

Genomic breeding values give better breeding decisions

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It is documented that genomic breeding values are more precise in finding the genetic superior heifers than ordinary breeding values. Genetic superior animals have themselves higher economic output, and they will also give the genetically best offspring in next generation. Combined with intensive use of sexed semen and beef semen genomic breeding values are efficient tools to increase the genetic potential for economy in your herd.

Genomic tests have become widely used in the Nordic countries in the recent years. In RDC and Jersey nearly 30% of the animals born in 2020 are genomically tested, while it is almost 20% for Holstein.

A genomic test can be used to improve mating plans by combining strong/weak traits in females and insemination bulls in a better way and to prevent heritable diseases. However, the most important use is to decide which females should be inseminated with sexed semen, in order to produce next generation of heifers, and which should be inseminated with beef semen. Today, females that should be inseminated with sexed semen are chosen based on parents' genetic level (parent average) for heifers or improved with own performance for cows. However, by identifying the superior heifers and cows and use sexed semen more precisely on these animals the genetic level of your future generation of heifers, and thus the economy of your herd, can be improved.

Higher genomic breeding values equals better performance

To show that genomic breeding values are more precise, data from 240 Nordic farms that use genomic tests is analyzed. In those herds heifers born in 2017 are used. All heifers get two NTM's based on either parents' average indices (NTM_{PA}) or indices where genomic information is included ($NTM_{genomic}$). Heifers are divided in two groups within herd based on either NTM_{PA} or $NTM_{genomic}$. Subsequently we calculate difference in performance between groups when heifers become cows and get own performance in 1st and 2nd lactation. Finally, mean differences across herds are calculated. Results across herds are shown in table 1.

Table 1. Differences in performance between groups with highest or lowest NTM within herd when grouping is based on $NTM_{genomic}$ or NTM_{PA}

Trait	Heifers grouped based on:		Favorable direction:
	$NTM_{genomic}$	NTM_{PA}	
1st lactation			
Milk yield (kg)	-280	-80	Lower = less milk
Fat yield (kg)	13.3	12.2	Higher = more fat
Protein yield (kg)	2.3	5.1	Higher = more protein
1 st to last insemination (days)	-5.7	-4.9	Lower = less days
Cows with mastitis (% points)	-1,5	-0.8	Lower = less mastitis
Udder (scale 1-9)	0,8	0.6	Higher = better score
Stillbirth (%)	-2.0	-1.0	Lower = fewer dead calves
Survival to 2 nd lactation (%)	1.9	1.8	Higher = better survival
2nd lactation			
Milk yield (kg)	-260	-80	Lower = less milk
Fat yield (kg)	19.1	14.9	Higher = more fat
Protein yield (kg)	6.4	7.2	Higher = more protein

1 st to last insemination (days)	-3.1	-1.6	Lower = less days
Cows with mastitis (% points)	-1.3	0.2	Lower = less mastitis
Survival to 3 rd lactation (%)	1.1	-1.5	Higher = better survival

Results show that total yield of milk solids are nearly the same no matter if groups are based on NTM_{PA} or NTM_{genomic}, however reduction in fluid is higher when grouping is based on NTM_{genomic}. If ARLA's payment model with negative value on milk is used, it means that the difference in economic value of milk production is nearly the same in both 1st and 2nd lactation, no matter if the grouping is based on NTM_{genomic} or NTM_{PA}.

For fertility, udder health, classification of udder and calving the differences between groups are bigger when grouping is done based on NTM_{genomic}. For survival there is no difference in performance in 1st lactation, while there is a large difference in performance in 2nd lactation in favor of NTM_{genomic}.

In general, genomic breeding values are better in finding the females that perform better themselves and have the highest economic potential. How much money you can earn by using genomic test in your herd depends also on the reproduction, longevity, and calf mortality in your herd.

Herds used in the analysis

Herds from Denmark, Sweden and Finland was included. Genomic tested heifer calves born in 2017 was the basis. Further it was required a minimum level of registration. Herds should have at least 20 animals with yield records and minimum 10 records for fertility, udder health and classification of conformation. If this was not the case the registrations for that particular trait group was deleted.