

**BYDGOSZCZ UNIVERSITY
OF SCIENCE AND TECHNOLOGY**



Identification of SNPs affecting conformation traits of dairy cows

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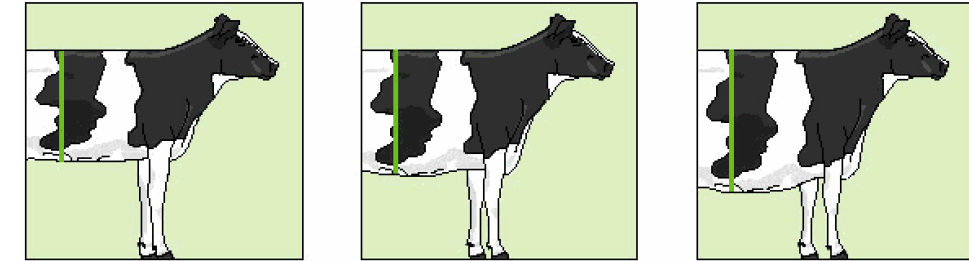


Introduction

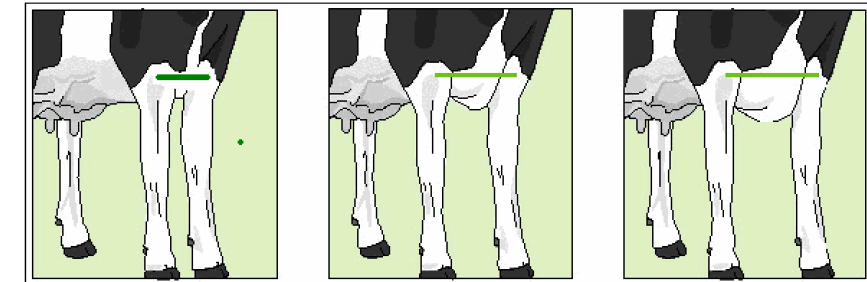
Conformation traits

- Conformation traits or the physical attributes of dairy cows are important in determining the efficiency, health and overall productivity of dairy operations.
- These traits, which include udder conformation, leg structure and body depth, have a direct impact on a cow's ability to produce milk efficiently and sustainably.
- These traits are important for breeding programs, as they impact the functional and economic efficiency of dairy operations.

Body Depth



Chest Width



1

2

3

4

5

6

7

8

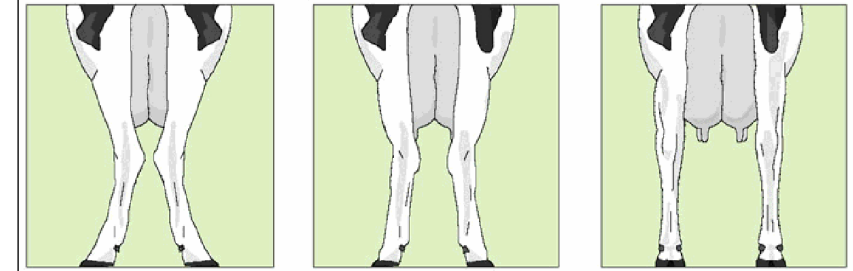
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Narrow

Intermediate

Wide

Rear Leg Rear View



1

2

3

4

5

6

7

8

9

Toes out

Intermediate

Parallel Bow-legged

Conformation traits

- Conformation traits are routinely assessed in dairy herds and understanding their genetic basis helps in selecting animals that are more likely to thrive in production environment.
- Understanding the relationship between a cow's physical structure and its milking performance is essential for optimizing dairy herd management and breeding programs.

Genetics

- The genetic makeup of dairy cows plays a fundamental role in shaping their conformation traits.
- Selective breeding has long been used to enhance desirable physical attributes that are linked to higher milk production, longevity and health.
- The advancement of genomic selection tools, particularly single nucleotide polymorphisms (SNP) microarrays, has allowed for the detailed examination of the genetics affecting these traits.

Objective of the study

To identify single nucleotide polymorphisms (SNPs) present on SNP Microarrays, that may be associated with conformation traits of Polish Holstein Friesian (PHF) cows.

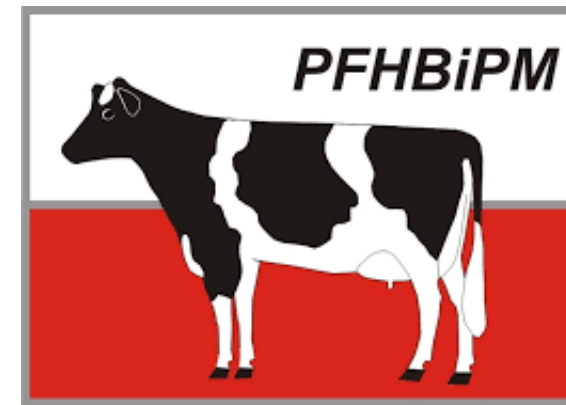




Material and methods

Cattle

- A total of 376 Polish Holstein Friesian (PHF) cows were examined in this study.
- Data on cow conformation traits was recorded by the Polish Federation of Cattle Breeders and Dairy Farmers (PFHBiPM), ensuring high-quality phenotypic information for analysis.



SNP Microarray Analysis

- Genomic data were collected in the process of routine genetic estimation of breeding value (GEBV) that is performed in Poland with the use of **EuroGenomics arrays**.
- 55,352 SNPs analyzed from microarray data.
- Data cleaning reduced SNPs to 41,705 for statistical analysis.



Statistical Analysis

- In total, 56 variables related to conformation traits were analyzed. These included traits such as udder position, hoof angle, body depth, and various aspects of body conformation.
- The analysis aimed to identify SNPs that had a statistically significant impact on specific conformation traits.
- The Bigstep analysis (Stepwise Selection for Large Data Sets), implemented in the R software package, was employed to identify SNPs significantly associated with conformation traits.

Statistical Analysis

- Bigstep method is particularly suited for handling large datasets (which exceed RAM capacity) and allows for selection of significant variables using modified stepwise procedure and modern selection criteria.
- The Bigstep Package in R allows for stepwise regression, which adds or removes SNPs based on their statistical significance, ensuring that the final model includes only the most relevant SNPs.
- The threshold for significance was set at $P < 0.001$ to ensure that only the most robust associations were reported.
- For the indicated SNPs, analysis of variance and multiple comparisons were performed to determine the effect of each genotype.



Results

Results

- Certain SNPs significantly ($P < 0.001$) influenced specific conformation traits
- One trait (Udder Depth) was affected by 4 SNPs.
 - One trait (Locomotion) by 3 SNPs
 - Six traits by 2 SNPs
 - Six traits by 1 SNP

Table 1. Number of SNPs affecting confirmation traits

Conformation trait	Number of SNP affecting the trait
Udder Depth	4
Locomotion	3
Foot angle	2
Body depth	2
Rear Leg Rear View	2
Rear teat placement	2
Suspension of the fore udder	2
Width of the udder	2
Front teat placement	1
height at the withers	1
Hindquarters' conformation	1
Legs and hooves	1
Rear Leg Side View	1
Udder	1

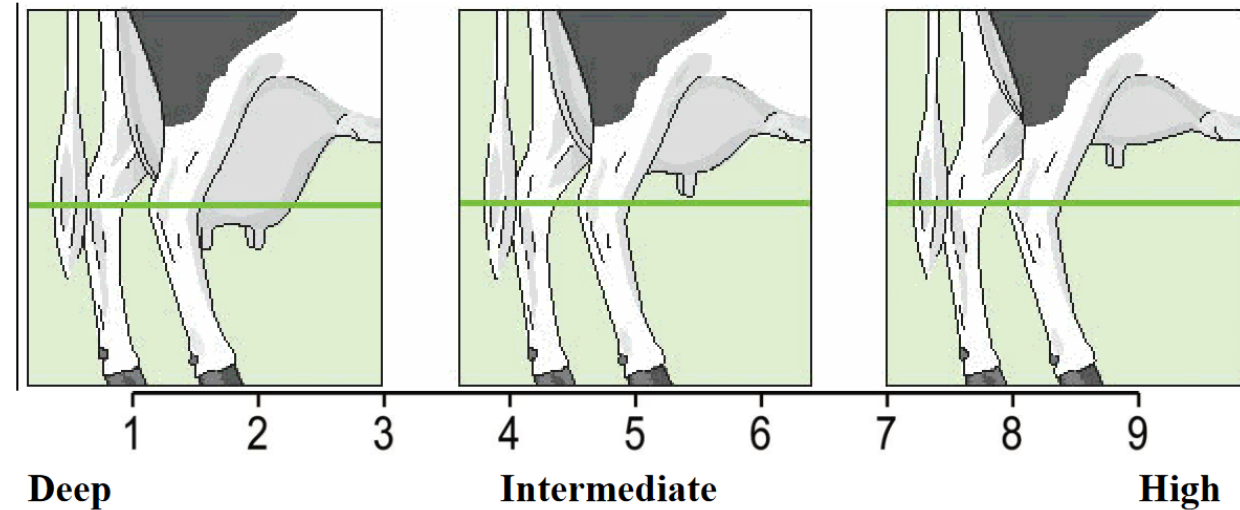
Udder Depth

➤ 4 SNPs from chromosome 2, 6, 24 and 29 (according to UMD_3.1 reference genome) affected Udder depth.

Udder bottom:

- 1** - 6 cm below hock level
- 3** - at hock level
- 5** - 6 cm above hock level
- 9** - 18 cm above hock level

Udder Depth



Udder depth is measured by comparing the distance between the deepest part of the udder and hock. The scale is 3 cm per point.

Udder Depth

Table 2. Number of cows for a given score

Conformation trait	Score (%)									
	0	1	2	3	4	5	6	7	8	9
Udder Depth	0 (0)	0 (0)	0 (0)	3 (0.8)	28 (7.4)	142 (37.8)	193 (51.3)	10 (2.7)	0 (0)	0 (0)

Table 3. The influence of selected SNPs on cow conformation traits (Least squares means, Scheffee)

SNP Name	Chromosome	Genotype		
		0	1	2
ARS-BFGL-BAC-31338	2	n/a	5.27 ^A	5.92 ^A
ARS-BFGL-NGS-103502	6	5.89 ^{A b}	5.58 ^A	5.31 ^b
Hapmap22754-BTA-157164	24	5.22 ^A	5.55 ^B	6.01 ^{AB}
ARS-BFGL-NGS-115406	29	5.80 ^{A b}	5.56 ^b	5.42 ^A

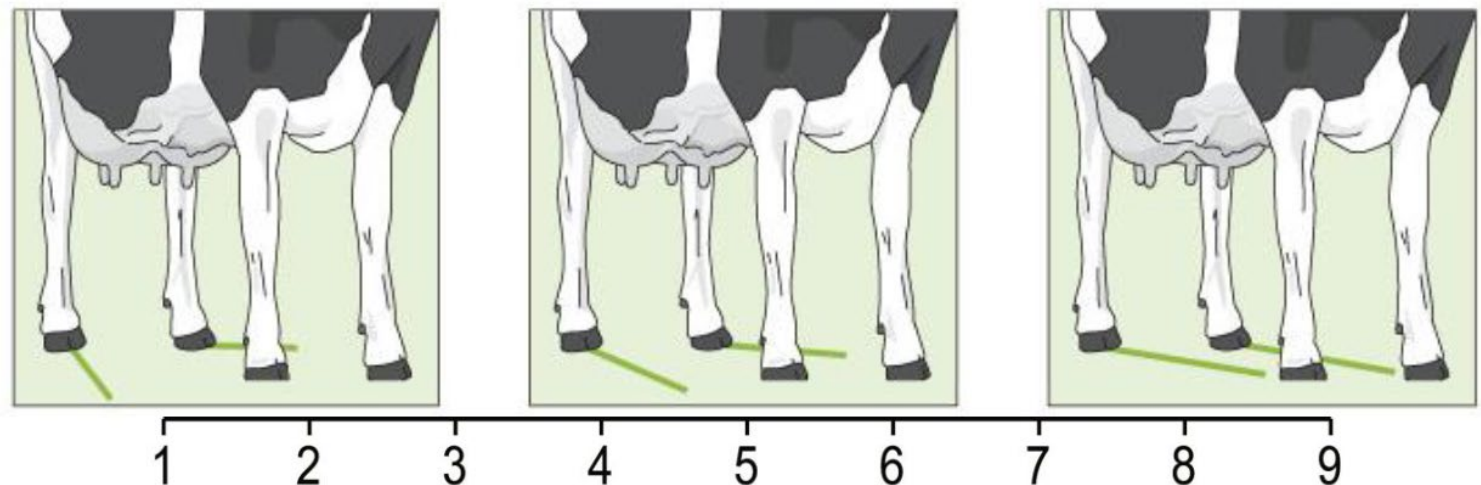
AA (aa) – Values are that are significantly different within a variable are marked with the same letters $P \leq 0.01$ ($P \leq 0.05$);

Locomotion

- Assessment of legs in motion - use of legs and hooves, length and direction of step
- 3 SNPs from chromosome 2, X affected Locomotion

Scores:

- 1** - Strong abduction - short step
- 5** - Light abduction - intermediate step
- 9** - No abduction - long step



Locomotion

Table 4. Number of cows for a given score

Conformation trait	Score (%)									
	0	1	2	3	4	5	6	7	8	9
Locomotion	67 (17.8)	1 (0.3)	0 (0)	2 (0.5)	4 (1.1)	35 (9.3)	0 (0)	182 (48.4)	80 (21.3)	5 (1.3)

Table 5. The influence of selected SNPs on cow conformation traits (Least squares means, Scheffee)

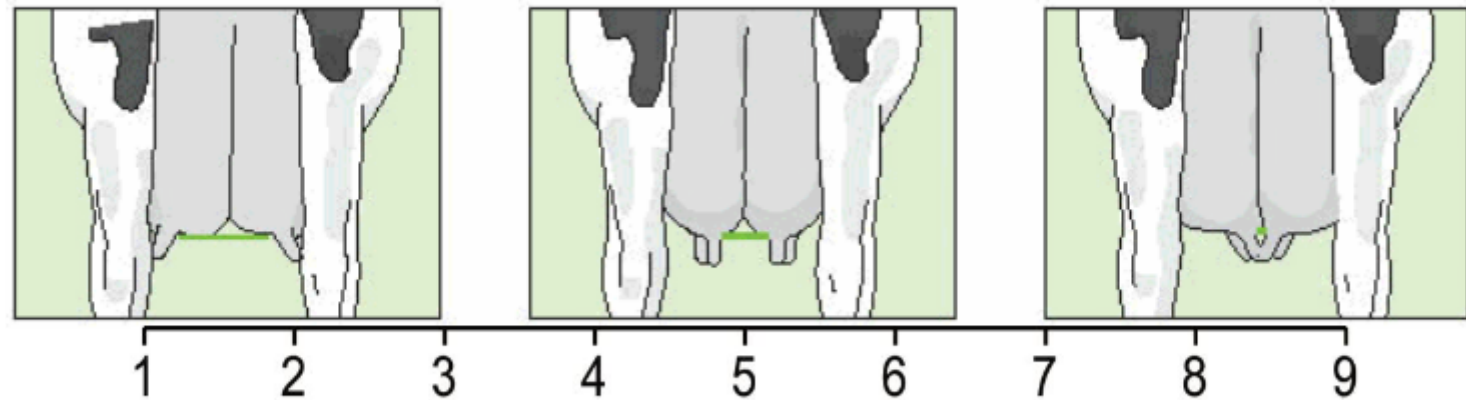
Name	Chromosome	Genotype		
		0	1	2
ARS-BFGL-NGS-36460	2	0.84 ^{A b}	2.65 ^b	3.35 ^A
ARS-BFGL-NGS-117757	X	2.46 ^{A B}	3.58 ^{Ac}	4.33 ^{Bc}
Hapmap59721-rs29025370	X	2.50 ^A	4.41 ^A	n/a

AA (aa) – Values are that are significantly different within a variable are marked with the same letters $P \leq 0.01$ ($P \leq 0.05$);

Rear teat placement

- 3 SNPs from chromosome 1,2 and 29 affected rear teat placement.

Rear Teat Placement Rear View



Wide

Intermediate

Close

Rear teat placement

Table 6. Number of cows for a given score

Conformation trait	Score (%)									
	0	1	2	3	4	5	6	7	8	9
Rear teat placement	0 (0)	0 (0)	0 (0)	1 (0.3)	38 (10.1)	71 (18.9)	163 (43.4)	87 (23.1)	14 (3.7)	2 (0.5)

Table 7. The influence of selected SNPs on cow conformation traits (Least squares means, Scheffee)

Name	Chromosome	Genotype		
		0	1	2
ARS-BFGL-NGS-62687	1	5.48 ^{AB}	5.80 ^{AC}	6.25 ^{BC}
snp2_14709182	2	6.50 ^{AB}	5.58 ^A	5.46 ^B
BTB-01216515	29	6.24 ^a	5.90 ^B	5.39 ^{aB}

AA (aa) – Values are that are significantly different within a variable are marked with the same letters $P \leq 0.01$ ($P \leq 0.05$);

Conclusions

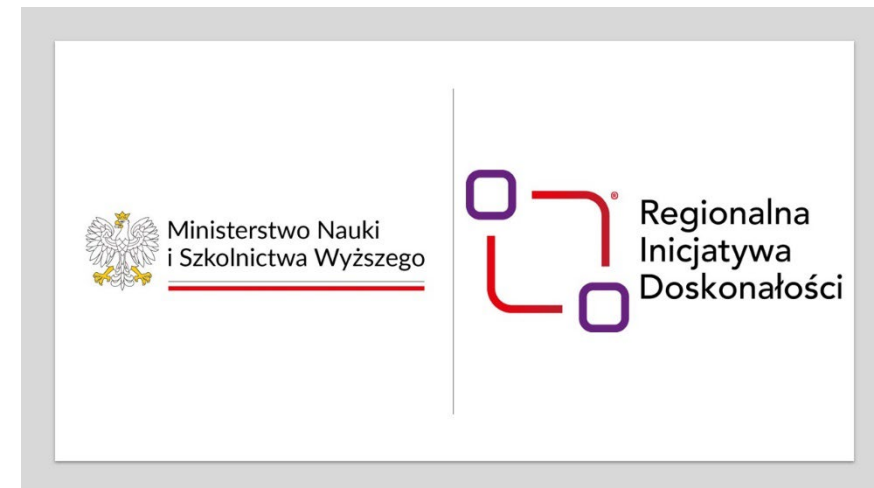
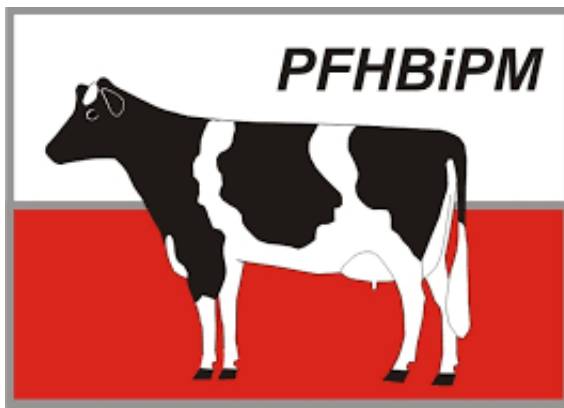
- Identified SNPs have significant potential in improving breeding programs when combined with performance data.
- SNP microarray data is a valuable tool for exploring the genetic basis of conformation traits in dairy cows.
- This approach may hold promise, particularly when combined with performance analysis, in exploring optimal conformation traits in cows predisposed to specific milking type.

Further research

- Different types of milking systems—conventional and automatic—place varying demands on the cow's body structure.
- Traditional milking systems rely on human operators or machine units attached manually.
- Automatic milking systems or robotic milking units require precise teat placement and udder conformation for optimal functioning.
- This may suggest that e.g. optimal teat placement and udder shape may differ for cows predisposed to different milking systems.
- Understanding how these factors interact can help optimize both milk yield and animal well-being.

Acknowledgments

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Thank you for your attention

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