values based on daughters and bull dam's phenotype

Rosman (2025)

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Summary

This work is intended to be used to disprove those who believes that the bull dam’s exterior and production should be taken into greater consideration when selecting breeding bulls. The breeding company Viking Genetics and their product manager for VikingRed Camilla Rosman has a strong believe that the bull dam’s exterior and production has a low correlation with the bulls estimated breeding values, but they want evidence to support this theory. In order to obtain a result, a correlation analysis has been made where the data from the dairy breeds Holstein, Nordic red and Jersey has been used. The data is based on bulls with estimated breeding values proved by daughters born between 2015 and 2020. The correlation is presented in a scatter diagram which includes a regression line to prove the correlation. The diagram also includes the coefficient of determination, which shows how much changes in the bull’s dam’s phenotypic breeding values actually affects the bull’s breeding values. Finaly, a significance analysis has also been made to determine whether the results are based on actual correlations or coincidences. The result shows that the correlation between the bull dam’s phenotypic breeding values and the bulls estimated breeding values are low. Above all, the coefficient of determination shows that there is a very high number of other factors that affect the bull’s breeding values. This confirms that the reliability of the bull dam’s breeding values is very low and should therefore not be taken into consideration when selecting bulls. The conclusion is that the most effective way to achieve economic and genetic progress is by using breeding values with high reliabilities and selecting breeding animals based on their Nordic total merit, NTM, and not based on the bull dam’s production and exterior.

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1 Introduction

This work has been carried out in consultation with the cattle breeding company Viking Genetics. The product manager for VikingRed Camilla Rosman has been the supervisor for the project and was the one suggested the aim on question. She is responsible for the breeding program for the VikingRed and through her work she often interacts with farmers. During these interactions she frequently gets into discussion about the breeding program using bulls from dam's who hasn't entered production yet or has a poor conformation score. Some farmers assume that the cow's performance in production and conformation has a high correlation with the bulls breeding values and that bulls in the breeding program should be after dams with high production and good exterior. This mindset causes farmers to do minimum selection where they reject bulls with high breeding qualities because of their dam's phenotypic performance (Rosman, 2025). Rosman and Viking Genetics has a strong believe that the correlation isn't that high and that the dam's performance should not be taken into such great consideration when searching for bulls. To investigate this theory Rosman and Viking Genetics wanted this work to be carried out and the result is intended to be used to address farmers when the discussion comes up. They hope that this work will lead to greater understanding among farmers and that this in turn may increase interest in genetic testing of their animals, which will benefit both the farmers and Viking Genetics breeding program.

2 Objectives

The aim for this project is to see if there is any correlation, and in that case how much correlation there is between bull's proven traits and the bull dam's phenotypic traits.

3 Method

To answer the question data about the bulls and bull dams has been collected from Viking Genetics database Viking Bull (Viking Genetics, 2025G) and through NAV bull search (NAV, 2025D). Data has only been included from bulls that have breeding values based on daughters, because it provides higher reliabilities in the data (Viking Genetics, 2025E). Bulls with estimated breeding values have daughters that are in production and have data registration of their production and health (Viking Genetics, 2025E). Thus, the youngest bulls are born in 2020. Originally it was planned to collect data from bulls born between 2017 and 2020, so that the breeding progress hadn't developed too much. The years had to be extended to 2015 to provide enough data. Data from 248 Nordic red, 294 Holsteins and 113 Jerseys has been used in the work. Nordic red includes the dairy breeds: Finnish Ayrshire, Swedish red and Danish Red (Viking Denmark, 2025). The result is presented with each trait and breed separately.

The correlation has been calculated using excels correlation analysis tool and then been presented as diagrams. The correlation analysis is used to measure how strong a correlation it's between two variables. The correlation is expressed with a correlation coefficient and it can have a value between -1 to 1. -1 describes a strong negative correlation where one variable decrease when the other increases. 1 describes a positive correlation where both variables increase. 0 means there is no correlation (Rybrand & Karp, 2025). To visualize the correlation the data points have been plotted in a scatter diagram and from there a regression line has been drawn and a coefficient of determination. The regression line describes the correlation between the x and y variables. Data samples that are close to the regression line indicate that there is a higher correlation between the variables (Rybrand & Karp, 2025).

R^2, the coefficient of determination, describes how much the values in the y axis are affected by changes in the x axis. The coefficient is read as a percentage and, unlike the correlation coefficient, can describe how large a proportion of the result is affected by factors other than those included in the model. For example, if R^2 is 0.96 it means that 96% of the result can be explained by factors included in the model. The remaining 4% are factors outside the model that have affected the result (Gunnarsson, 2020).

In order to make assumptions and draw conclusions based on the correlation, a significance analysis is needed. Statistical significance describes how likely it is that a correlation observed in data is real and not just a coincidence. When determining whether a correlation is statistically significant, one starts from the correlations p-value. The p-value is used to determine whether the null hypothesis can be rejected or not. The null hypothesis believes that there is no correlation, but if the p-value for the result is below 0.05, 5%, it suggests that it's unlikely that the result is due to chance, and the null hypothesis can be rejected. If the p-value is higher than 5%, the correlation might be a coincidence and therefore the null hypothesis remains (Första kursen, 2025). Significance may not be achieved if there is too little data collected or if there is a large spread in the material. The large spread weakens the correlation and significance may not be achieved (Figueiredo, 2013).

Initially the bull dam's average production through all the lactations was used when the correlation between production traits was investigated. To ensure that it did not give a misleading result the diagram was redone with the average production for the first lactation. The result where similar as in the first diagram, but the decision was made to continue using average data from the first lactation, in order to use as equivalent data as possible. Since genetic development occurs for each generation, there was also interest in seeing whether the correlation changed over the years. This was investigated by dividing the data material based on the bull's birth year and making diagrams by year. The result showed that it was not possible to discern any trend for the correlation over the years and thus it was decided that combining the years did not give misleading results.

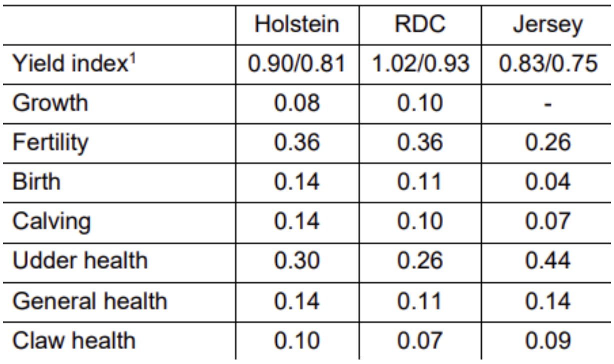
4 Background

Nordic cattle genetic evaluations, NAV, established 2002 with the aim of implementing a united breeding plan for dairy cows in Sweden, Finland and Denmark. Landbrug & Fodevarver, Faba and Växa Sverige are the members of NAV (NAV, 2025). Lanbrug & Fodervarver are since 2009 a merger of several agricultural organizations in Denmark. Today it´s a member organization that works for the Danish agricultural sector (Landbrug & Fodevarer, 2025). Faba is a Finnish company that works to develop Finnish dairy and beef production. Their main focus is to develop reproduction, breeding and health of the cows (Faba, 2025). Växa Sverige is a member organisation who offers services and products which will promote the Swedish agriculture (Växa, 2025). Viking Genetics is a breeding company owned by Landbrug & Fodevarver, Faba and Växa Sverige (Viking Genetics, 2025H) and their aim is to create a breeding program that will improve the dairy cow's health and performance (Viking Genetics, 2025C). In order to achieve their goal they use NTM (Viking Genetics, 2025B).

Nordic total merit, NTM, was established by NAV in 2008. The purpose of NTM is to provide a total index of all economically valuable characteristics of cattle (NAV, 2025). NTM can be used as a guide in breeding planning to provide a more effective breeding development (Viking Genetics, 2025B). NAV (2024) believes that if the selection of breeding material is based on NTM the farmer will provide higher profit. The next generation will also perform better than the previous one, both in production and profit (NAV, 2024). NAV (2020) explains that one NTM unit result in 9 €, euro, more per cow each year. In a herd with 150 cows who has an average of 10 in NTM would result in almost 15,000 € more in income each year, just through higher NTM (NAV, 2020).

NTM is a total index based on 15 subindex, which are: yield, growth, fertility, birth, calving, udder health, general health, claw health, feet & legs, udder, milkability, temperament, longevity, youngstock survival and saved feed (NAV, 2024). The 15 subindex are based on 90 subindices (Viking Genetics, 2025B). For example, the subindex yield is based on the subindices milk, fat and protein (NAV, 2025H).

When calculating NTM all the subindices are given a specific value which is then weighed together to a subindex. Figure 1 shows weights for some of the different subindices for each breed. The economic valuation of the subindex is based on the current economic situation and on the future situation over the next eight to ten years and it also varies depending on which breed it applies (NAV, 2024). Holsteins for example have a higher value for health traits than Nordic Red and Jersey, while the weight on production is higher for them (Viking Genetics, 2025A). The weight of traits can be adjusted towards a lower economic gain, if it instead benefits animal welfare, ethical views, climate and environment (NAV, 2024).



	Holstein	RDC	Jersey
Yield index[1]	0.90/0.81	1.02/0.93	0.83/0.75
Growth	0.08	0.10	-
Fertility	0.36	0.36	0.26
Birth	0.14	0.11	0.04
Calving	0.14	0.10	0.07
Udder health	0.30	0.26	0.44
General health	0.14	0.11	0.14
Claw health	0.10	0.07	0.09

Figure 1: Example on weight factors for dairy breeds, which are used when calculating NTM (NAV, 2024).

The individual breeding values, subindices, has an average value of 100 and for NTM it´s 0 (Växa, 2023) and the average is supposed to correspond to the base population (Viking Genetics, 2025D). Växa (2023) describes that most of the population will be close to the average breeding values and NTM, but a few individuals have breeding values that are extremely high or low. The individual breeding values has a spread of 70 – 130 and NTM -30 – 30 (Växa, 2023). Figure 2 shows the spread of breeding values and NTM in a population.

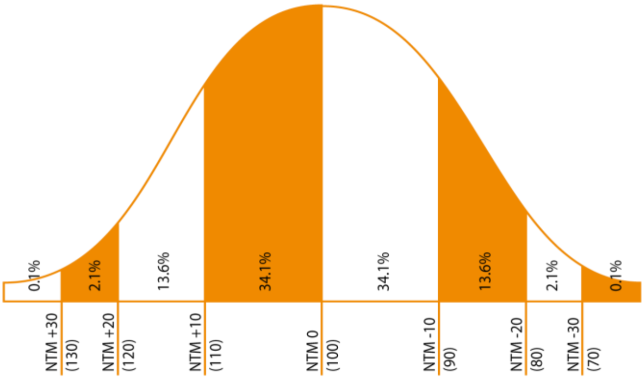
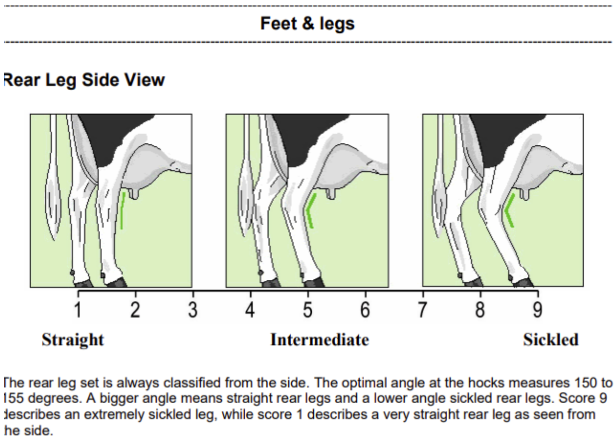


Figure 2: Describes the distribution of breeding values within a population (Växa, 2023).

Viking Genetics (2025D) use NTM to find the best individual in the population, so that they can be used in the breeding program and generate the greatest genetic development. Since genetic development occurs with each generation, a comparison group is needed to be able to test future breeding candidates (Växa, 2023). The base group contains cows who are three to five years old and there average in individual breeding values are 100 and 0 in NTM. After every breeding evaluation the base group changes to follow the development (Växa, 2023).

Breeding values can be determined in several ways, but the different methods provide various reliabilities in the breeding values (Växa, 2025A). Växa (2020) describes that the breeding values can be determined by pedigree and registrations about the animal. The registrations can for example contain information about the animal's health in general and in hoof and udder (Växa, 2024A). Breeding values based on pedigree and registrations are called phenotypic breeding values (Växa, 2025A). The phenotype describes the characteristics that are visible and can be measured (Genetiknämnden, 2024). The reliabilities in these breeding values can be a maximum of 12 % according to Rosman (2025). NAV (2024) tells that animals with breeding values based on pedigree gets a lower NTM due to the low reliabilities. Dairy cattle get their phenotype valid by exterior evaluation and it´s an impartial estimation that should evaluate the functional properties (Växa, 2024). Figure 3 shows an example on how feet and legs get valid during the exterior evaluation.



Feet & legs

Rear Leg Side View

The rear leg set is always classified from the side. The optimal angle at the hocks measures 150 to 155 degrees. A bigger angle means straight rear legs and a lower angle sickled rear legs. Score 9 describes an extremely sickled leg, while score 1 describes a very straight rear leg as seen from he side.

Figure 3: Example of how traits are valued in the conformation assessment (International Committee for Animal Recording, w,y).

Breeding values can also be determined by DNA and then they are called genotypic breeding values and they have a maximum reliability of 72%, regardless of whether the trait has high or low heritability (Växa, 2025A). The genotype contains the genetic factors that affects the appearance and production (Genetiknämnden, 2025) and the genetic breeding values are necessary when making an effective breeding plan according to Växa (2020). The highest reliabilities of breeding values are achieved by bulls that are progeny tested with a maximum reliability of 95% (Växa, 2025A). The progeny test has a high level of reliabilities as the bull's daughters are in production and confirm which characteristics are inherited from the bull (Viking Genetics, 2025E). Figure 4 shows the reliability for the different breeding values according to Viking Genetics (Rosman, 2025). The phenotypic breeding values are updated four times a year and the genomic values monthly (Växa, 2020A).

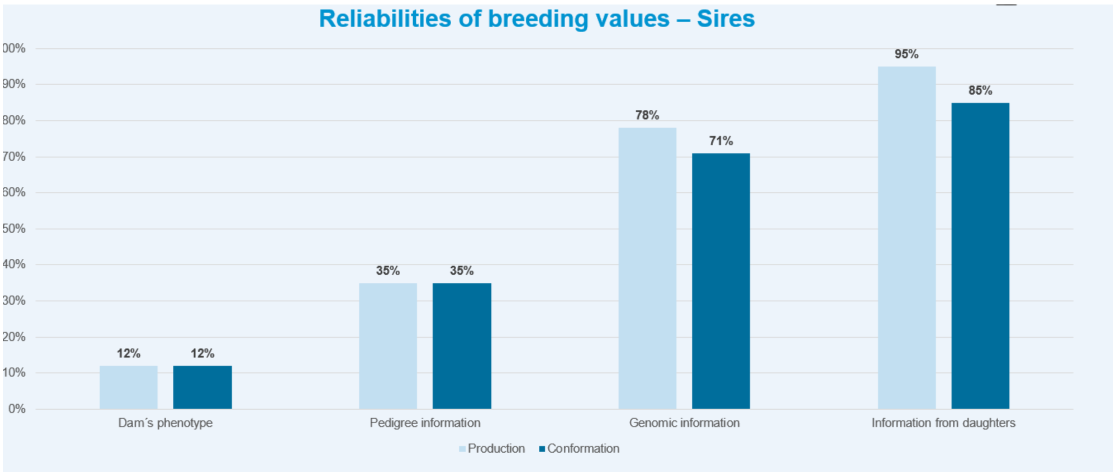
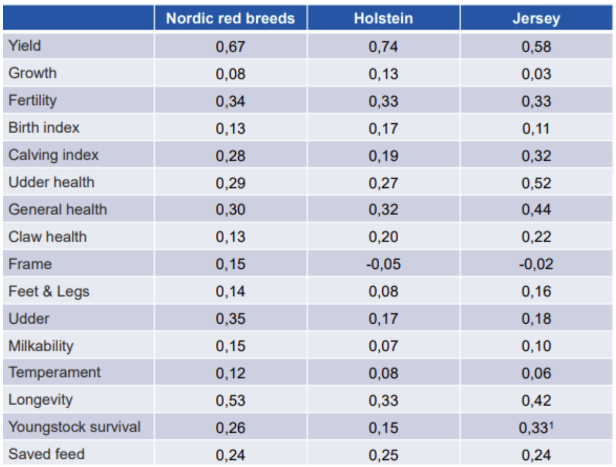


Figure 4: Diagram showing the reliabilities in different breeding values according to Viking Genetics (Rosman, 2025)

Correlation of traits is also taken into consideration when planning the breeding (Viking Genetics, 2025F). The correlation in this case shows how strong the relationship is between two characteristics. NAV (2025B) state that breeding that are based on NTM leads to several traits being improved simultaneously and NAV (2025A) expresses that they use correlation to see how much development will occur for each subindices. Figure 5 shows that Nordic red has a correlation of 0.67 for yield, which means that 67% development can be expected in the yield trait when breeding is based on NTM (NAV, 2025A). Maximum development can be achieved if breeding work aims to develop only one trait at a time (NAV, 2024).



	Nordic red breeds	Holstein	Jersey
Yield	0,67	0,74	0,58
Growth	0,08	0,13	0,03
Fertility	0,34	0,33	0,33
Birth index	0,13	0,17	0,11
Calving index	0,28	0,19	0,32
Udder health	0,29	0,27	0,52
General health	0,30	0,32	0,44
Claw health	0,13	0,20	0,22
Frame	0,15	-0,05	-0,02
Feet & Legs	0,14	0,08	0,16
Udder	0,35	0,17	0,18
Milkability	0,15	0,07	0,10
Temperament	0,12	0,08	0,06
Longevity	0,53	0,33	0,42
Youngstock survival	0,26	0,15	0,33[1]
Saved feed	0,24	0,25	0,24

Figure 5: Correlation weights between NTM and subindex (NAV, 2025A).

Figure 6 illustrates the genetic progress that has occurred on dairy cows over the last 20 years in Denmark, Finland and Sweden. To achieve the most efficient breeding planning possible Växa (2023) state that the genetically best animals must be located and used in a thoughtful way. A crucial factor for effective breeding planning is that both the cow and bull have a breeding evaluation (Växa, 2020) and it is the genomic breeding evaluation that provides the highest level of reliabilities (Växa, 2025A). Denmark's development is higher than Finland's and Sweden's and Rosman (2025) believes this is because they use animals with high NTM to a higher extent. She witnesses that in Sweden and Finland ancient ways of thinking remain when valuing breeding animals. In the past, bulls were selected based on the bull dam's conformation and production. The bull was then progeny valued after his daughters came into production (Rosman, 2025). Rosman (2025) describes that this strategy involved high uncertainty in the breeding values and that the breeding work was ineffective. Today this is expressed in farmers doing minimum selection where they don´t use bulls with high NTM, because the bull dams have one or more traits with low phenotypic breeding values.

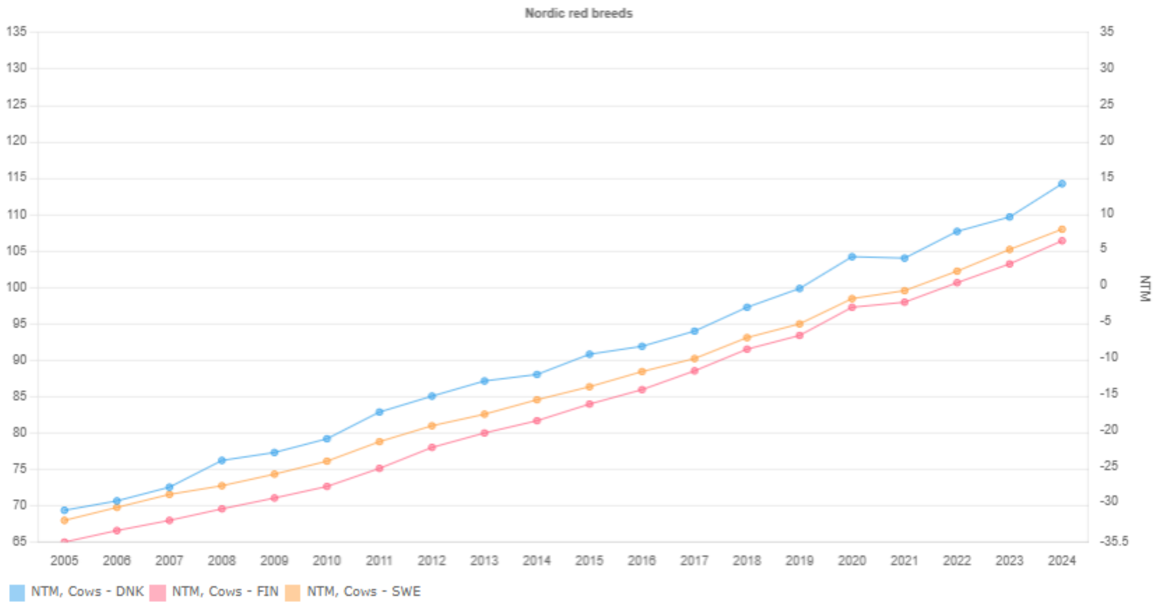
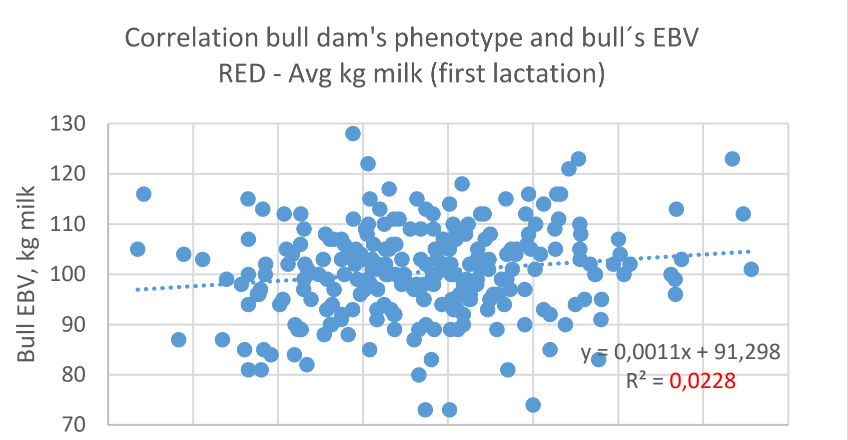


Figure 6: Diagram of the genetic trend on cows from the Nordic red breeds throughout the last twenty years. It includes cows from Denmark, Sweden and Finland. The breeding values are shown on the y axis to the left and NTM on y axis to the right (NAV, 2025C).

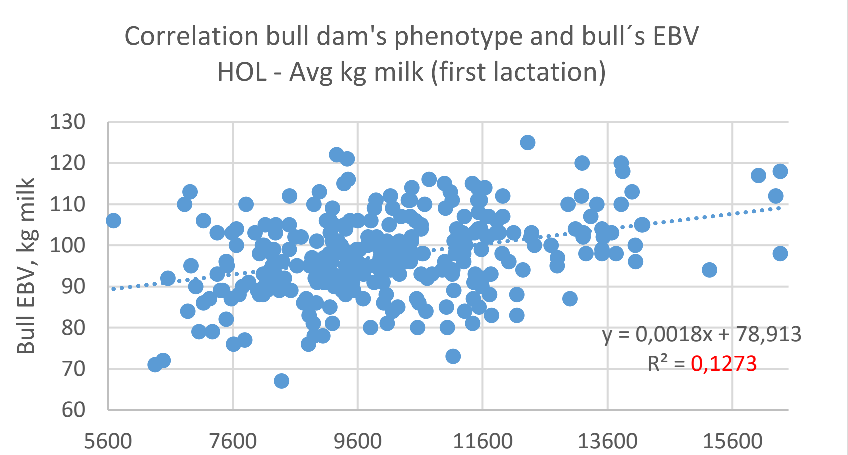
5 Results

Below, values from both conformation and production will be individually presented in breeding order, Nordic red, Holstein and Jersey. The result will describe the correlation between the bull dam’s phenotype and bull’s estimated breeding values, EBV. In the diagrams it will be possible to read the correlation coefficient, p-value, coefficient of determination and regression line equation.

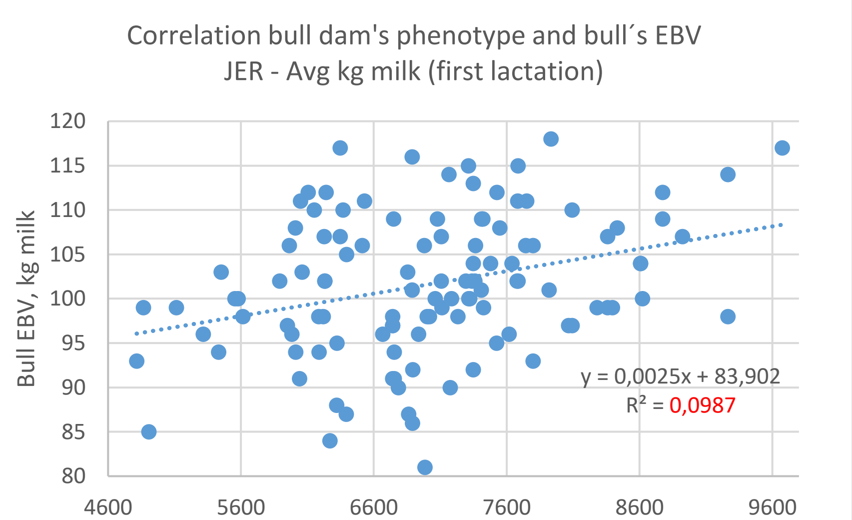
5.1 Kg of milk



Correlation: 0.15
P = 0.017

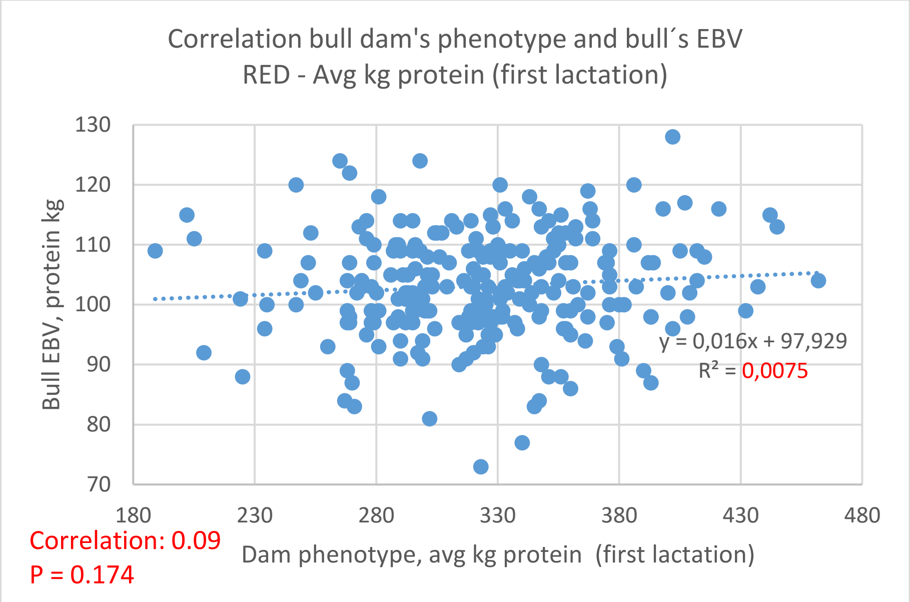


Correlation: 0.36
P = 9,11377E-19

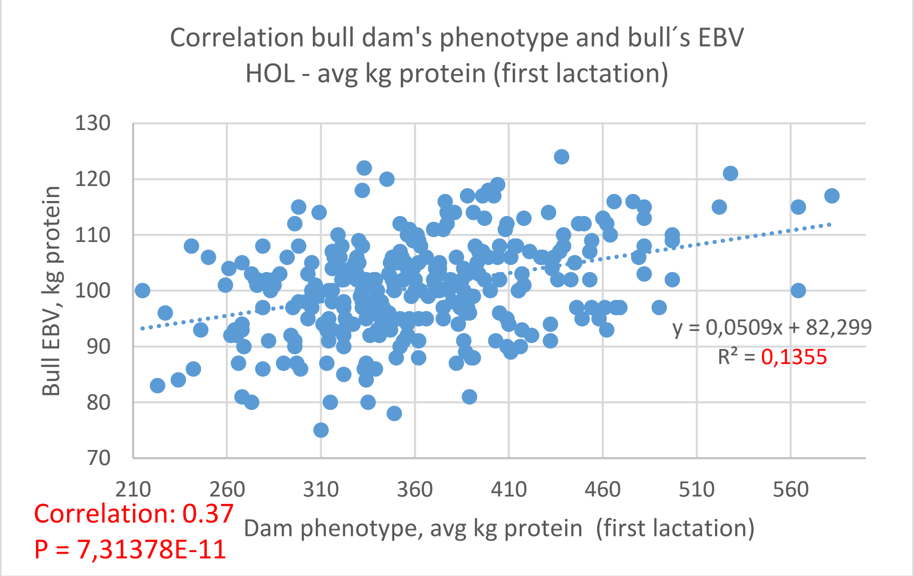


Correlation: 0.31
P = 0.00066

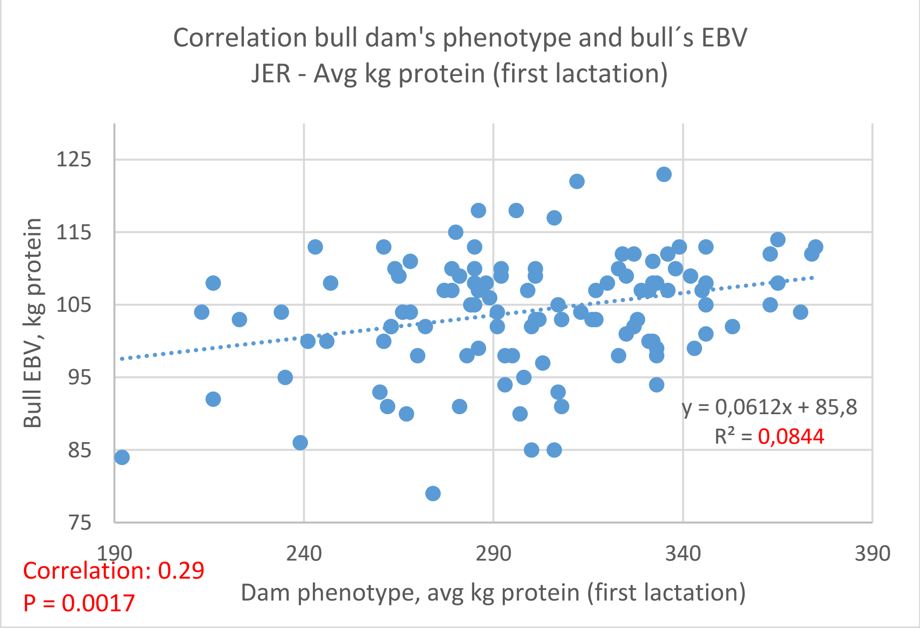
5.2 Protein



Correlation: 0.09
P = 0.174

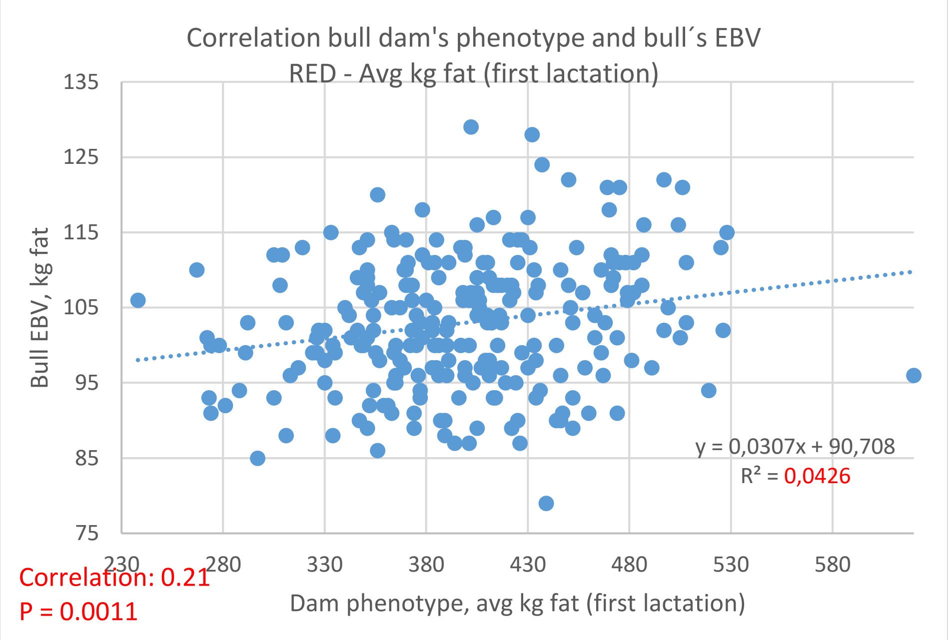


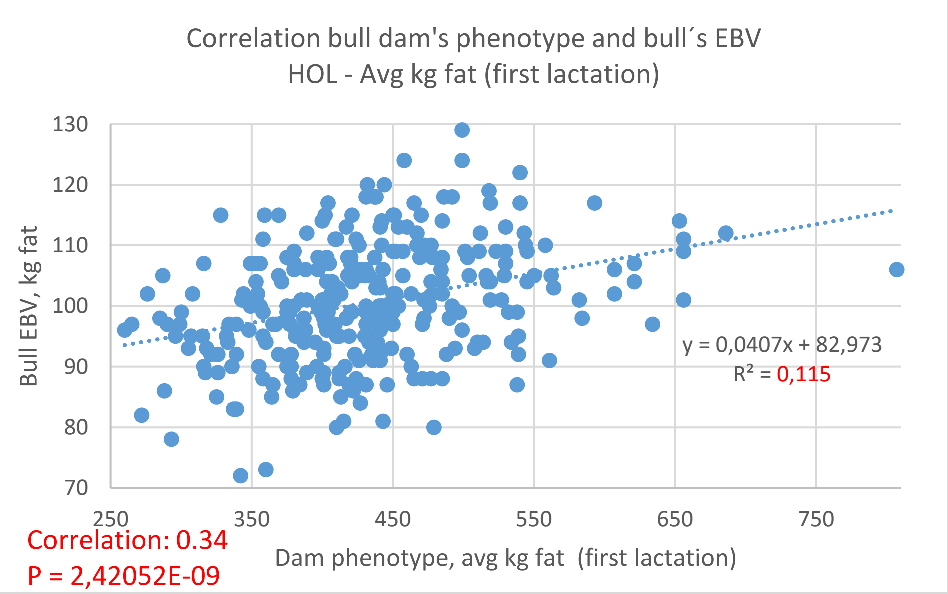
Correlation: 0.37
P = 7,31378E-11

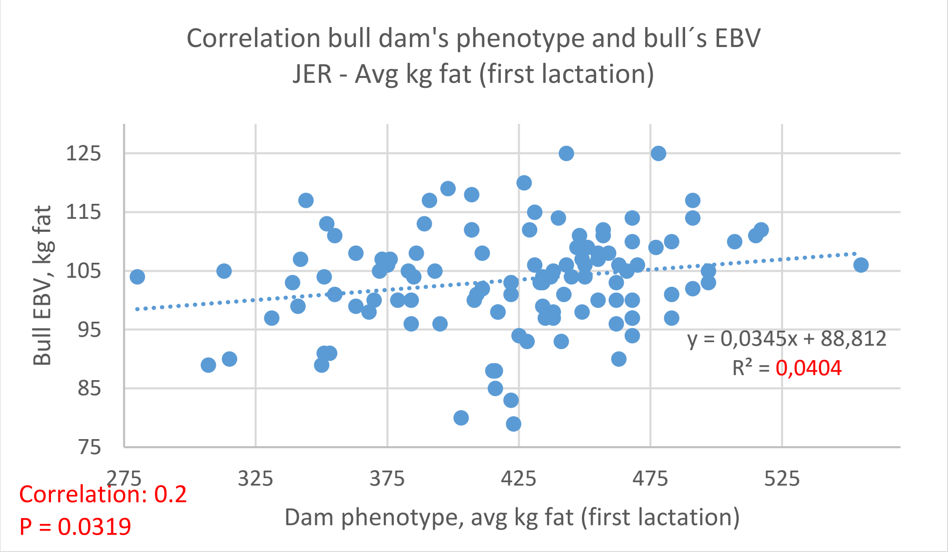


Correlation: 0.29
P = 0.0017

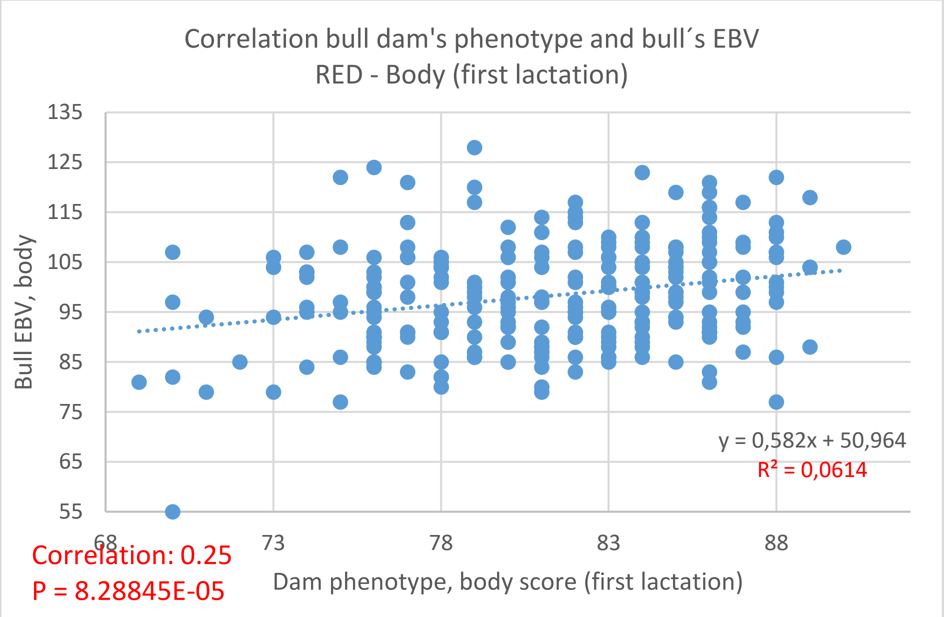
5.3 Fat

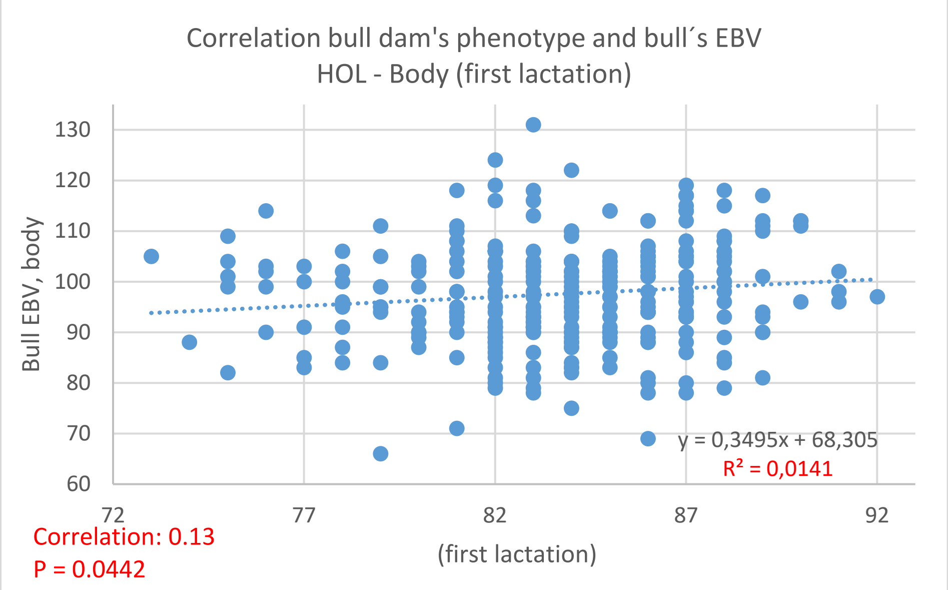

Correlation bull dam's phenotype and bull´s EBV
RED - Avg kg fat (first lactation)
Bull EBV, kg fat
135
125
115
105
95
85
75
230
280
330
380
430
480
530
580
Dam phenotype, avg kg fat (first lactation)
y = 0,0307x + 90,708
R² = 0,0426
Correlation: 0.21
P = 0.0011

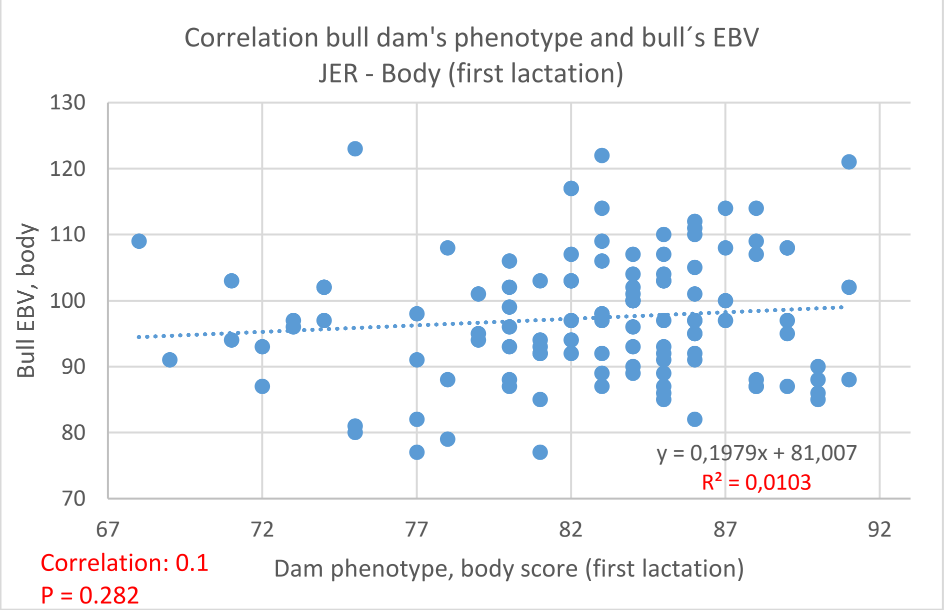

Correlation bull dam's phenotype and bull´s EBV
HOL - Avg kg fat (first lactation)
Bull EBV, kg fat
130
120
110
100
90
80
70
250
350
450
550
650
750
Dam phenotype, avg kg fat (first lactation)
y = 0,0407x + 82,973
R² = 0,115
Correlation: 0.34
P = 2,42052E-09


Correlation bull dam's phenotype and bull´s EBV
JER - Avg kg fat (first lactation)
Bull EBV, kg fat
125
115
105
95
85
75
275
325
375
425
475
525
Dam phenotype, avg kg fat (first lactation)
y = 0,0345x + 88,812
R² = 0,0404
Correlation: 0.2
P = 0.0319

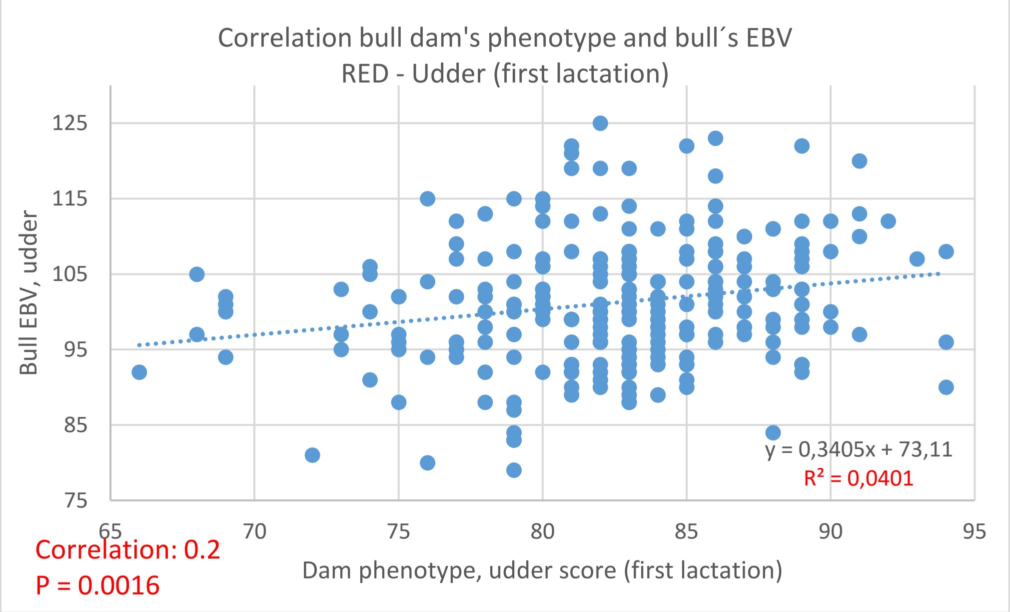
5.4 Body

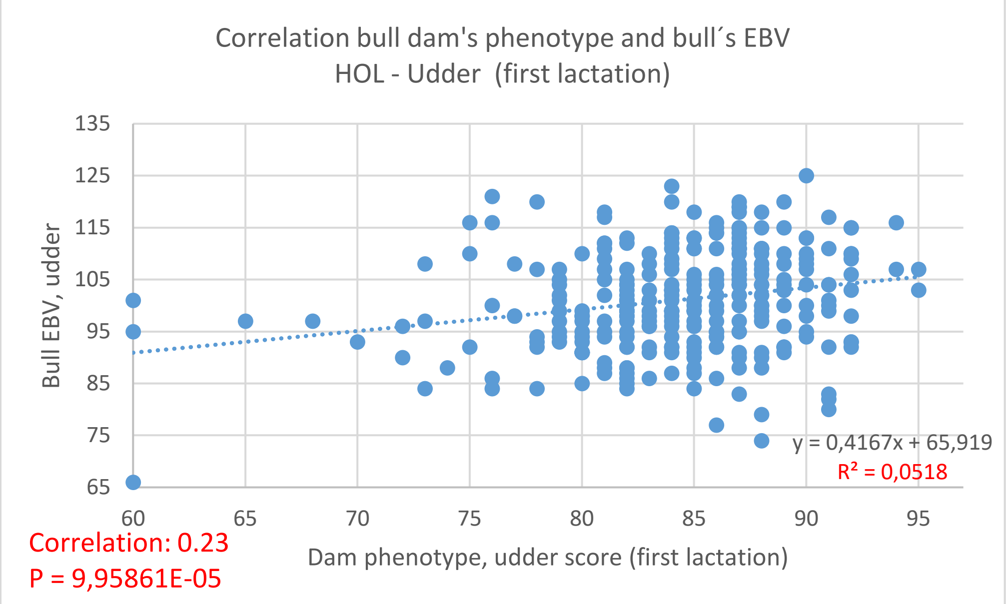

Correlation bull dam's phenotype and bull´s EBV
RED - Body (first lactation)
Bull EBV, body
135
125
115
105
95
85
75
65
55
68
73
78
83
88
Dam phenotype, body score (first lactation)
y = 0,582x + 50,964
R² = 0,0614
Correlation: 0.25
P = 8.28845E-05

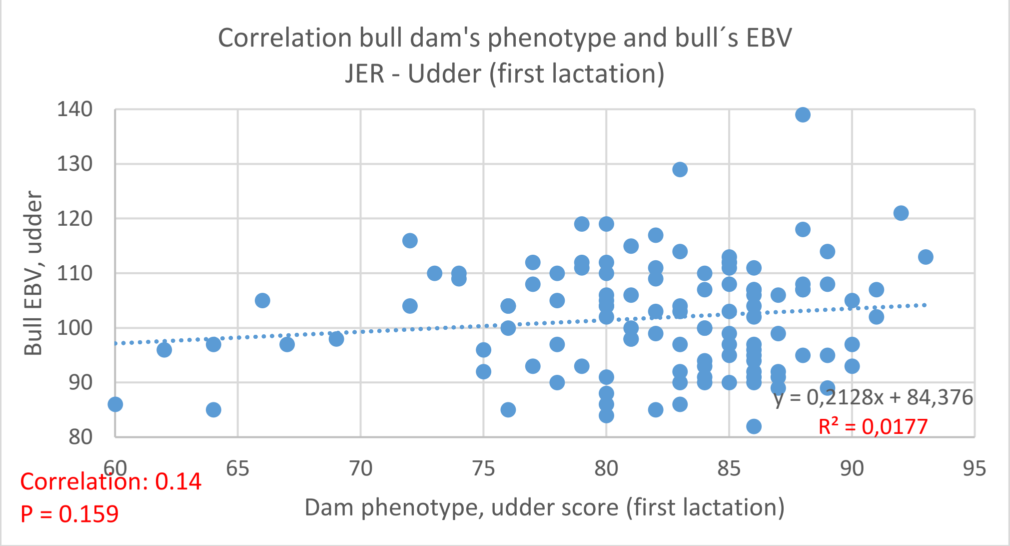

Correlation bull dam's phenotype and bull´s EBV
HOL - Body (first lactation)
Bull EBV, body
130
120
110
100
90
80
70
60
72
77
82
87
92
(first lactation)
y = 0,3495x + 68,305
R² = 0,0141
Correlation: 0.13
P = 0.0442


Correlation bull dam's phenotype and bull´s EBV
JER - Body (first lactation)
Bull EBV, body
130
120
110
100
90
80
70
67
72
77
82
87
92
Dam phenotype, body score (first lactation)
y = 0,1979x + 81,007
R² = 0,0103
Correlation: 0.1
P = 0.282

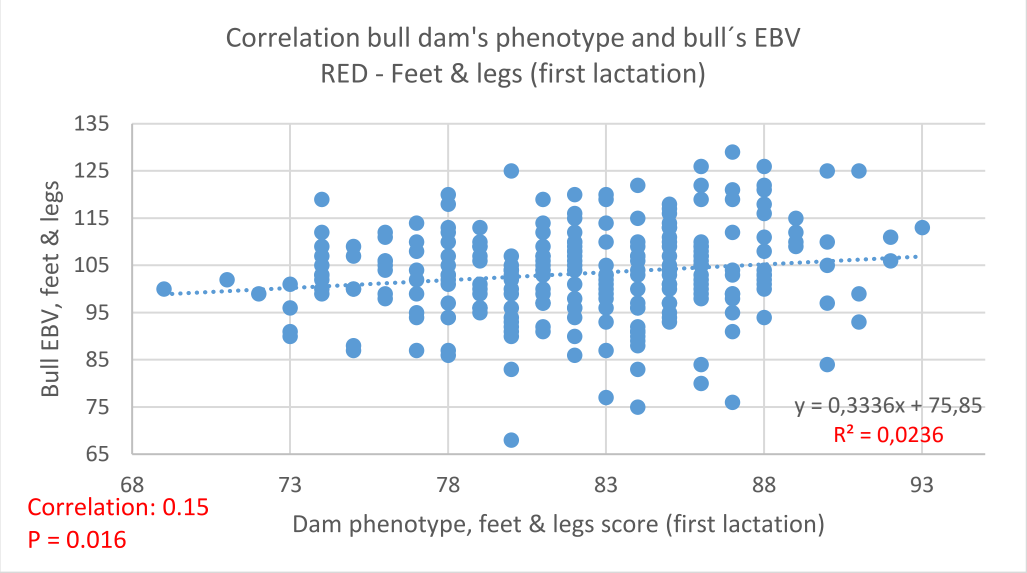
5.5 Udder


Correlation bull dam's phenotype and bull´s EBV
RED - Udder (first lactation)
Bull EBV, udder
125
115
105
95
85
75
65
70
75
80
85
90
95
Dam phenotype, udder score (first lactation)
y = 0,3405x + 73,11
R² = 0,0401
Correlation: 0.2
P = 0.0016


Correlation bull dam's phenotype and bull´s EBV
HOL - Udder (first lactation)
Bull EBV, udder
135
125
115
105
95
85
75
65
60
65
70
75
80
85
90
95
Dam phenotype, udder score (first lactation)
y = 0,4167x + 65,919
R² = 0,0518
Correlation: 0.23
P = 9,95861E-05

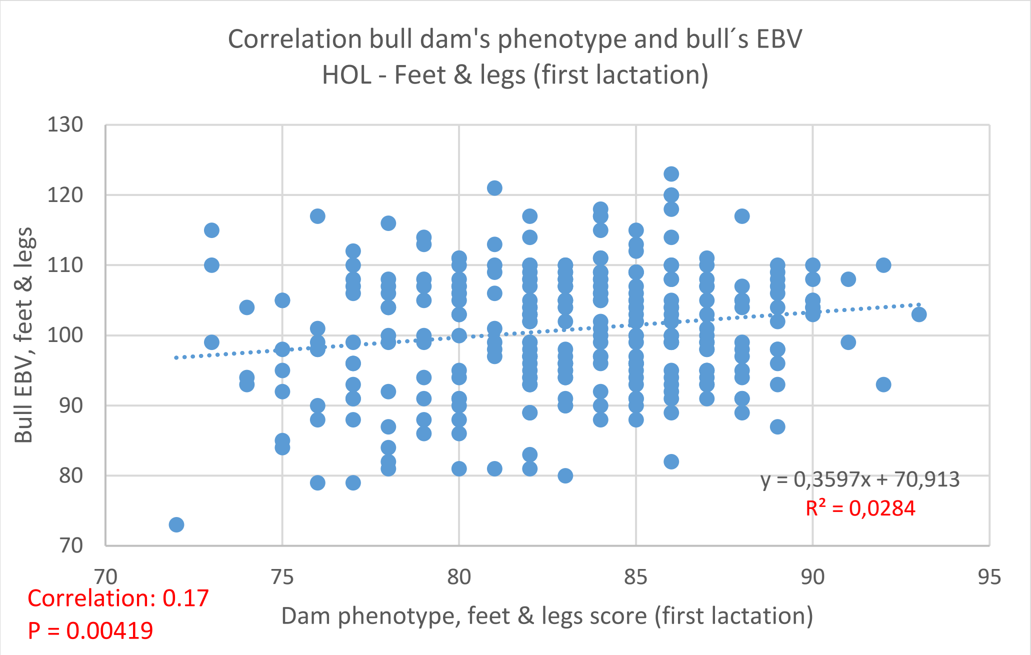

Correlation bull dam's phenotype and bull´s EBV
JER - Udder (first lactation)
Bull EBV, udder
140
130
120
110
100
90
80
60
65
70
75
80
85
90
95
Dam phenotype, udder score (first lactation)
y = 0,2128x + 84,376
R² = 0,0177
Correlation: 0.14
P = 0.159

5.6 Feet & legs



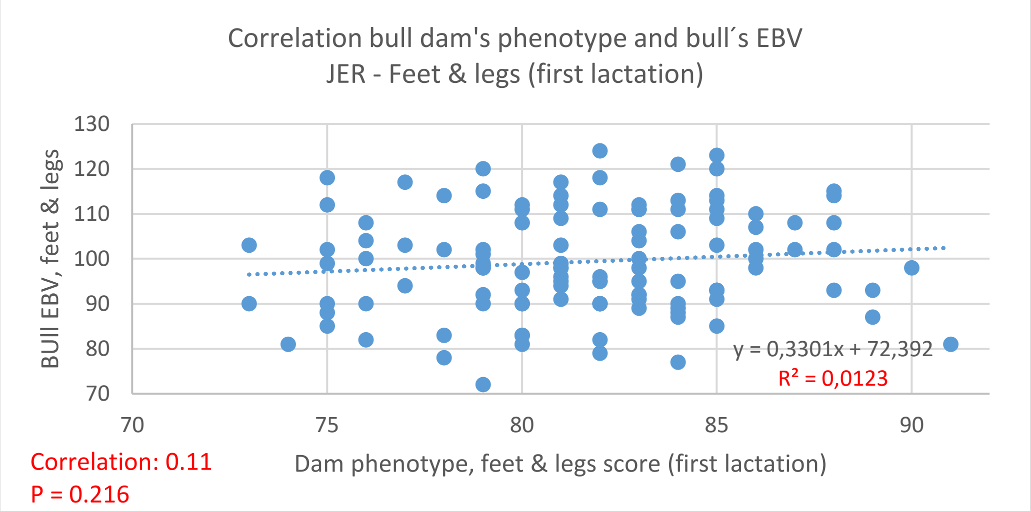
Correlation bull dam's phenotype and bull´s EBV
RED - Feet & legs (first lactation)

Correlation: 0.15
P = 0.016



Correlation bull dam's phenotype and bull´s EBV
HOL - Feet & legs (first lactation)

Correlation: 0.17
P = 0.00419



Correlation bull dam's phenotype and bull´s EBV
JER - Feet & legs (first lactation)

Correlation: 0.11
P = 0.216

6 Discussion

Kilograms, kg, of milk shows a relatively similar correlation for Holstein and Jersey. For the Nordic red, the correlation is much lower. All the correlations are significant which suggests that it´s probably not a coincidence that there is a correlation between the bull dam's phenotypic breeding values and the bulls breeding values. Even though there is a real correlation for all breeds, R^2 shows that changes in the bull dam's phenotypic breeding values have a low impact on the bulls estimated breeding values. For Holstein the bull dam's phenotype affects the breeding values of the bull by 13%. For Jersey it´s 10% and for Nordic red it´s only 2%. The remaining 87%, 90% and 98% are other factors that affects the bulls breeding values that are not included in this model.

For the trait kg protein, Holstein and Jersey have both quite high correlation compared to the Nordic red and they are significant. The reds' correlation is much lower and it's not significant, so it's difficult to draw conclusions from that data. Just because the correlation is not significant does not mean that there is no correlation. It can be, but then it can be either higher or lower. It may also be that the correlation is non-existent and it´s just a coincidence that it appears in this diagram. I however doubt this since there is a significant correlation for the other breeds, so it most likely should also be the case for the Nordic red. Another theory as to why it´s no significant correlation could be that the data is so small that it cannot disprove coincidence. This may seem strange since the data for Nordic red is more than twice as large as for Jersey. The reason that the material is not sufficient could be because the spread within the breed is large, therefore the correlation is weakened. It is possible to assume that the correlation for the Nordic red would be similar to the other breeds if the data were larger and the correlation significant. R^2 shows, just as for kg milk, that the relationship in the correlation has a low impact, for Holstein it´s 14% and for Jersey 8%. This means for Holsteins that if the dam's phenotypic breeding values increase by one unit it affects the bulls breeding value only by 14%.

For the trait kg fat, all breeds have a significant correlation. It is possible to see a clear difference in the correlation for Nordic red, which now with significant correlation is more consistent with the other breeds. R^2 shows that the bull dam's phenotypic breeding values affects the bull's breeding values by almost 12% and for Jersey and Nordic Red by 4%.

For the body trait Nordic red has the highest correlation and significance. Holstein's correlation is lower but significant. Jersey has a lower correlation and it´s not significant. The reason why the red breed has a higher correlation than Holstein is not established, but it could be a larger spread in Holstein which weakens the correlation. Or it is just a coincidence that the result turned out that way. For Jersey the low correlation and lack of significance might be because there is too little data.

For udder the correlation is almost the same for Holstein and Nordic red, and for both it´s significant. For Jersey the p-value is higher than 5%, so the correlation is not significant. R^2 shows that the dam's phenotypic breeding values affects the bulls breeding values by 5% for Holstein and 4% for Nordic Red. For Jersey it is almost 2%, but it is misleading since it lacks significance.

For the last trait, feet & legs, the correlation is just as with udders relatively similar between Holstein and Nordic red. R^2 also shows a similar influence of 2% to 3% from the phenotypic breeding values of the bull dam. Jersey again has a correlation that is not significant and therefore the low correlation and R^2 are misleading.

The reason why Jersey does not get any significant correlation for the exterior traits might be because it´s too little data to determine a result on. Based on the correlations that Holstein and Nordic red have shown for the exterior traits it´s lower than it´s for the production traits. If the correlation is low a larger amount of data is probably needed to be able to prove that the correlation is not a coincidence. Because of that you probably would have needed a larger amount of data to define a significant correlation for the exterior traits for Jersey.

The result shows that there is a correlation between the bull dam's phenotypic breeding values and the bull's estimated breeding values. The significant correlation varies between 0.2-0.37 for production traits and between 0.13-0.25 for conformation. However, what the result also are showing is that the correlation does not have a major impact. For production the bull dam's phenotypic breeding values affect the bull's estimated breeding values by 2-14%. The remaining % are other external factors that affect the bull's estimated breeding values, but those factors are not included in this model. For conformation the phenotypic breeding values of the bull dam's affect the bull's breeding values only by 1-6%.

The results confirm that there is a very high uncertainty in choosing a bull based on the phenotypic breeding values of the dam. The diagrams show that several bulls with high breeding values have dams with low breeding values and vice versa. It's therefore not possible to assume that a dam with high production and conformation will pass it on, but what is passed on is what is in the genes. Animals with genetically poor breeding values can have a good exterior and high production, but then it's due to other factors or coincidence. However, it´s possible to say with significantly higher certainty what is passed on if the breeding animals are genomically tested and especially if the bulls are proven. The dam's phenotypic breeding values are also problematic to take into account, as they are affected by the herd and management she comes from. It's also a human evaluation that is made in the confirmation assessment, which generates a higher uncertainty. The dam's breeding value is also already included in the bull's own breeding value, so when selecting based on the dam she is valued twice.

By choosing breeding bulls based on the phenotypic breeding values of the dam and not based on the bull's NTM, you miss out on profits. NTM aims to develop traits that have an economic impact and the animals' traits are valued based on that. Animals with high NTM have genetic qualities which means they are more feed efficient, healthier, have high fertility and more. Just by increasing NTM by one unit, income will increase by 9 € per year and animal. It is in the genes, so nothing else is required for income to increase. The advantage of breeding based on NTM is that several traits are improved simultaneously. Maximum development of one trait can be achieved, but it´s at the expense of another trait. For example maximum development of yield would lead to a decrease in fertility. NTM is calculated so that development can occur, without it costing another trait.

NTM is a total index which provides a combined assessment of all the economically valuable characteristics that an animal has. This means that individual traits may have a breeding value that is lower than the average, but overall the animal can have an NTM above the average. The animal then has other economically valuable traits that outweigh the trait that is lower than the average. If you then make a minimum selection and decides to exclude a breeding animal due to a one low rated trait you miss out on genetic progress in other economically valuable traits. This makes it problematic to have minimum selection as a strategy in breeding planning. It is more advantageous to look at NTM and select breeding animals based on that, because then you know that there will be a development for several traits.

To generate high reliabilities in NTM the breeding values must have high reliabilities and it´s the genomic breeding values that will provide the highest. If you have reliable breeding values you know what breeding material you may work with and you can plan the breeding work, so that it becomes ideal for each individual. Proven bulls have the highest reliabilities in their breeding values, but they only generate half the truth about what the offspring will be like. The dam, who is the other half, is just as important and should therefore also have reliable breeding values!

7 Conclusion

The correlation between the bull dam's phenotypic breeding values and the proved bulls breeding values are low. There are also many other factors that affect the bull's breeding values that are not related to the bull dam´s phenotype. The reliabilities in the bull dam's phenotypic breeding values are low and irrelevant and should therefore not be considered when planning the breeding work. To ensure that the breeding work generates a higher income and development, the easiest and safest way is to invest in animals with reliable breeding values and high NTM.

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