

## **Udder Coordinates from Lely Milking Robots 2015**

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Conformation traits for the udder have been recorded for many years in Denmark by individual assessment of the cow, and the recordings are used in the breeding values estimations. However, conformation traits are usually only been recorded once per cow per parity. It has, therefore, not been possible to follow potential changes within lactation period of the cow. With the introduction of milking robots in the some Danish milking herds; it is possible to transfer multiple observations for the udder conformation from the national database and use these additional observations for the udder conformations in the breeding value estimations.

The purpose of this preliminary study was to estimate heritabilities for Udder Conformation Traits observed with milking robots; and to find the genetic and phenotypic correlations between the traits observed with milking robots and the records from the individual assessment of the cow across the three first parities.

### **Data from Milking Robots and Individual Assessments**

The data consist of two datasets for each of the three breeds Holstein, RDM and Jersey; one dataset with milking records for the udder coordinates from Lely Milking Robots from and another dataset with the individual assessments of Udder Conformation Traits. The data for both milking robots and assessments of Udder Conformation Traits are from first, second and third parity. The milking robot data are from 2008 and onwards and observed in the interval 30 day to 60 days after last calving.

The assessments of Udder Conformation Traits are used in the routine breeding value evaluation and the data from the milking robot are new data. Therefore, Table 1 to 5 shows only means and standard deviations for the data from the milking robots. Table 1 to 3 shows the means of the data for all three breeds before and after editing. The milking robots measure the distance of specific points of the udder for each milking from a fixed set point. However, the observations performed by the milking robots are expressed on a fictitious scale without actual unit.

Table 1 Holstein: Mean, standard deviations, minimum and maximum before and after editing (single observations)

	Variable	N	Mean	SD	Min	Max
Before editing	Front Teat Placement		150.15	33.42	-110	435
	Rear Teat Placement		71.05	25.17	-161	259
	Distance, front - rear	4,966,954	124.41	28.83	-583	531.5
	Udder Balance		14.73	16.30	-197.5	264.5
	Udder Depth		587.00	69.80	293	801.75
After editing	Front Teat Placement		150.15	33.35	1	435
	Rear Teat Placement		71.05	25.10	1	259
	Distance, front - rear	3,706,151	124.37	28.55	0	531.5
	Udder Balance		14.74	16.12	-60	70
	Udder Depth		587.05	69.76	293	801.75

Table 2 RDM: Mean, standard deviations, minimum and maximum before and after editing (single observations)

	Variable	N	Mean	SD	Min	Max
Before editing	Front Teat Placement		168.93	37.25	10	381
	Rear Teat Placement		83.07	28.79	16	263
	Distance, front - rear	377,449	120.93	27.26	-6.5	303.5
	Udder Balance		3.22	15.74	-88.5	73.5
	Udder Depth		534.08	73.55	294.5	753.5
After editing	Front Teat Placement		169.86	37.32	10	381
	Rear Teat Placement		81.13	28.50	16	242
	Distance, front - rear	233,961	120.65	27.26	0	237.5
	Udder Balance		4.21	15.08	-59.5	70
	Udder Depth		561.91	62.36	347.75	742.5

Table 3 Jersey: Mean, standard deviations, minimum and maximum before and after editing (single observations)

	Variable	N	Mean	SD	Min	Max
Before editing	Front Teat Placement		149.53	30.81	20	296
	Rear Teat Placement		80.27	25.88	14	224
	Distance, front - rear	276,675	120.08	25.99	-262.5	496.5
	Udder Balance		7.34	15.39	-98	76
	Udder Depth		485.73	61.85	288.5	669.75
After editing	Front Teat Placement		147.37	30.86	35	296
	Rear Teat Placement		78.16	25.63	14	224
	Distance, front - rear	210,747	121.21	25.86	32.5	218
	Udder Balance		8.21	15.30	-60	67.5
	Udder Depth		494.61	56.42	344	666.5

Table 4 shows the frequency of number of cows over the years with data from Lely milking robot separate for each breed. Table 5 shows mean, standard deviations, minimum and maximum before editing divided up into breed, AMS type and control type for each trait.

Table 4 Frequency of number of cows over the years with data from a Lely milking robot before and after editing divided up into Holstein, RDM and Jersey

	Year	Parity 1		Parity 2		Parity 3	
		Before	After	Before	After	Before	After
Holstein	2008	4	4	2	2		
	2009	32	29	17	15	5	5
	2010	289	247	223	169	146	96
	2011	3527	2785	2696	2013	1748	1236
	2012	8259	6090	6617	4699	4040	2813
	2013	8795	6232	6909	4752	4514	2992
	2014	6928	4856	5286	3599	3446	2220
	Total	27,834	20,243	21,750	15,249	13,899	9362
RDM	2010	3	1	2	2	7	7
	2011	149	115	110	79	84	62
	2012	684	433	565	337	374	205
	2013	749	412	585	304	379	196
	2014	617	370	519	330	299	170
	Total	2,202	1,331	1,781	1,052	1,143	640
Jersey	2010			3			
	2011	87	16	47	1	56	22
	2012	319	235	332	16	186	144
	2013	506	393	513	251	389	288
	2014	455	377	402	382	291	227
	Total	1,367	1,021	1,297	650	922	681

Tabel 5 Mean, standard deviations, minimum and maximum before editing. The data was divided up into breed, AMS type and control type for each traits

Breed	AMS	Control	N	Front Teat Placement				Rear Teat Placement				Distance, front - rear				Udder Balance				Udder Depth			
	type	type		Mean	STD	Min	Max	Mean	STD	Min	Max	Mean	STD	Min	Max	Mean	STD	Min	Max	Mean	STD	Min	Max
RDM	A2	C2	32,886	168.13	41.03	73	359	84.85	31.37	23	263	120.02	28.13	17.5	303.5	2.39	16.63	-87	73.5	463.30	62.18	298.5	604.25
		C3	86,389	169.60	36.07	60	372	86.00	28.53	19	241	120.25	26.94	52.5	217.5	0.33	14.77	-78	54	483.04	66.94	294.5	679.75
	A3	C2	17,143	168.83	32.45	89	297	81.51	26.88	21	191	121.86	24.54	43.5	216.5	3.72	15.92	-53	52.5	560.48	59.75	347.75	722.25
		C3	223,655	169.00	37.44	10	381	81.63	28.05	16	235	120.22	27.41	-6.5	267.5	4.07	15.46	-88.5	72.5	559.71	63.33	357	742.5
	A4	C3	12,495	170.67	36.96	82	333	89.70	31.02	21	242	127.10	28.45	55	229.5	2.57	15.21	-51.5	40	558.76	60.52	387	705
Holstein	A2	C2	328,293	151.40	33.32	28	369	72.36	25.53	1	259	123.19	29.00	18	531.5	10.52	16.34	-85	82	517.40	60.58	293	707
		C3	762,797	150.79	32.64	1	370	72.59	24.67	11	244	123.45	28.82	-583	300.5	12.65	15.61	-86.5	264.5	538.54	68.95	293	764.25
	A3	C2	687,741	149.39	33.67	36	353	69.78	25.00	11	255	124.20	28.36	25	284.5	15.84	16.35	-107.5	89.5	599.11	62.62	340.75	798.75
		C3	2717,656	150.35	33.74	-110	435	71.19	25.33	-161	239	124.99	29.07	-27.5	527	15.49	16.49	-197.5	89	604.34	62.22	351	801.75
	A4	C3	428,996	148.09	32.30	15	351	68.55	24.77	10	237	123.79	27.90	-12.5	251.5	14.90	15.43	-102.5	77	596.28	61.20	354	778.75
Jersey	A2	C2	27,826	158.18	29.10	41	257	85.32	25.62	17	192	116.19	26.75	17	496.5	2.99	14.82	-64	58.5	414.79	58.29	288.5	566.75
		C3	13,408	158.22	31.58	79	265	87.27	29.06	23	190	117.61	30.42	-262.5	195.5	6.77	14.83	-58	46	436.00	54.24	294	579.75
	A3	C2	6780	152.27	32.30	47	244	83.25	24.59	22	149	125.63	26.95	58	194	10.12	14.38	-33	46.5	500.20	61.66	351.25	629.25
		C3	164,684	147.73	30.88	33	296	79.68	25.81	14	224	121.63	25.83	-4.5	232.5	8.42	15.41	-64	76	489.12	55.90	344	666.5
	A4	C3	60,810	147.92	30.40	48	292	77.58	25.45	14	187	120.10	26.04	32.5	215	7.48	16.05	-46	70.5	502.29	57.61	346	644.75
RDH	A2	C2	2270	157.01	33.79	90	255	75.08	20.89	34	148	136.91	34.29	63	265	8.61	13.26	-32	47	482.32	55.00	378	599.25
		C3	3932	158.56	31.05	89	241	73.08	23.01	23	143	133.48	32.04	55.5	219.5	14.11	16.85	-51.5	53.5	539.33	76.95	400.25	731
	A3	C2	1675	161.08	30.92	102	229	75.67	20.72	32	118	146.35	30.76	75	226.5	2.31	13.06	-29.5	27.5	561.39	40.59	480.5	673.75
		C3	52,140	153.60	31.32	24	326	71.45	25.07	17	208	134.17	29.55	62	218.5	19.83	16.39	-36	82	615.00	61.00	409.5	781
	A4	C3	1962	153.57	37.87	94	263	72.41	25.43	32	138	125.92	24.22	73	182	11.09	14.71	-34	42	606.03	61.91	460.25	736.5
Cross	A2	C2	43,606	160.84	35.25	61	336	80.01	27.04	19	223	120.04	27.37	9	478	8.47	14.85	-47	72.5	486.59	58.54	311.5	652
		C3	83,278	161.52	34.99	9	374	79.38	25.57	14	257	121.46	27.66	45.5	228	7.14	16.16	-75.5	86	492.90	67.28	289.75	724
	A3	C2	40,849	155.84	35.66	52	322	71.91	25.23	17	208	120.51	25.45	50.5	221	12.21	15.24	-64.5	66	589.94	61.93	364.75	746.75
		C3	272,764	156.84	35.00	-129	337	75.42	26.90	-177	245	122.07	29.79	21	556	10.29	16.84	-223	74	580.42	68.69	337.25	773.75
	A4	C3	24,122	154.78	31.40	63	340	72.04	24.02	12	189	117.42	27.09	60.5	202.5	10.94	15.59	-103	53	573.72	59.65	348.75	705

### Editing of the data

Figure 1 to 5 shows the frequency of the five traits observed with milking robots (Front Teat Placement, Rear Teat Placement, Distance Front – Rear Teats, Udder Balance and Udder Depth) before the data was edited. For the traits Front Teat Placement and Rear Teat Placement negative values were deleted. For the trait Udder Balance observations that were less than -60 and higher than 70 were deleted.

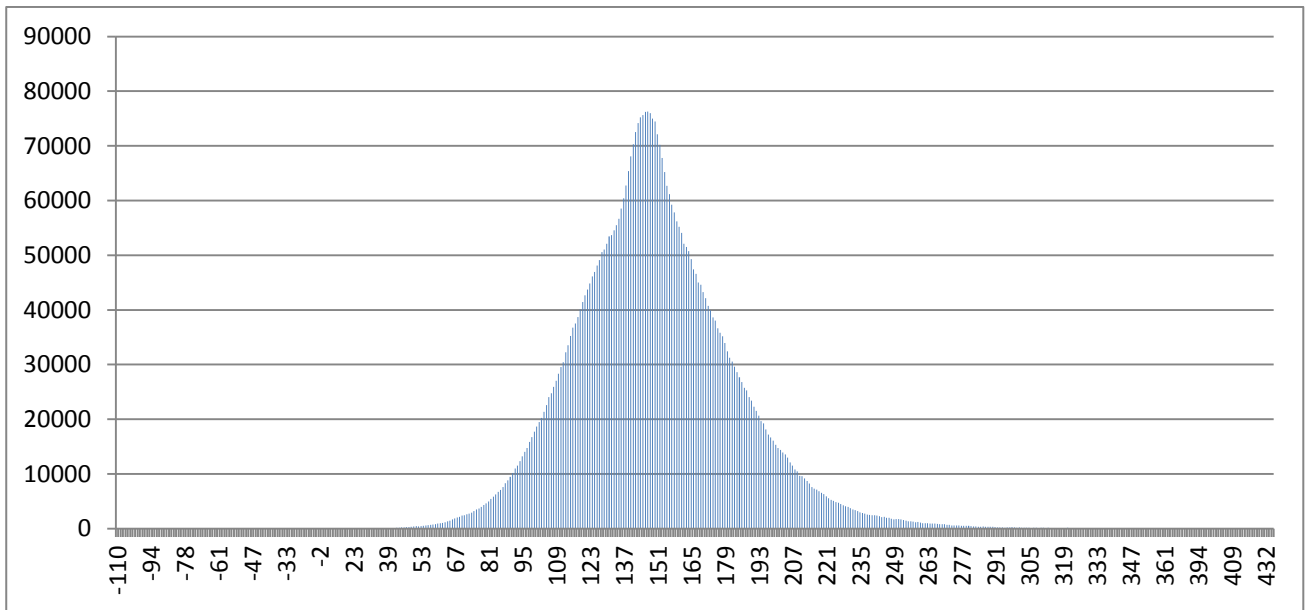


Figure 1 Front Teat Placement for Holstein before editing of data

For the trait Rear Teat Placement there were outliers in the interval 94 to 100 (Figure 2), which is due to that the coordinates come from cows with only three working teats. For the cows with three teats, a standard coordinated between 94 and 100 were given by the robot software. In order to correct these data, all the observations for the cow from these specific milking were deleted. However, it would be possible to delete only the Rear Teat Placement coordinate for the specific milking and leave the observations from the other traits for the specific cow.

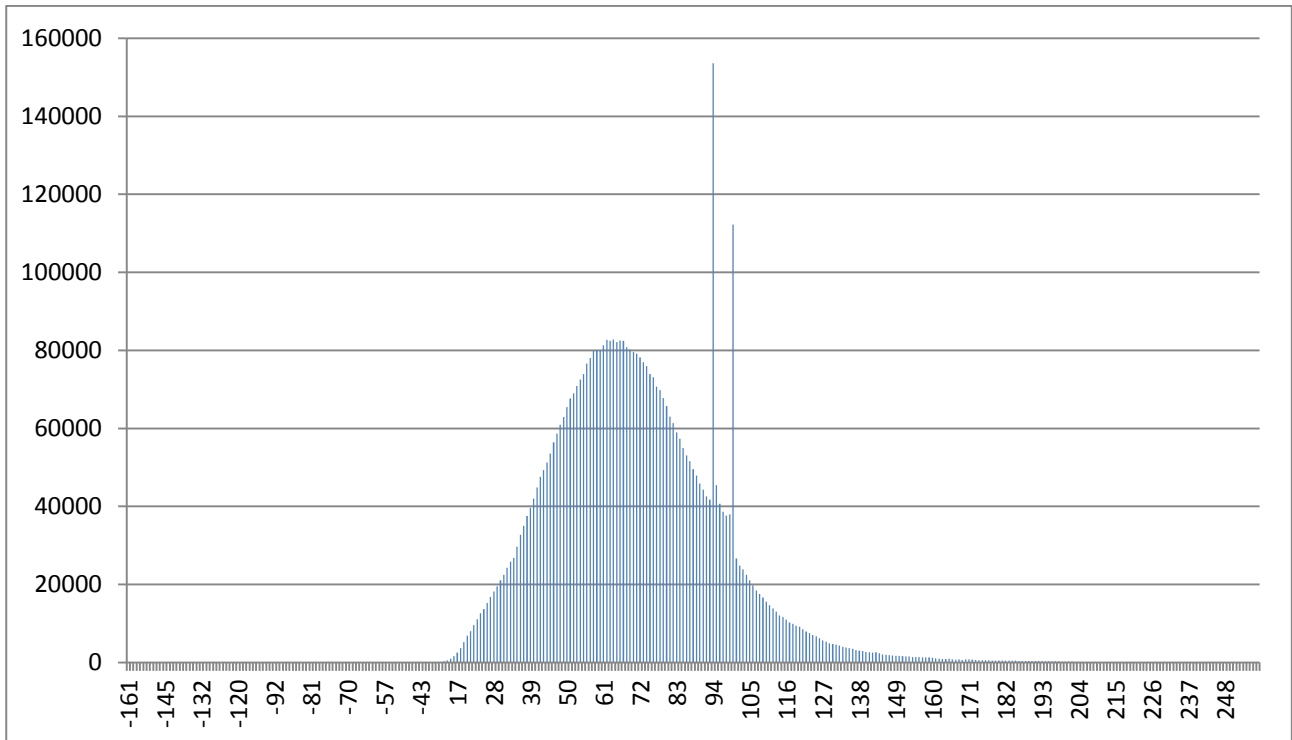


Figure 2 Rear Teat Placement for Holstein before editing of data

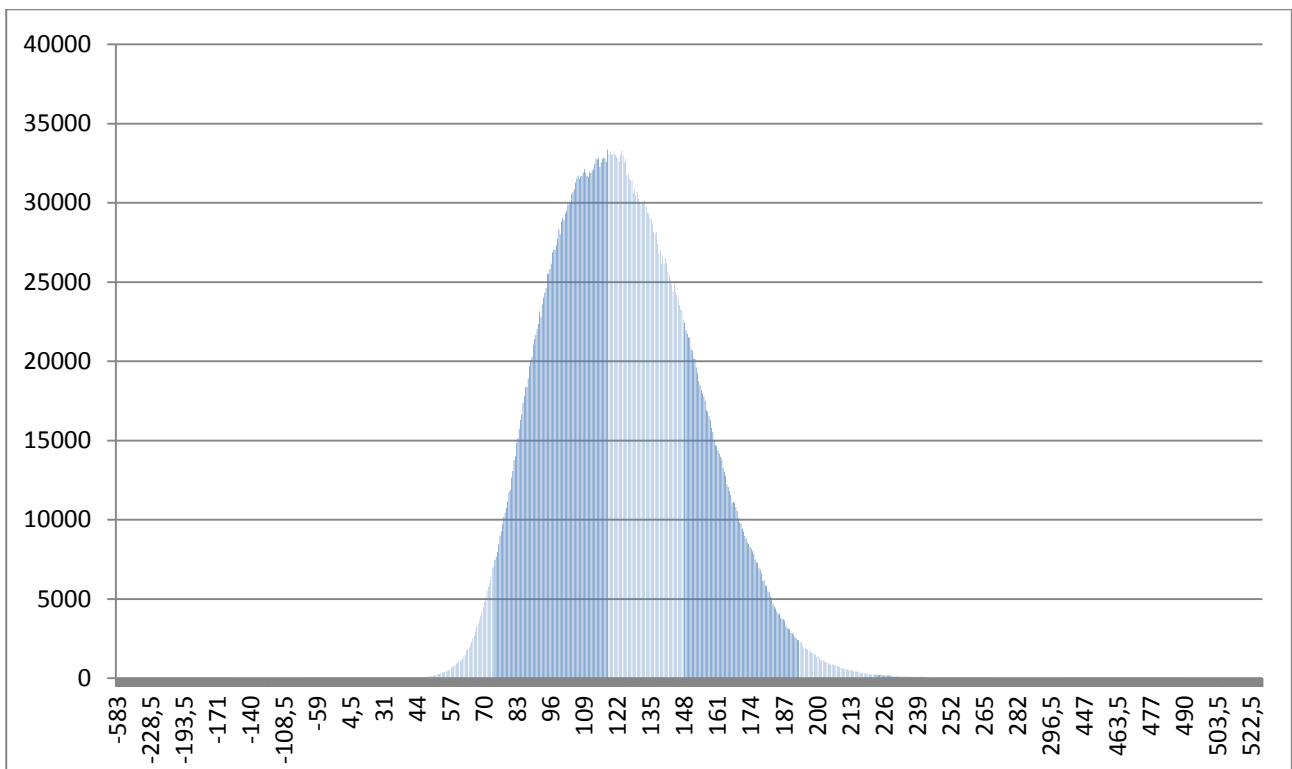


Figure 3 Distance Front – Rear Teats for Holstein before editing of data

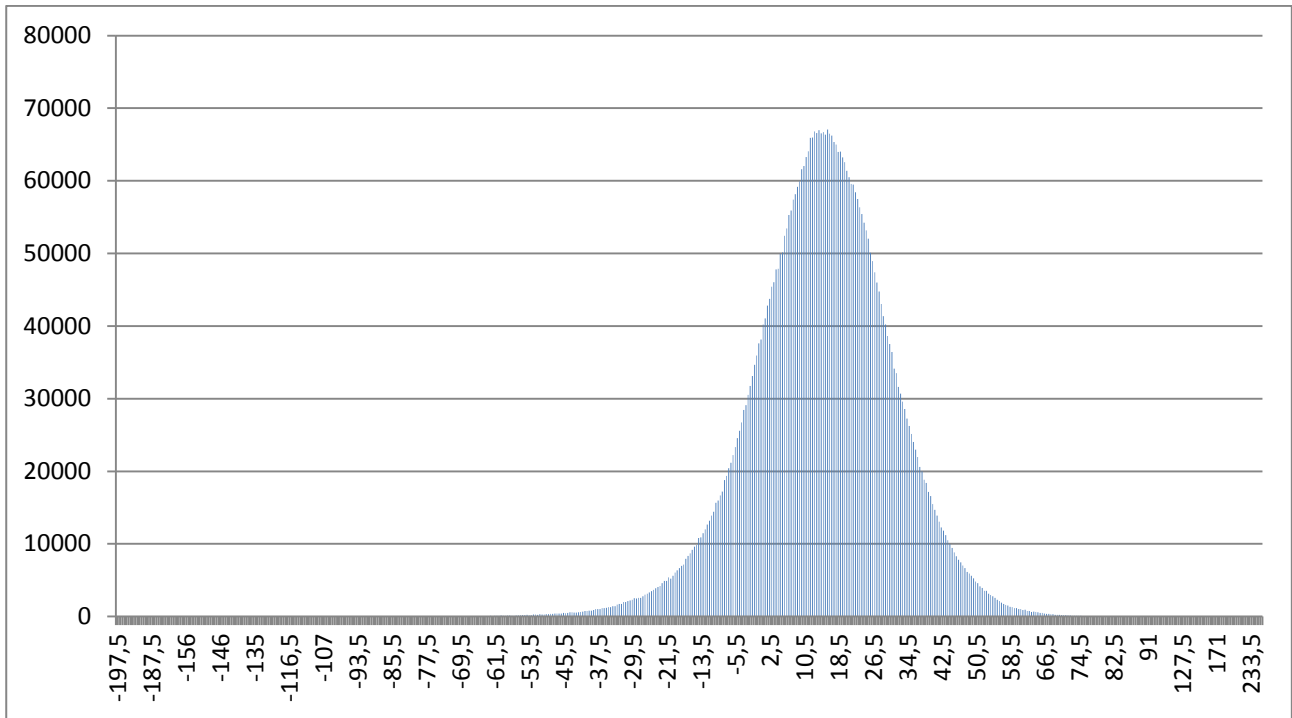


Figure 4 Udder Balance for Holstein before editing of data

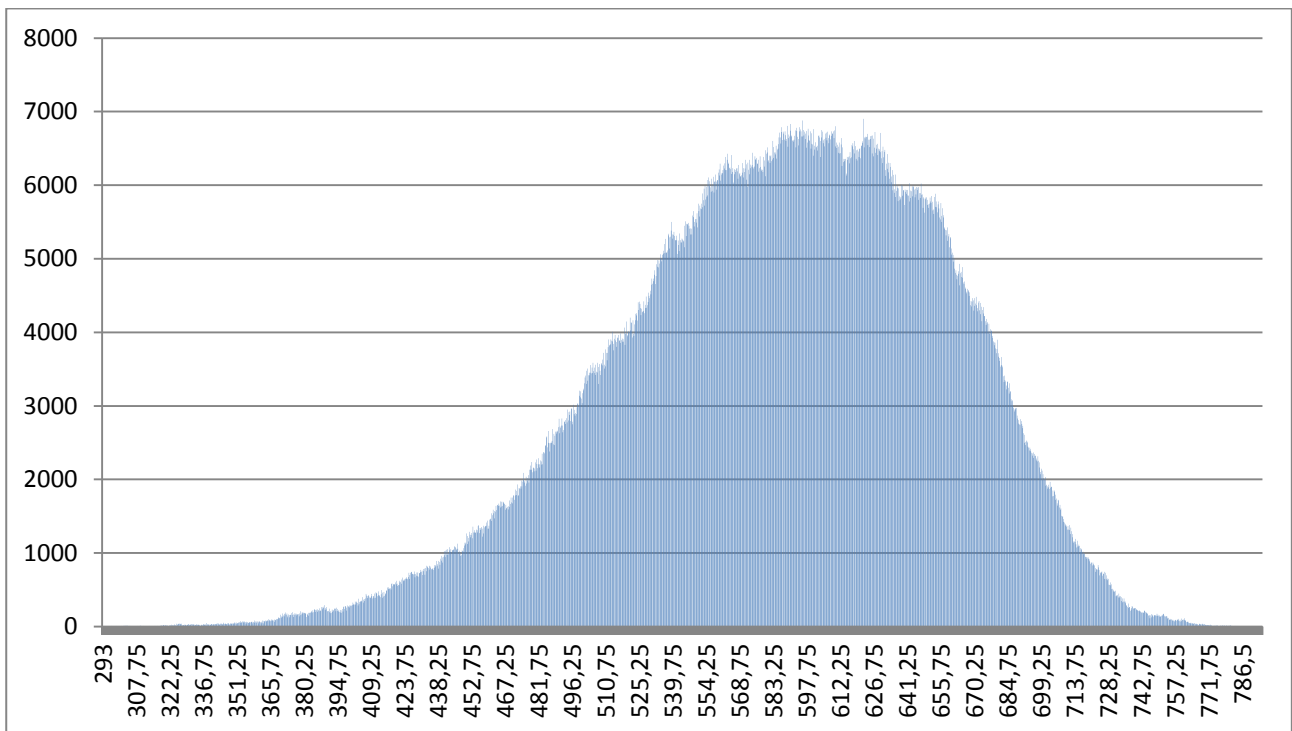


Figure 5 Udder Depth for Holstein before editing of data

Editing of the data is specified in details in Table 6 to 8 (Holstein = table 6, RDM = Table 7 and Jersey = Table 8). Table 6 to 8 shows which errors that need to be corrected, which editing that where performed and number of milking, cow and herds after editing.

Table 6 Editing for Holstein AMS

Error	Editing - deleted	N Milking	N Cows	N Herds
Number of animals before editing		5029856	46119	282
Negative values: for teat distance	Rear teat distance less than 0	5029456	46117	282
Negative values: rear teat distance	Teat distance less than 0	5029448	46116	282
Negative values: For-rear teat distance	For-rear teat distance is less than 0	5029146	46115	282
Balance is -197.5 to 264.5	Balance less than -60 and higher than 70	5027250	46110	282
Rear teat RR output is 0	Coordinate: lrmilkyield = 0	4551298	42282	270
Missing rear teat RR performance	Coordinate: rrmilkyield =.	3983555	35440	217**
Rear teat LR output is 0	Coordinate: rrmilkyield = 0	3882530	34662	217
Missing rear teat LR performance	Coordinate: rrmilkyield =.	3882530	34662	217
Teat RF output is 0	Coordinate: rfmilkyield = 0	3770780	33832	217
Lack teat RF performance	Coordinate: rfmilkyield =.	3770780	33832	217
Teat LF output is 0	Coordinate: lfmilkyield = 0	3671093	33072	217
Lack teat LF performance	Coordinate: lfmilkyield =.	3671093	33072	217
Average cow / lactation and minimum 10 milkings per average*	Under 10 milkings per lactation		32972	

\* average of milking, \*\* 65 herds without observations for lfmilkyield, rfmilkyield, lrmilkyield og rrmilkyield.

Table 7 Editing for RDM AMS data

Error	Editing - deleted	N Milking	N Cows	N Herds
Number of animals before editing		377449	3858	87
Negative values: rear teat distance	Rear teat distance less than 0	377449	3858	87
Negative values: teat distance	Teat distance less than 0	377449	3858	87
Negative values: For-rear teat distance	For-rear teat distance is less than 0	377448	3858	87
Balance is -88.5 to 73.5	Balance less than -60 and higher than 70	377213	3855	87
Rear teat RR output is 0	Coordinate: lrmilkyield = 0	335950	3531	81
Missing rear teat RR performance	Coordinate: rrmilkyield =.	254519	2524	60**
Rear teat LR output is 0	Coordinate: rrmilkyield = 0	248420	2479	60
Missing rear teat LR performance	Coordinate: rrmilkyield =.	248420	2479	60
Teat RF output is 0	Coordinate: rfmilkyield = 0	240916	2419	59
Lack teat RF performance	Coordinate: rfmilkyield =.	240916	2419	59
Teat LF output is 0	Coordinate: lfmilkyield = 0	233961	2359	58
Lack teat LF performance	Coordinate: lfmilkyield =.	233961	2359	58
Average cow / lactation and minimum 10 milkings per average	Under 10 milkings per lactation		2348	

\* average of milking, 29 herds without observations for lfmilkyield, rfmilkyield, lrmilkyield og rrmilkyield.



Table 8 Editing for Jersey

Error	Editing – deleted	N Milking	N Cows	N Herds
Number of animals before editing		276675	2815	25
Negative values: rear teat distance	Rear teat distance less than 0	276675	2815	25
Negative values: teat distance	Teat distance less than 0	276675	2815	25
Negative values: For-rear teat distance	For-rear teat distance is less than 0	276593	2815	25
Balance is -98 to 76	Balance less than -60 and higher than 70	276593	2815	25
Rear teat RR output is 0	Coordinate: lrmilkyield = 0	241109	2499	24
Missing rear teat RR performance	Coordinate: rrmilkyield =.	229213	2360	22**
Rear teat LR output is 0	Coordinate: rrmilkyield = 0	222952	2298	22
Missing rear teat LR performance	Coordinate: rrmilkyield =.	222952	2298	22
Teat RF output is 0	Coordinate: rfmilkyield = 0	217093	2252	22
Lack teat RF performance	Coordinate: rfmilkyield =.	217093	2252	22
Teat LF output is 0	Coordinate: lfmilkyield = 0	210747	2185	22
Lack teat LF performance	Coordinate: lfmilkyield =.	210747	2185	22
Average cow / lactation and minimum 10 milkings per average*	Under 10 milkings per lactation		2180	

\* average of milking, 3 herds without observations for lfmilkyield, rfmilkyield, lrmilkyield og rrmilkyield.

Figure 6 to 10 shows the frequency of the data per traits (Front Teat Placement, Rear Teat Placement, Distance Front – Rear, Udder Balance and Udder Depth) after the data was edited.

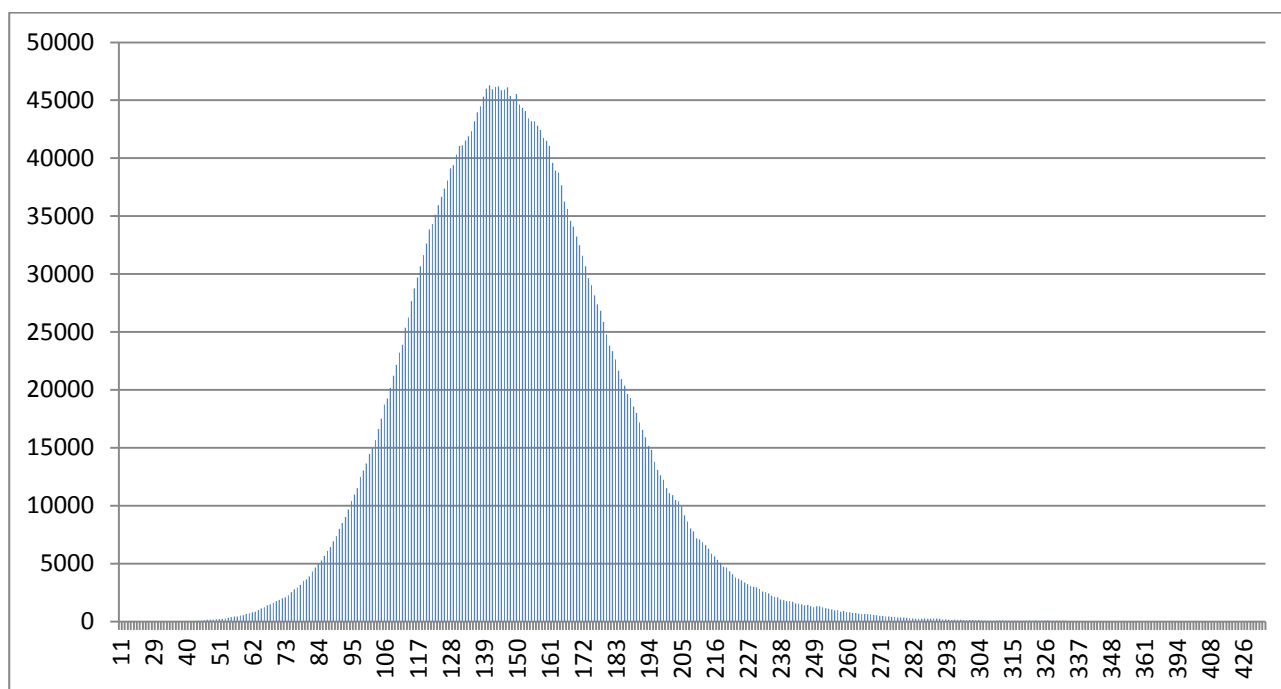


Figure 6 Front Teat Placement for Holstein after editing of data

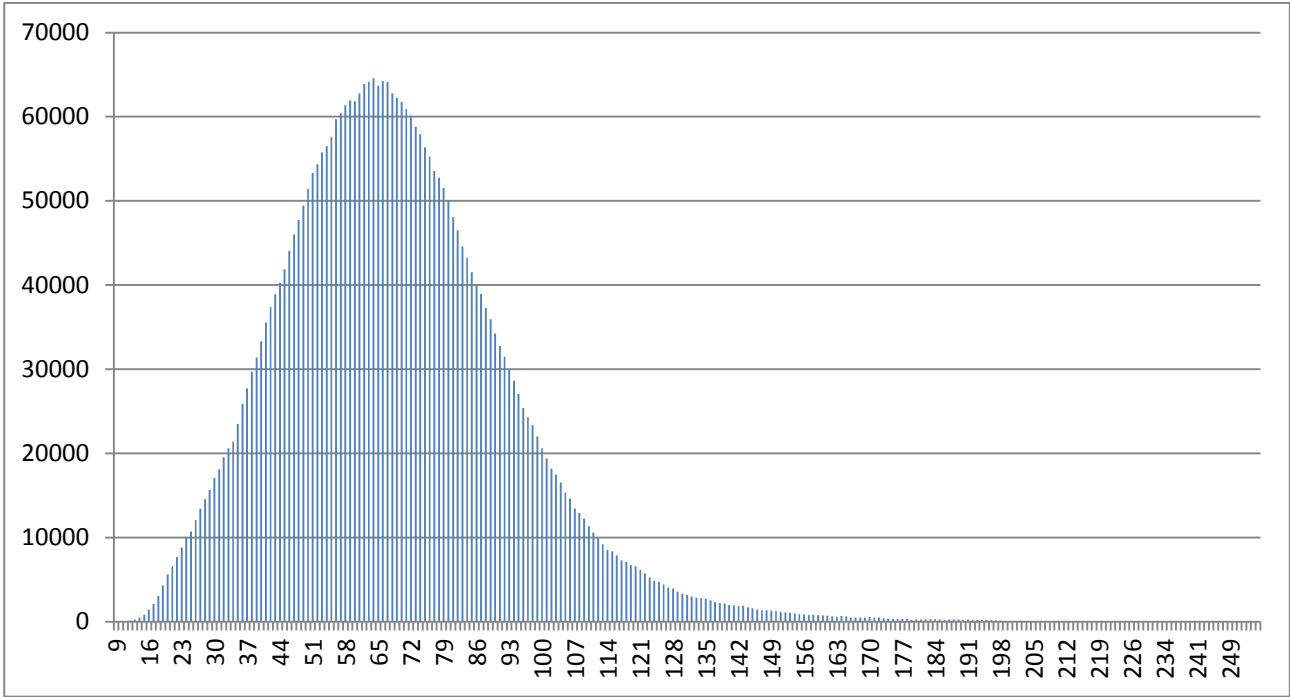


Figure 7 Rear Teat Placement for Holstein after editing of data

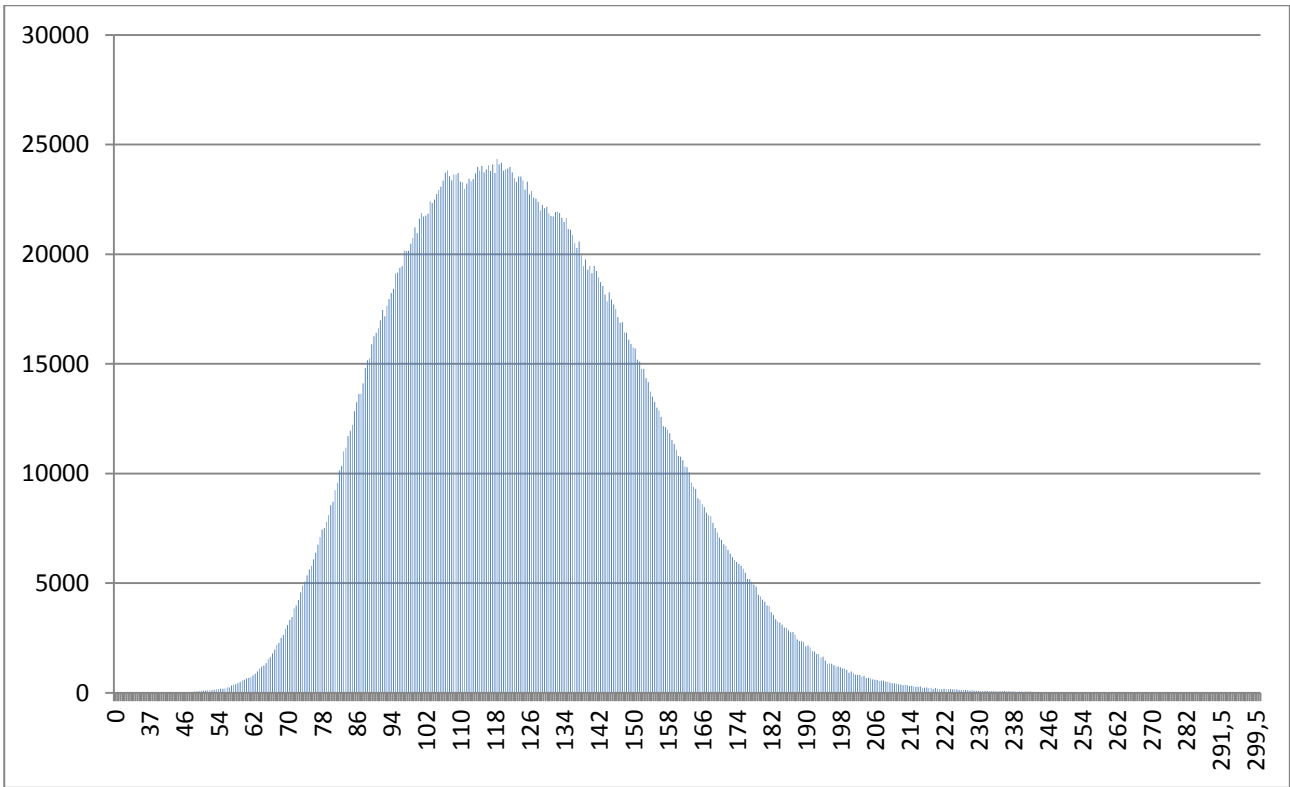


Figure 8 Distance Front – Rear Teats for Holstein after editing of data

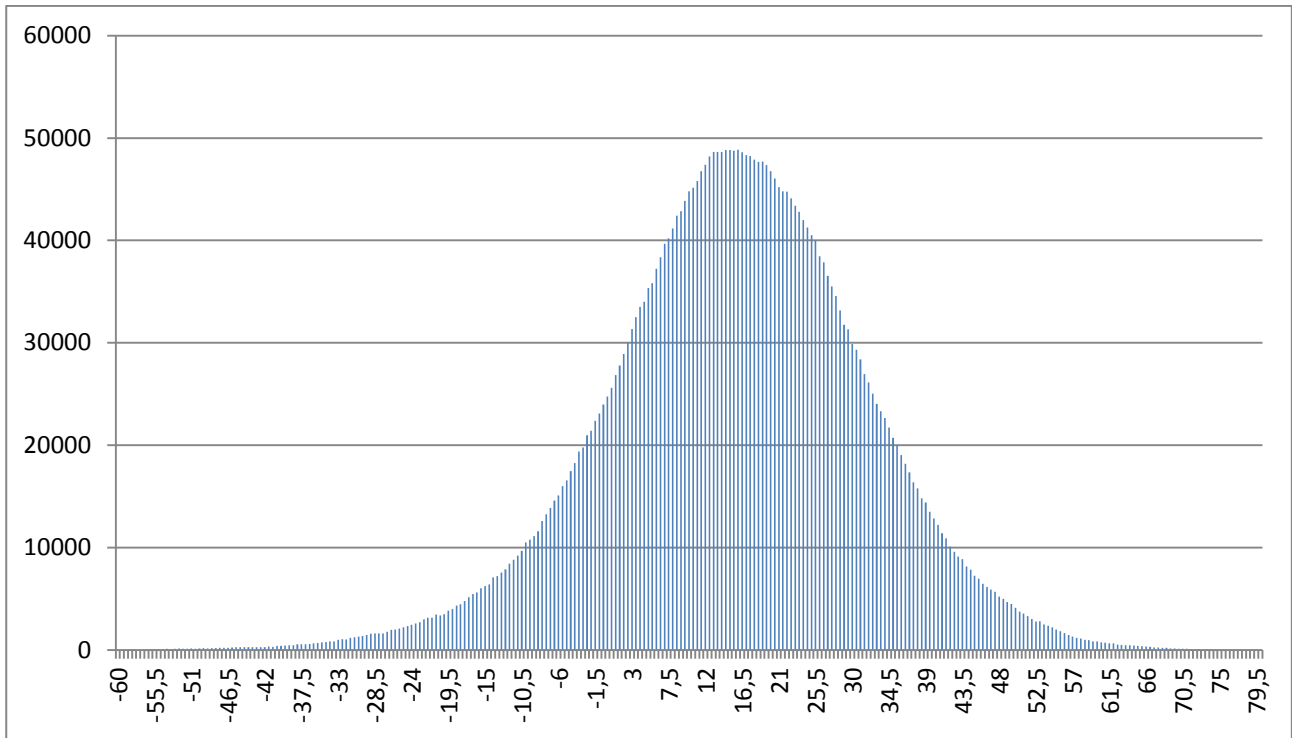


Figure 9 Udder Balance for Holstein after editing of data

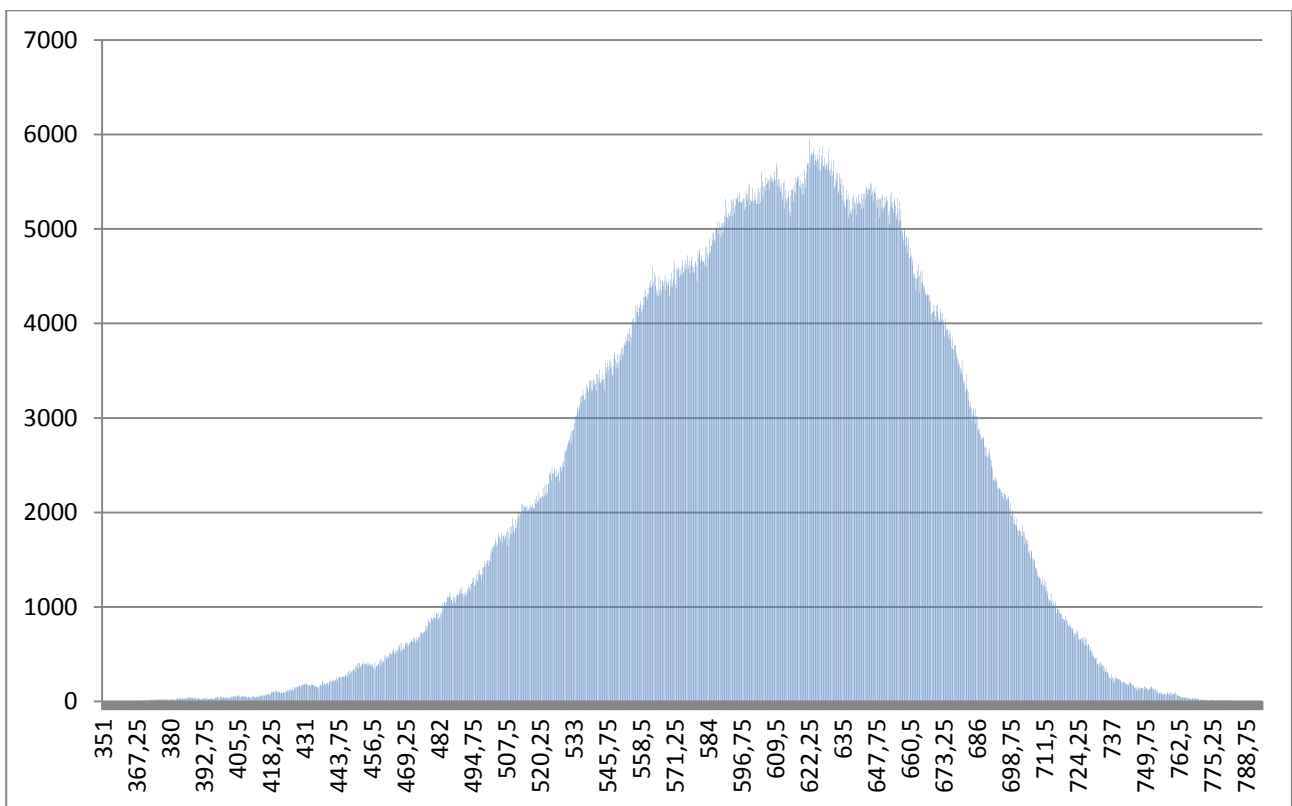


Figure 10 Udder Depth for Holstein after editing of data

## Linear data

The linear data consist of observations of the individual cow from first, second and third parity. The data was reduced for Holstein and RDM in order to estimate genetic correlation with milking robots measure for the traits Front Teat Placement, Rear Teat Placement, Udder Balance and Udder Depth. Table 9 shows the number of single observation used in the analysis. The full data converted for Jersey, except for Front Treat Placement and Udder Depth in first parity. Therefore, where only Front Treat Placement and Udder Depth in first parity reduced.

Table 9 Number of observations used from Linear traits observations

Linear traits	Parity 1	Parity 2	Parity 3
	<b>Holstein</b>		
Front Teat Placement	46115	8970	5627
Rear Teat Placement	41388	6820	4317
Udder Balance	34310	4005	2265
Udder Depth	46115	8970	5627
<b>RDC</b>			
Front Teat Placement	23795	6019	6019
Rear Teat Placement	23966	3735	3735
Udder Balance	17965	3235	3735
Udder Depth	25048	6134	5464
<b>Jersey</b>			
Front Teat Placement	63868	24261*	25623*
Rear Teat Placement	182429*	15124*	20586*
Udder Balance	140833*	7625*	10757*
Udder Depth	63868	24261*	25623*

\*Not reduced data

## Statistical analysis of udder conformation

The AMS data and the linearly scored conformation data were analysed using bi-variate or tri-variate linear animal models by means of DMU (Madsen and Jensen, 2008).The model used for analysing AMS data was as following:

$$y_{AMS} = \text{herd year} + \text{parity age} + \text{month of calving} + \text{nav\_id} + e$$

where herd year was the effect of herd-year group, parity age was the effect of age at calving in months, and month of calving was the effect of month of calving.

The model used to assessments of Udder Conformation Traits was the same as model used for the routine breeding value estimations.

## Genetic Parameters

The following tables (Table 10 to 14) show the genetic parameters for the udder conformation traits from both robots milking systems and individual assessment.

Heritability was estimated for the trait Distance Front – Rear Teats from only the robot milking machine. Genetic correlations and phenotypic correlations were estimated between first, second and third parity for Distance Front – Rear Teats for each of the breeds Holstein, RDM and Jersey (Table 10).

Table 10 Heritability (**in diagonal**) for Distance Front – Rear Teats for Holstein, Jersey and RDM divided into parity 1, 2 and 3. Genetic correlation (above diagonal) and phenotypic correlation (below diagonal). Standard error for genetic correlation is in subscript

		Parity 1	Parity 2	Parity 3
Holstein	Parity 1	<b>0.62</b> <sub>0.02</sub>	0.97 <sub>0.007</sub>	0.96 <sub>0.01</sub>
	Parity 2	0.84	<b>0.59</b> <sub>0.02</sub>	0.998 <sub>0.002</sub>
	Parity 3	0.80	0.91	<b>0.58</b> <sub>0.02</sub>
Jersey	Parity 1	<b>0.69</b> <sub>0.1</sub>	0.95 <sub>0.03</sub>	0.99 <sub>0.06</sub>
	Parity 2	0.89	<b>0.59</b> <sub>0.01</sub>	0.99 <sub>0.03</sub>
	Parity 3	0.87	0.91	<b>0.53</b> <sub>0.11</sub>
RDM	Parity 1	<b>0.59</b> <sub>0.1</sub>	0.99 <sub>0.02</sub>	0.99 <sub>0.06</sub>
	Parity 2	0.87	<b>0.47</b> <sub>0.1</sub>	0.99 <sub>0.03</sub>
	Parity 3	0.78	0.92	<b>0.41</b> <sub>0.1</sub>

Heritabilities for the traits Front Teat Placement, Rear Teat Placement, Udder Balance and Udder Depth were estimated on the basis of observations from both the robot milking machine and observations from the assessments of Udder Conformation Traits. Genetic correlations and phenotypic correlations were estimated between these eight traits divided into first, second and third parity using bi-variate models. Tri-variate models were used to estimate genetic and phenotypic correlation between traits observed with robot milking machine within first, second and third parity.

The results are shown in Table 11 for Holstein, Table 12 for RDM and Table 13 for Jersey. Genetic and residual variance from the estimations can be found in the Excel file “covariance-matrix”. For Holstein, the genetic correlation between robot observations and linear traits were high, and most of the genetic correlations over 0.90 and only a few correlations around 0.80. For RDM, the several of genetic correlations between the robot observations and linear traits were low with a high standard error or some a realistic correlation with a high standard error. The low correlations or high standard deviation seem to be caused by small numbers (under 50) of overlapping observations (cows with both linear and robot observations). These low genetic correlations or high standard errors are shown in the Table 12 in brackets. For Jersey, most of the genetic correlations were high and over 0.90. However, two of correlations (Udder Balance – linear trait third parity and robot observations parity three and Udder Depth – linear trait parity three and robot observations second parity) were low due to small number of overlapping observations (cows with

both linear and robot observations). Heritabilities for Balance second and third parity for RDM and Jersey are bit lower than the same heritabilities for Holstein. The same is the same for heritabilities for Udder Depth all three parities for Jersey are bit lower than the same heritabilities for Holstein and RDM.

Table 11 Heritability and genetic correlations for Holstein. Heritabilities are **in diagonal** and Genetic correlation (above diagonal) and phenotypic correlation (below diagonal). Standard error for genetic correlation is in subscript

		AMS			Linear traits			
		Parity 1	Parity 2	Parity 3	Parity 1	Parity 2	Parity 3	
Front Teat Placement	AMS	Parity 1	<b>0.61</b> <sub>0.02</sub>	0.86 <sub>0.07</sub>	0.84 <sub>0.01</sub>	-0.91 <sub>0.02</sub>	-0.80 <sub>0.05</sub>	-0.98 <sub>0.40</sub>
		Parity 2	0.79	<b>0.59</b> <sub>0.1</sub>	0.98 <sub>0.06</sub>	-0.91 <sub>0.02</sub>	-0.91 <sub>0.04</sub>	-0.94 <sub>0.06</sub>
		Parity 3	0.72	0.87	<b>0.61</b> <sub>0.1</sub>	-0.90 <sub>0.02</sub>	-0.91 <sub>0.05</sub>	-0.95 <sub>0.05</sub>
	Linear traits	Parity 1	-0.66	-0.61	-0.53	<b>0.37</b> <sub>0.01</sub>	–	–
		Parity 2	-0.64	-0.58	0.64	–	<b>0.35</b> <sub>0.03</sub>	–
		Parity 3	-0.77	-0.65	-0.77	–	–	<b>0.29</b> <sub>0.05</sub>
Rear Teat Placement	AMS	Parity 1	<b>0.48</b> <sub>0.02</sub>	0.93 <sub>0.01</sub>	0.85 <sub>0.03</sub>	-0.93 <sub>0.02</sub>	-0.86 <sub>0.05</sub>	-0.88 <sub>0.07</sub>
		Parity 2	0.74	<b>0.46</b> <sub>0.02</sub>	0.97 <sub>0.01</sub>	-0.91 <sub>0.02</sub>	-0.89 <sub>0.04</sub>	-0.93 <sub>0.6</sub>
		Parity 3	0.65	0.84	<b>0.41</b> <sub>0.02</sub>	-0.92 <sub>0.02</sub>	-0.92 <sub>0.04</sub>	-0.98 <sub>0.04</sub>
	Linear traits	Parity 1	-0.67	-0.61	-0.40	<b>0.34</b> <sub>0.01</sub>	–	–
		Parity 2	-0.60	-0.74	-0.67	–	<b>0.33</b> <sub>0.03</sub>	–
		Parity 3	-0.53	-0.63	-0.77	–	–	<b>0.30</b> <sub>0.003</sub>
Udder Balance	AMS	Parity 1	<b>0.48</b> <sub>0.02</sub>	0.94 <sub>0.01</sub>	0.91 <sub>0.02</sub>	0.90 <sub>0.02</sub>	0.93 <sub>0.05</sub>	0.89 <sub>0.09</sub>
		Parity 2	0.80	<b>0.48</b> <sub>0.02</sub>	0.99 <sub>0.005</sub>	0.90 <sub>0.02</sub>	0.98 <sub>0.04</sub>	1 <sub>0.09</sub>
		Parity 3	0.71	0.86	<b>0.45</b> <sub>0.03</sub>	0.90 <sub>0.03</sub>	0.99 <sub>0.04</sub>	0.97 <sub>0.06</sub>
	Linear traits	Parity 1	0.60	0.49	0.47	<b>0.21</b> <sub>0.01</sub>	–	–
		Parity 2	0.57	0.68	0.54	–	<b>0.22</b> <sub>0.04</sub>	–
		Parity 3	0.54	0.58	0.61	–	–	<b>0.23</b> <sub>0.07</sub>
Udder Depth	AMS	Parity 1	<b>0.67</b> <sub>0.02</sub>	0.98 <sub>0.005</sub>	0.96 <sub>0.01</sub>	0.97 <sub>0.01</sub>	0.90 <sub>0.04</sub>	0.83 <sub>0.06</sub>
		Parity 2	0.88	<b>0.66</b> <sub>0.02</sub>	0.99 <sub>0.003</sub>	0.96 <sub>0.01</sub>	0.99 <sub>0.02</sub>	0.90 <sub>0.05</sub>
		Parity 3	0.82	0.92	<b>0.64</b> <sub>0.02</sub>	0.92 <sub>0.02</sub>	0.98 <sub>0.05</sub>	0.92 <sub>0.04</sub>
	Linear traits	Parity 1	0.76	0.71	0.67	<b>0.42</b> <sub>0.03</sub>	–	–
		Parity 2	0.73	0.80	0.71	–	<b>0.44</b> <sub>0.03</sub>	–
		Parity 3	0.79	0.78	0.78	–	–	<b>0.35</b> <sub>0.05</sub>

Table 12 Heritability and genetic correlations for RDM. Heritabilities are in **diagonal** and Genetic correlation (above diagonal) and phenotypic correlation (below diagonal). Standard error for genetic correlation is in subscript. Note: The correlations and standard error in brackets are unrealistic correlations due to small number of overlapping observations (cows with both linear and robot observations).

		AMS			Linear traits			
		Parity 1	Parity 2	Parity 3	Parity 1	Parity 2	Parity 3	
Front Teat Placement	AMS	Parity 1	<b>0.65</b> <sub>0.08</sub>	0.92 <sub>0.05</sub>	0.95 <sub>0.06</sub>	-0.87 <sub>0.05</sub>	(-0.73 <sub>0.32</sub> )	(-0.44 <sub>0.5</sub> )
		Parity 2	0.78	<b>0.67</b> <sub>0.1</sub>	0.92 <sub>0.06</sub>	-0.83 <sub>0.07</sub>	(-0.58 <sub>0.42</sub> )	-0.96 <sub>(0.85)</sub>
		Parity 3	0.82	0.83	<b>0.53</b> <sub>0.1</sub>	-0.87 <sub>0.07</sub>	-0.99 <sub>(0.45)</sub>	-0.96 <sub>0.14</sub>
	Linear traits	Parity 1	-0.60	-0.49	-0.44	<b>0.30</b> <sub>0.03</sub>	-	-
		Parity 2	-0.61	0.43	-0.55	-	<b>0.28</b> <sub>0.07</sub>	-
		Parity 3	-0.93	-0.84	-0.68	-	-	<b>0.22</b> <sub>0.02</sub>
Rear Teat Placement	AMS	Parity 1	<b>0.54</b> <sub>0.1</sub>	0.81 <sub>0.1</sub>	0.86 <sub>0.1</sub>	-0.89 <sub>0.04</sub>	-0.92 <sub>(0.36)</sub>	(-0.72 <sub>0.13</sub> )
		Parity 2	0.74	<b>0.46</b> <sub>0.1</sub>	0.98 <sub>0.1</sub>	-0.87 <sub>0.07</sub>	-0.90 <sub>0.13</sub>	-0.89 <sub>0.09</sub>
		Parity 3	0.74	0.79	<b>0.49</b> <sub>0.1</sub>	-0.99 <sub>0.07</sub>	-0.92 <sub>(0.5)</sub>	-0.93 <sub>0.10</sub>
	Linear traits	Parity 1	-0.61	-0.53	-0.46	<b>0.26</b> <sub>0.02</sub>	-	-
		Parity 2	-0.75	-0.72	-0.82	-	<b>0.37</b> <sub>0.2</sub>	-
		Parity 3	-0.52	-0.63	-0.82	-	-	<b>0.24</b> <sub>0.03</sub>
Udder Balance	AMS	Parity 1	<b>0.50</b> <sub>0.09</sub>	0.92 <sub>0.07</sub>	0.98 <sub>0.15</sub>	0.92 <sub>0.05</sub>	(0.31 <sub>0.2</sub> )	0.99 <sub>0.07</sub>
		Parity 2	0.80	<b>0.27</b> <sub>0.08</sub>	0.98 <sub>0.13</sub>	0.95 <sub>0.05</sub>	0.99 <sub>(2)</sub>	1 <sub>0.10</sub>
		Parity 3	0.73	0.82	<b>0.16</b> <sub>0.09</sub>	0.94 <sub>0.10</sub>	(0.56 <sub>0.6</sub> )	0.98 <sub>0.19</sub>
	Linear traits	Parity 1	0.48	0.44	0.32	<b>0.17</b> <sub>0.02</sub>	-	-
		Parity 2	0.27	0.89	0.45	-	<b>0.96</b> <sub>0.74</sub>	-
		Parity 3	0.45	0.44	0.59	-	-	<b>0.15</b> <sub>0.02</sub>
Udder Depth	AMS	Parity 1	<b>0.73</b> <sub>0.08</sub>	0.98 <sub>0.1</sub>	0.96 <sub>0.1</sub>	0.95 <sub>0.03</sub>	1 <sub>0.05</sub>	0.83 <sub>0.08</sub>
		Parity 2	0.78	<b>0.7</b> <sub>0.1</sub>	0.95 <sub>0.04</sub>	0.88 <sub>0.18</sub>	1 <sub>0.13</sub>	0.95 <sub>0.04</sub>
		Parity 3	0.82	0.83	<b>0.57</b> <sub>0.1</sub>	0.99 <sub>(0.26)</sub>	0.99 <sub>0.08</sub>	0.93 <sub>0.10</sub>
	Linear traits	Parity 1	0.74	0.87	0.77	<b>0.39</b> <sub>0.02</sub>	-	-
		Parity 2	-0.10	0.96	0.80	-	<b>0.30</b> <sub>0.07</sub>	-
		Parity 3	0.56	0.64	0.89	-	-	<b>0.27</b> <sub>0.02</sub>



Table 13 Heritability and genetic correlations for Jersey. Heritabilities are in **diagonal** and Genetic correlation (above diagonal) and phenotypic correlation (below diagonal). Standard error for genetic correlation is in subscript. Note: The correlations and standard error in brackets are unrealistic correlations due to small number of overlapping observations (cows with both linear and robot observations).

		AMS			Linear traits			
		Parity 1	Parity 2	Parity 3	Parity 1	Parity 2	Parity 3	
Front Teat Placement	AMS	Parity 1	<b>0.64</b> <sub>0.11</sub>	0.83 <sub>0.08</sub>	0.81 <sub>0.12</sub>	-0.99 <sub>0.03</sub>	-0.95 <sub>0.07</sub>	-0.97 <sub>0.07</sub>
		Parity 2	0.79	<b>0.59</b> <sub>0.1</sub>	0.97 <sub>0.07</sub>	-0.89 <sub>0.05</sub>	-0.88 <sub>0.08</sub>	-0.92 <sub>0.07</sub>
		Parity 3	0.68	0.87	<b>0.51</b> <sub>0.11</sub>	-0.92 <sub>0.07</sub>	-0.92 <sub>0.10</sub>	-0.88 <sub>0.10</sub>
	Linear traits	Parity 1	-0.62	-0.58	-0.56	<b>0.31</b> <sub>0.01</sub>	–	–
		Parity 2	-0.63	-0.69	-0.80	–	<b>0.32</b> <sub>0.02</sub>	–
		Parity 3	-0.58	-0.70	-0.73	–	–	<b>0.25</b> <sub>0.01</sub>
Rear Teat Placement	AMS	Parity 1	<b>0.44</b> <sub>0.1</sub>	0.91 <sub>0.08</sub>	0.93 <sub>0.1</sub>	-0.93 <sub>0.06</sub>	-0.99 <sub>0.07</sub>	-0.99 <sub>0.08</sub>
		Parity 2	0.72	<b>0.38</b> <sub>0.1</sub>	0.99 <sub>0.06</sub>	-0.89 <sub>0.06</sub>	-0.99 <sub>0.07</sub>	-0.96 <sub>0.08</sub>
		Parity 3	0.78	0.83	<b>0.42</b> <sub>0.1</sub>	-0.91 <sub>0.06</sub>	-0.98 <sub>0.07</sub>	-0.95 <sub>0.07</sub>
	Linear traits	Parity 1	-0.68	-0.58	-0.57	<b>0.31</b> <sub>0.01</sub>	–	–
		Parity 2	-0.51	-0.82	-0.85	–	<b>0.29</b> <sub>0.03</sub>	–
		Parity 3	-0.13	-0.75	-0.82	–	–	<b>0.26</b> <sub>0.02</sub>
Udder Balance	AMS	Parity 1	<b>0.52</b> <sub>0.1</sub>	0.96 <sub>0.05</sub>	0.94 <sub>0.09</sub>	0.89 <sub>0.05</sub>	0.92 <sub>0.09</sub>	0.81 <sub>0.15</sub>
		Parity 2	0.80	<b>0.30</b> <sub>0.09</sub>	0.99 <sub>0.05</sub>	0.96 <sub>0.05</sub>	0.95 <sub>0.14</sub>	0.74 <sub>0.22</sub>
		Parity 3	0.68	0.85	<b>0.35</b> <sub>0.1</sub>	0.91 <sub>0.09</sub>	0.88 <sub>0.12</sub>	(0.63 <sub>0.22</sub> )
	Linear traits	Parity 1	0.61	0.50	0.37	<b>0.20</b> <sub>0.01</sub>	–	–
		Parity 2	0.39	0.57	0.44	–	<b>0.21</b> <sub>0.04</sub>	–
		Parity 3	0.52	0.72	0.77	–	–	<b>0.19</b> <sub>0.03</sub>
Udder Depth	AMS	Parity 1	<b>0.41</b> <sub>0.09</sub>	<b>0.94</b> <sub>0.06</sub>	<b>0.94</b> <sub>0.07</sub>	<b>0.93</b> <sub>0.04</sub>	<b>0.91</b> <sub>0.10</sub>	<b>0.82</b> <sub>0.12</sub>
		Parity 2	<b>0.83</b>	<b>0.47</b> <sub>0.09</sub>	<b>0.99</b> <sub>0.03</sub>	<b>0.89</b> <sub>0.05</sub>	<b>0.73</b> <sub>0.13</sub>	<b>(0.69</b> <sub>0.25</sub> )
		Parity 3	0.76	0.85	<b>0.47</b> <sub>0.1</sub>	<b>0.86</b> <sub>0.09</sub>	<b>0.94</b> <sub>0.11</sub>	<b>0.98</b> <sub>0.10</sub>
	Linear traits	Parity 1	<b>0.67</b>	<b>0.70</b>	<b>0.65</b>	<b>0.39</b> <sub>0.01</sub>	–	–
		Parity 2	<b>0.69</b>	<b>0.79</b>	<b>0.91</b>	–	<b>0.42</b> <sub>0.02</sub>	–
		Parity 3	<b>0.91</b>	<b>0.84</b>	<b>0.91</b>	–	–	<b>0.30</b> <sub>0.02</sub>

Table 14 shows the genetic and phenotypic correlations between the five traits (Front Teat Placement, Rear Teat Placement, Distance Front – Rear Teats, Udder Balance and Udder Depth) assessed with the robot milking system (first parity). Heritability is not shown, since it is shown in the previous tables.

Table 14 Genetic correlation (above diagonal) and phenotypic correlation (below diagonal) between the traits (Front Teat Placement, Rear Teat Placement, Distance Front – Rear Teats, Udder Balance and Udder Depth) observed with AMS (milking robots). Standard error for genetic correlation is in subscript

		Front Teat Placement	Rear Teat Placement	Distance Front – Rear Teats	Udder Balance	Udder Depth
Holstein	Front Teat Placement	–	0.58 <sub>0.03</sub>	0.28 <sub>0.04</sub>	-0.20 <sub>0.04</sub>	-0.27 <sub>0.04</sub>
	Rear Teat Placement	0.63	–	0.05 <sub>0.04</sub>	-0.23 <sub>0.05</sub>	-0.26 <sub>0.04</sub>
	Distance Front – Rear Teats	0.27	0.09	–	0.15 <sub>0.04</sub>	-0.23 <sub>0.04</sub>
	Udder Balance	-0.17	-0.25	0.13	–	0.19 <sub>0.04</sub>
	Udder Depth	-0.25	-0.22	-0.26	0.12	–
RDM	Front Teat Placement	–	0.66 <sub>0.1</sub>	0.25 <sub>0.14</sub>	-0.38 <sub>0.15</sub>	-0.24 <sub>0.13</sub>
	Rear Teat Placement	0.62	–	0.04 <sub>0.15</sub>	-0.45 <sub>0.15</sub>	-0.31 <sub>0.14</sub>
	Distance Front – Rear Teats	0.24	0.09	–	-0.10 <sub>0.16</sub>	-0.07 <sub>0.13</sub>
	Udder Balance	-0.27	-0.38	0.07	–	0.12 <sub>0.16</sub>
	Udder Depth	-0.26	-0.29	-0.17	0.15	–
Jersey	Front Teat Placement	–	-0.40 <sub>0.16</sub>	0.02 <sub>0.21</sub>	-0.4 <sub>0.16</sub>	0.02 <sub>0.20</sub>
	Rear Teat Placement	-0.27	–	-0.78 <sub>0.16</sub>	-0.05 <sub>0.2</sub>	-0.07 <sub>0.22</sub>
	Distance Front – Rear Teats	-0.20	0.08	–	0.30 <sub>0.17</sub>	-0.47 <sub>0.17</sub>
	Udder Balance	-0.27	-0.26	0.18	–	-0.77 <sub>0.17</sub>
	Udder Depth	-0.20	-0.22	-0.33	0.08	–