

Improvement of genomic breeding values

Anders Fogh, Emma Carlén and Terhi Vahlsten

In February 2018 genomic breeding values for calving, fertility, claw health, general health and longevity are improved by adding females in reference population. This has the largest impact for claw health and general health (all breeds), but also an impact for calving for RDC and Jersey.

More cows are being genomic tested. This means that more information from cows is available for genomic prediction. Therefore, NAV has improved genomic evaluation by including female information for many traits. In February, it also happens for calving, fertility, claw health, general health and longevity, and the only remaining trait is youngstock survival.

Largest change for general health and claw health

The effect of adding females to the reference group depends on how much information we had previously. The traits with the lowest amount of information based on bulls alone is claw health and general health. For these traits and calving for RDC and Jersey, the biggest change in breeding values are observed. In table 1 changes are shown for young genotyped bulls, but similar changes are observed for genotyped heifers.

Table 1. Frequency (%) of young genotyped bulls, born 2015-2016, with certain change in breeding values for calving, fertility, general health, claw health and longevity between official run in November and February 2018

Index units	Calving			Fertility			General health			Claw health			Longevity		
	RDC	HOL	JER	RDC	HOL	JER	RDC	HOL	JER	RDC	HOL	JER	RDC	HOL	JER
< -9										5		6			
-9 - -7			2	2	5	1			1	14	1	7	1		2
-6 - -4	6	1	10	13	23	13	6	10	5	13	11	13	17	1	21
-3 - 3	56	98	57	83	72	80	85	87	65	44	72	53	81	98	76
4 - 6	29	1	16	2		6	9	3	19	7	11	9	1	1	1
7 - 9	6		5						10	8	5	8			
> 9	3		10							9	1	4			

Genomic evaluation for claw health for Jersey

Besides the improvements mentioned above, genomic evaluation for claw health is introduced for Jersey. This means that in the calculation of NTM for genomic tested young animals pedigree indices are substituted. This gives a NTM with a higher reliability