

Improved genomic prediction

- Females in reference for more traits**

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Nordic Cattle Genetic Evaluation

Reference population

January 2018

	Reference population	
	Bulls	Cows
Holstein	35,800 ^{a)}	31,600
RDC	8,900 ^{b)}	33,500
Jersey	2,630 ^{c)}	18,200

a) Includes proven bulls from NLD, FRA, DEU, ESP, POL

b) Includes proven bulls from NOR

c) Includes proven bulls from USA

Tested females per country and birth year

Year	Holstein			RDC			Jersey		
	DNK	FIN	SWE	DNK	FIN	SWE	DNK	FIN	SWE
2011	1,775	1,142	366	903	3,613	1,921	4,099	6	90
2012	2,725	1,817	587	1314	3,760	2,144	4,636	6	112
2013	4,277	2,618	1,633	1,642	3,489	2,451	3,535	13	84
2014	4,720	2,846	2,264	1,814	3,683	2,853	4,369	29	92
2015	5,977	3,532	2,577	2,159	4,789	3,886	5,421	36	141
2016	9,583	4,846	3,793	2,708	6,867	5,183	5,328	44	145
2017	7,409	5,438	3,143	1,961	5,494	3,714	4,095	38	123
Total	40,096	22,866	14,892	13,241	34,462	23,725	25,513	126	659
	HOL total: 77,854			RDC total: 71,428			Jersey total: 34,949		
	New since last year: 26,176			17,555			8,651		

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Level of genomic tested Holstein

November 2017

	Bulls with HB	NTM	Bulls with out HB	NTM	Females	NTM
Born	Number		Number		Number	
2011	192	6,5	1,541	-0,7	3,283	-2,0
2012	211	10,0	1,970	2,4	5,129	0,4
2013	173	13,5	2,224	5,2	8,528	2,4
2014	130	18,9	3,045	7,4	9,830	4,7
2015	97	23,6	2,609	11,1	12,086	7,0
2016	77	27,5	2,745	15,3	18,222	10,6
2017	24	30,1	2,477	18,9	15,990	13,0

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Level of genomic tested RDC

November 2017

	Bulls with HB		Bulls without HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2011	260	3.2	1,552	1,6	6,436	-1,9
2012	208	7,8	2,131	2,6	7,218	-0.2
2013	196	9,6	2,156	3,4	7,580	2,0
2014	139	13,4	2,194	5.3	8,347	3.4
2015	101	17,3	2,178	8,3	10,826	5.9
2016	96	21,8	2,130	11.8	14,749	8,6
2017	57	18,7?	1,995	14.3	11,424	10.9

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Level of genomic tested Jersey

November 2017

	Bulls with HB	NTM	Bulls without HB	NTM	Females	NTM
Born	Number		Number		Number	
2012	59	6,2	369	3,1	4,765	-1,1
2013	67	6,7	391	2,3	3,631	0,7
2014	67	9,3	428	3,2	4,488	1,9
2015	53	14,9	492	7,3	5,298	4,5
2016	31	18,4	456	9,7	5,513	7,0
2017	7	23,0	429	13,5	4,256	9,3

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Changes to be introduced

- Females in reference population for more traits: (calving, fertility, general health, claw health and longevity)
- Genomic evaluation for claw health for JER
- Calculation of ERC instead of EDC(technical change, no further comments)
- Calculation of DRP separately for males and females(technical change, no further comments)

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Efficiency of genomic prediction

(compared to pedigree information)

	HOL	RDC	JER
Yield	*****	****	****(*)
Growth	****(*)	***(*)	
Body	*****	*****	*****
Feet & legs	****	***	****(*)
Udder	*****	****(*)	*****
Milking speed	*****	*****	****(*)

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Efficiency of genomic prediction

(compared to pedigree information)

	HOL	RDC	JER
Fertility	****	**	*(*)
Birth	***(*)	****	-
Calving	***(*)	**(*)	*
Udder health	****(*)	****	***(*)
General health	**(*)	**(*)	**
Claw health	**	**	* (new trait)
Temperament	***	**	(*)
Longevity	***	**	*
Y. Stock survival	*	*	No evaluation

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Extra reliability due to females in reference

	HOL	RDC	JER
Fertility	*	*	(*)
Birth	-	*	-
Calving	-	*	-
General health	**	**(*)	**
Claw health	***	***	***
Longevity	*	-	*

Gain by adding females is largest when number of bulls in reference is smallest

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Reranking of genotyped heifers and bull calves due to females in reference and other changes

	HOL	RDC	JER
Fertility	-	**	**
Birth	-	*	**
Calving	-	**	***
General health	*	**	***
Claw health	***	***	New trait
Longevity	-	*	**

Reranking is largest when relative gain is largest

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Relative no. of females in reference population - compared to production

	HOL			RDC			JER
	DNK	FIN	SWE	DNK	FIN	SWE	DNK
Prod. (%)	100	100	100	100	100	100	100
Type (%)	75	72	68	85	74	74	82
Temp. (%)	10	59	40	23	60	57	17

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Summary

- Females in reference: calving, fertility, general health, claw health and longevity
- Largest improvement for traits where females add biggest proportion of extra reference information (claw health for all breeds)
- Reranking of genotyped heifers and bull calves within traits dependents on extra reliability

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Summary (continued)

- Registrations of temperament on more cows in DK can improve genomic prediction.
- Changes are planned to be introduced in the February run.

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