

## **Improved genetic progress after introduction of genomic selection –a red dairy cattle example**

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### **Summary**

The VikingRed breeding program received the first genomic enhanced breeding values (GEBV) from Nordic Cattle Breeding Evaluation (NAV) in autumn 2009. Genetic trends are compared for both bulls and females between two periods, 2001-2008 and 2009-2016. The data consists of records on 3,104 AI-bulls and more than 2.4 million females. 14 traits included in the Nordic Total Merit index (NTM) are included in this study. All studied traits, in both males and females, have had a positive genetic trend since the introduction of genomic selection (GS). The annual genetic progress, both before and after the introduction of GS, was highest in NTM, yield index, udder conformation and longevity for both males and females. The traits with the largest genetic improvement in bulls, after the introduction of GS, are feet & legs, daughter fertility, longevity, mastitis resistance, claw health, yield index and birth index. The improvement of the individual traits generated a major increase of the NTM. The traits with the largest improvement in females, since 2009, are claw health, young stock survival, feet & legs and daughter fertility. The genetic progress has been larger in the end of the "genomic era" than in the beginning. A gradual adjustment of the breeding program has occurred; improvement of reliability of GEBV, increase of selection intensity through a reduction of the number of AI-bulls and a decrease of the generation interval through the promotion of young bulls as sires in the breeding program and an increased proportion of females inseminated with semen from superior young genomic tested bulls.

*Keywords: Stålhammar, Red dairy cattle, GEBV, genetic gain*

### **Introduction**

Meuwissen *et al.* (2001) suggested that selection using genome wide dense marker maps would dramatically increase genetic gain due to improved accuracies and decreased generation intervals. This also include traits with low heritability. Schaeffer (2006) applied a strategy for genome-wide selection in dairy cattle, resulting in an improved genetic gain at a lower cost. Since then, GS has changed the way cattle breeding companies organize their breeding work.

The autumn of 2009, GEBV became available for VikingGenetics for Red Dairy Cattle from the NAV. From the beginning, the reference population consisted of domestic bulls from Sweden, Finland and Denmark. Over the years, the reference population has extended to include bulls from Norway (NRF) and Germany (Angler) and a large number of females. In August 2017, the reference populations consisted of 8,212 bulls and 32,315 females.

Several major changes of the breeding program have been performed; the number of AI-bulls has decreased from 266 bulls born in 2000 to 101 bulls born in 2015. One in 30

genomic tested candidates is selected based on GEBV. The sires in the breeding program have become young genomic tested bulls. The dams are to an increasing proportion heifers and a growing proportion of candidates are born by ET-recipients. Dairy farmers in Denmark, Finland and Sweden have largely accepted the bulls with genomic proofs. The proportion of sold doses of daughter proven bulls on the domestic market has gradually decreased from 75 % to less than 5 %.

The aim of this study is to compare the genetic trends for both bulls and females between two periods, before and after the introduction of GS, for Nordic Total Merit index and the 14 traits included in the index.

## Material and methods

The data consists of records on 3,104 AI-bulls and more than 2.4 million females, born between 2001 and 2016. Trends for males and females are studied separately. Investigated traits are the 14 traits included in NTM and the NTM. The data is from the official breeding estimation done in August 2017 by NAV, <http://www.nordicebv.info/ntm-and-breeding-values/genetic-trends>. The animals were divided into four groups; bulls and females born before and after the introduction of GS. The proofs are expressed with a mean of 0/100 for NTM/sub-traits and a standard deviation (STD) of 10 index units.

## Results

Table 1 and 2 show the annual genetic progress before and after the introduction of GS. Before the introduction of GS the genetic gain exceeded 1/10<sup>th</sup> of a STD in both males and females in only NTM, yield index, udder conformation and longevity. For several traits (daughter fertility, general health, claw health, birth index and young stock survival), the genetic trend was close to zero or even negative in both sexes. After the introduction of GS, all traits in both sexes had a positive genetic trend. Males had after the introduction of GS also exceeded 1/10<sup>th</sup> of a STD threshold for mastitis resistance, daughter fertility, feet & legs and milkability. The rate of genetic gain for AI-bulls had improved for 12 of 14 sub-traits. Corresponding figures for females was 11 of 14 sub-traits. The traits in AI-bulls with the largest increase in genetic trend, after the introduction of GS, were feet & legs, daughter fertility, longevity, mastitis resistance, claw health, yield index and birth index. The improvement of the individual traits generated a major increase of the NTM. The traits in females with the largest improvement in rate of genetic gain, since 2009, were claw health, young stock survival, feet & legs and daughter fertility.

After the introduction of GS, the genetic gain in males was considerable higher than in females. The improvement of the trend in NTM was 5 times higher in males than in females. However, the rate of improvement of the mean for the 14 sub-traits differed less between the sexes. This was due to decreased trend in yield index for females. Yield index is the individual trait with the highest weight in NTM.

In table 3, the period after the introduction of GS was divided into two periods, 2009-2013 and 2013-2016. The genetic gain was higher in the later period in both sexes for NTM as well as for the yield index.

*Table 1. Rate of genetic gain for the Nordic Total Merit index and the 14 sub-traits for AI-*

*bulls born between 2001-2008 and 2009-2016.*

Trait	AI-bulls		
	2001-2008	2009-2016	Difference
NTM	1.92	3.42	+1.50
Yield index	1.15	1.79	+0.64
Daughter fertility	0.02	1.00	+0.98
Mastitis resistance	0.25	1.05	+0.80
General health	-0.08	0.37	+0.45
Claw health	-0.21	0.53	+0.74
Birth index	-0.04	0.53	+0.57
Calving index	0.59	0.40	-0.19
Frame	0.52	0.62	+0.13
Feet and legs	0.44	1.48	+1.04
Udder conformation	1.30	1.40	+0.10
Longevity	1.13	2.07	+0.94
Young stock survival	-0.07	0.22	+0.29
Temperament	0.70	0.30	-0.40
Milkability	0.76	1.07	+0.31

*Table 2. Rate of genetic gain for the Nordic Total Merit index and the 14 sub-traits for females born between 2001-2008 and 2009-2016.*

Trait	Females		
	2001-2008	2009-2016	Difference
NTM	1.88	2.16	+0.28
Yield index	1.41	1.20	-0.21
Daughter fertility	-0.19	0.33	+0.52
Mastitis resistance	0.17	0.52	+0.35
General health	-0.09	0.10	+0.19
Claw health	-0.27	0.47	+0.74
Birth index	0.00	0.25	+0.25
Calving index	0.50	0.55	+0.05
Frame	0.44	0.43	-0.01
Feet and legs	0.34	0.89	+0.55
Udder conformation	1.06	1.13	+0.07
Longevity	1.07	1.36	+0.29
Young stock survival	-0.27	0.47	+0.74
Temperament	0.73	0.29	-0.44
Milkability	0.60	0.77	+0.17

*Table 3. Rate of genetic gain for the Nordic Total Merit index and the yield index for females*

and AI-bulls born between 2009-2013 and 2013-2016.

Sex	Females		AI-bulls	
	2009-2013	2013-2016	2009-2013	2013-2016
NTM	2.38	2.47	3.04	4.06
Yield	1.18	1.38	1.73	2.24

## Discussion

We are in the transition period between the past, progeny-testing breeding schemes, and the future, breeding schemes design for GS. Schaeffer, 2006, predicted a situation with a large reduction in the generation intervals. Today the VikingRed breeding program have implemented a short generation interval; young sire in the breeding program and more than 95 % of the sold doses on the domestic market are from young bulls. Furthermore, the number of genotyped bull calves per year has increased to 3,000 and the number of AI-bulls per year has decreased to 100, giving a higher selection intensity. In the example of a traditional progeny-testing scheme presented by Schaeffer, 2006, the annual genetic gain was 0.195 genetic standard deviation. The progress achieved by the VikingGenetics precursors is in the same size. In the genome-wide selection scheme of Schaeffer 2006, the annual gain was 3.88 times higher than the traditional scheme. Since 2009, the genetic gain in the VikingRed program has increased 78 % and for the last 4 years, the improvement was 111 % in males.

Meuwissen *et al.* (2001) forecasted the shorter generation interval and a dramatically increased rate of genetic gain, especially in traits where selection on phenotypic records is difficult (including traits with low heritability), in future breeding programs. Since 2009, the genetic trend for functional traits such as daughter fertility, mastitis resistance, claw health, and birth index have improved considerable. The genetic trend for all traits in both sexes have been positive since the introduction of GS.

The transition into the “genomic era” is faster for AI-bulls than for the national female population. All AI-bull candidates have been selected on their DNA-profiles. The superiority of the selected AI-bulls will be transmitted to the next generation of females.

## Conclusions

Since the introduction of GS, the genetic trends have been positive for all traits included in the NTM in both sexes. The improvement of genetic gain was more pronounced for AI-bulls than for the national female population. However, the females are expected to follow the same enhanced trend.

## List of References

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