Genomic regions associated with somatic cell score in dairy cattle

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Acknowledgements

www.robustmilk.eu

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RobustMilk

- Collaboration 6 research institutes
  - Belgium, Ireland, the Netherlands, Scotland, Sweden

- Develop new technologies with focus on milk quality and robustness
  - Enable farmers and dairy industry to reconsider selection decisions

- Unique combined dataset:
  - Research dairy herds
  - Detailed somatic cell count recordings
  - Dense DNA information on cows

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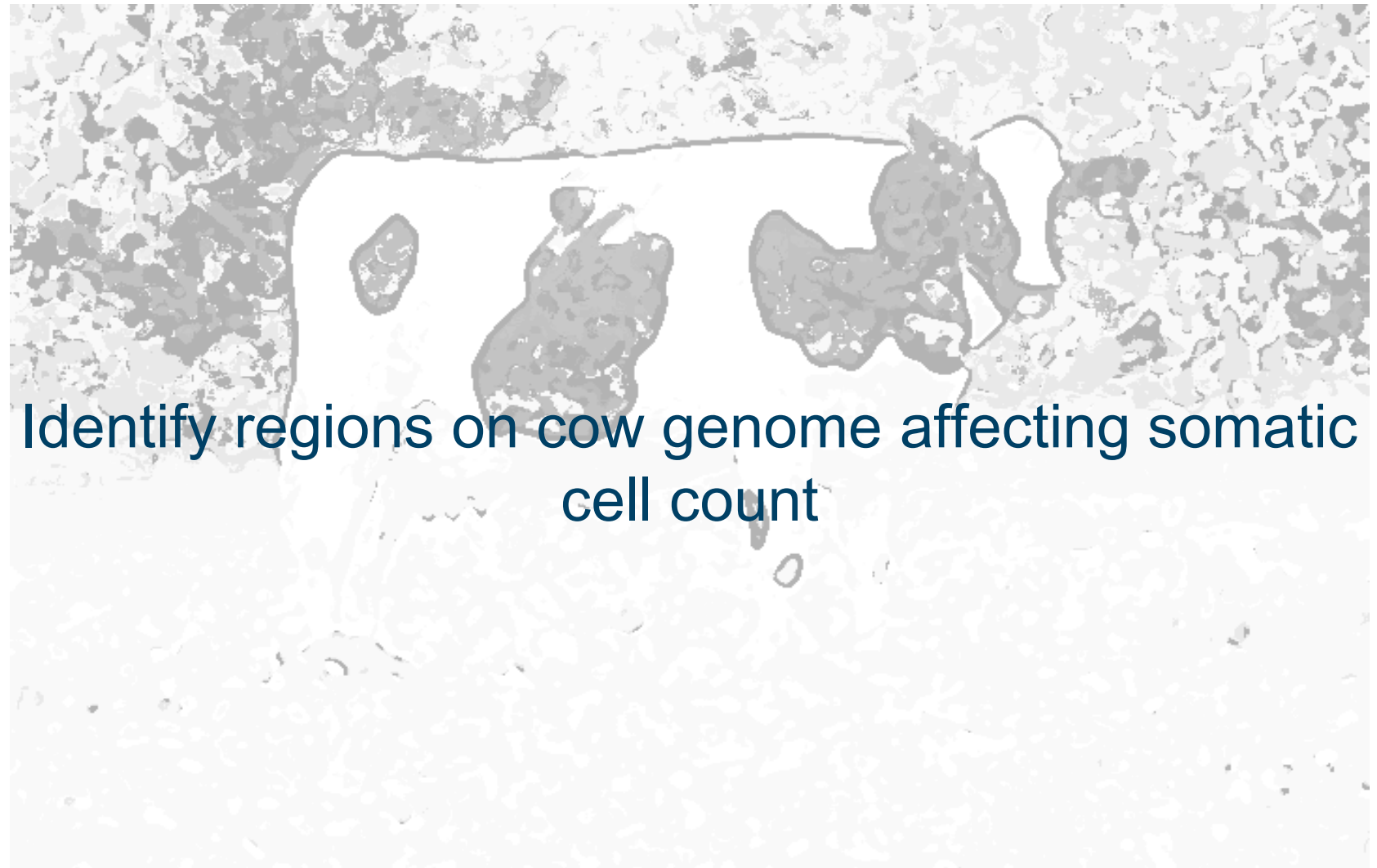
Identify regions on cow genome affecting somatic cell count

Animals

- ■ 1,484 Holstein cows
  - ● Genotyped, pedigree checked using DNA info

Country	Cows	Herds	SCC records
Ireland	329	3	8,795
The Netherlands	574	2	17,024
Scotland	390	2	13,312
Sweden	191	1	7,751

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Phenotypes

- Lactation-average SCC (LSCS)
- Within individual SCC variation (SCS-SD)

- 46,900 first lactation SCC records
- On average 31 SCC records per cow
  - Range 10 to 52 records
  - Recorded before 350 days in milk

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DNA

1,484 cows
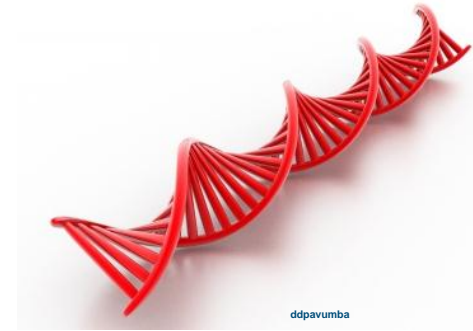
marker

Cow 1	AATC**G**GTCA	maternal DNA
	AATC**G**GTCA	paternal DNA
Cow 2	AATC**G**GTCA	maternal DNA
.	AATC**C**GTCA	paternal DNA
.		
.		
Cow 1,484	AATC**C**GTCA	maternal DNA
	AATC**C**GTCA	paternal DNA

± 50,000 Markers (SNP)

Genome-wide association study

■ Essence: find markers with an effect on SCS

Simplified example

Marker	GG (AA)	GC (AB)	CC (BB)
SCS	10.5	5.9	2.1

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Analysis

- **Model accounted for effects due to:**
  - Country of origin
  - Herd
  - Year and season of calving
  - Dietary treatment
  - Birth year
  - <u>Marker</u>
  - Family relationships
    - pedigree 9,400 individuals
    - 9 generations

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Analysis

- Multiple testing (±50,000 individually tested markers)

- Increased risk of false positives

- False Discovery Rate (FDR)

  - Results < FDR 0.20 presented
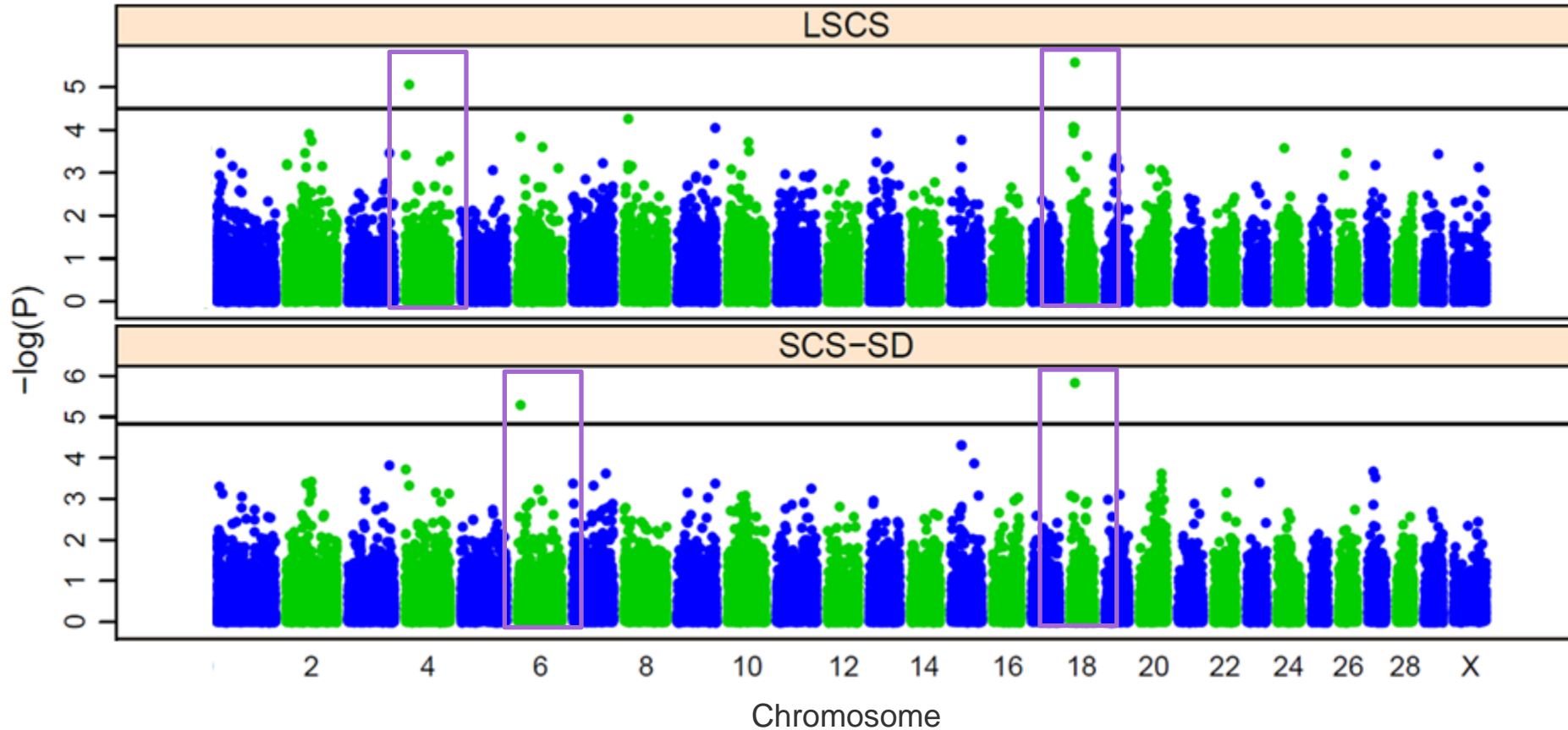 - 80% chance finding is a true relation

Genetic parameters

- ■ Heritability:
  - ● Degree to which phenotypic differences are genetic
  - ● LSCS 0.17
  - ● SCS-SD 0.14
  - ● Good agreement with literature

- ■ Genetic correlation 0.96
  - ● Genetic component of traits not significantly different

Genome-wide association study

Implication relation marker - SCC

- **LSCS:**
  - Chr. 4: AA variant > 51,000 cells/mL > BB variant
  - Chr. 18: AA variant > 87,000 cells/mL > BB variant

- **SCS-SD:**
  - Chr. 6: AB variant > 235,000 cells/mL > AA variant
  - Chr. 18: AA variant > 197,000 cells/mL > BB variant

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Candidate genes

- Marker itself may not be causative for effect, but may be linked to gene that is

- 200,000 base pair window around marker

Chr.	Trait	Gene	Function
4	LSCS	*TFPI2*	Proliferation, death smooth muscle cells
		GNGT1, GNGT11	Signal transductors cell migration, adhesion
6	SCS-SD	-	-
18	LSCS, SCS-SD	*SMAR1*	Cell cycle, death, signalling
		P22-PHOX	Cell death

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Conclusion

- Few markers related to LSCS and SCS-SD
  - Effects of most genes not large enough to be detected
  - SCC influenced by multiple genes spread across genome, each a relatively small effect

- Findings need to be verified in other independent studies

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Knowledge on genetic control needed to...

- **Enable higher selection response**
  - Particularly valuable for bull dams

- **Find genes mastitis resistance**

- **Understand genetic mechanisms mastitis**
  - Discovery targets mastitis therapeutics

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