THE
Resilient Dairy
GENOME PROJECT

Genetic architecture of fertility traits in hormonally synchronized and heat detected dairy cows

GA Oliveira Junior[1], **CM Rochus**[1], L Alcantara[1], C Lynch[1], FS Schenkel[1], CF Baes[1,2]

[1]Centre for the Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph
[2]Institute of Genetics, Department of Clinical Research and Veterinary Public Health, University of Bern

UNIVERSITY of GUELPH
Improve Life.
DEPARTMENT OF ANIMAL BIOSCIENCES
CGIL
DAIRY at GUELPH
CANADA'S DAIRY UNIVERSITY

Acknowledgements

THE
Resilient Dairy
GENOME PROJECT

GenomeCanada

GenomeAlberta

GenomeQuébec

Genome BritishColumbia
Leading ▸ Investing ▸ Connecting

Ontario Genomics

UNIVERSITY of GUELPH

UNIVERSITÉ LAVAL

UNIVERSITY OF ALBERTA

UBC THE UNIVERSITY OF BRITISH COLUMBIA

McGill

UNIVERSITY OF CALGARY

UNIVERSITY of Prince Edward ISLAND

Ministry of
Economic Development,
Job Creation &
Trade

Ministry of
Agriculture, Food &
Rural Affairs

Ontario
Ministry of
Research and Innovation

Agriculture and
Agri-Food Canada

Alberta
Agriculture
and Forestry

Lactanet

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

USDA

FFAR
Foundation for Food
and Agriculture Research

WISCONSIN
UNIVERSITY OF WISCONSIN–MADISON

MICHIGAN STATE UNIVERSITY

IOWA STATE UNIVERSITY

PURDUE UNIVERSITY

UNIVERSITY OF GEORGIA

UF
UNIVERSITY of FLORIDA

unesp

VICTORIA
State
Government
Jobs,
Precincts
and Regions

INIA
Instituto Nacional de Investigación
y Tecnología Agraria y Alimentaria

CONAFE
Confederación de Asociaciones de Frisona Española

QUALITAS

Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

ETH zürich

vit
Service & Daten aus einer Quelle

C A U
Kiel University
Christian-Albrechts-Universität zu Kiel

Freie Universität Berlin

AARHUS UNIVERSITY

GENTORE

INRAE

illumina

afimilk

SEMEX
Genetics for Life

DAIRY FARMERS OF CANADA
LES PRODUCTEURS LAITIERS DU CANADA

Allflex
Livestock Intelligence™

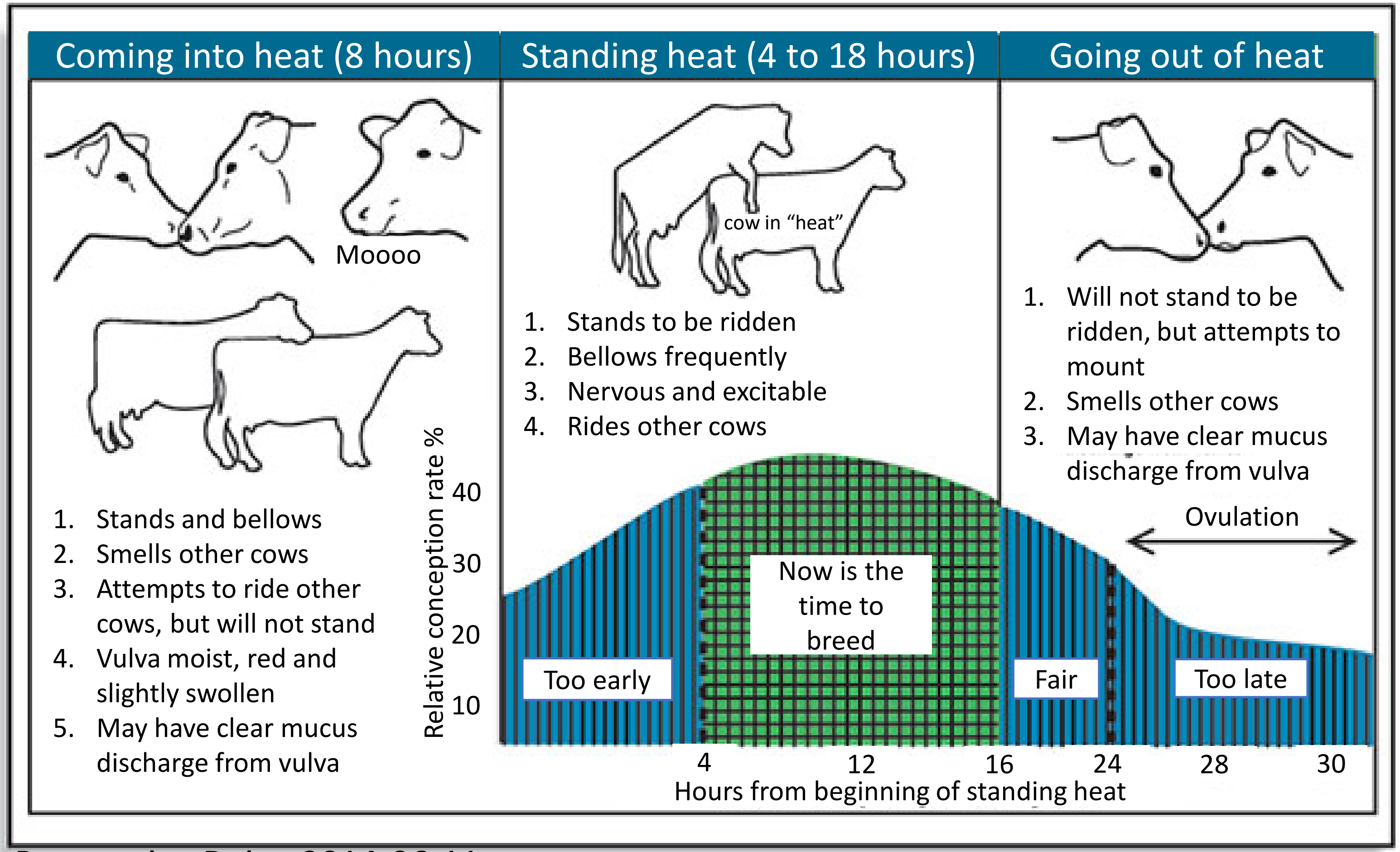
nedap

DAIRY RESEARCH CLUSTER 3
GRAPPE RECHERCHE LAITIÈRE 3

CANADIAN AGRICULTURAL PARTNERSHIP

Canada

Estrus detection



Coming into heat (8 hours)

1. Stands and bellows
2. Smells other cows
3. Attempts to ride other cows, but will not stand
4. Vulva moist, red and slightly swollen
5. May have clear mucus discharge from vulva

Standing heat (4 to 18 hours)

1. Stands to be ridden
2. Bellows frequently
3. Nervous and excitable
4. Rides other cows

Going out of heat

1. Will not stand to be ridden, but attempts to mount
2. Smells other cows
3. May have clear mucus discharge from vulva

Progressive Dairy, 2014-06-11

- High-producing cows may have:
  - Shortened estrus
  - Reduced behavioural signs

(MacMillan, 2010; Walsh et al., 2011; Wiltbank et al., 2011)

- Accurate estrus detection is required for successful artificial insemination (AI)

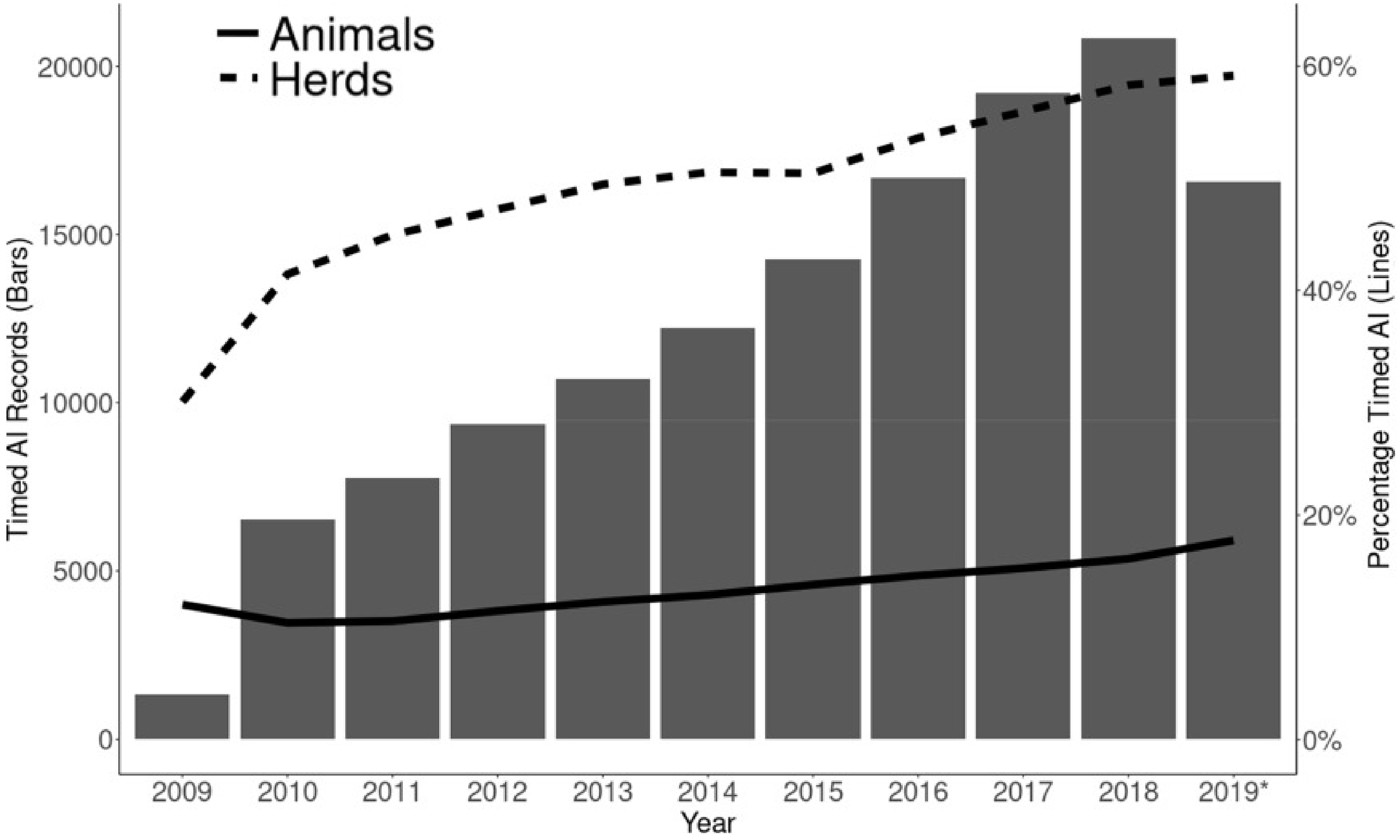
(Sales et al., 2011)

Timed artificial insemination (TAI)

- TAI: Estrus synchronization, combined with artificial insemination

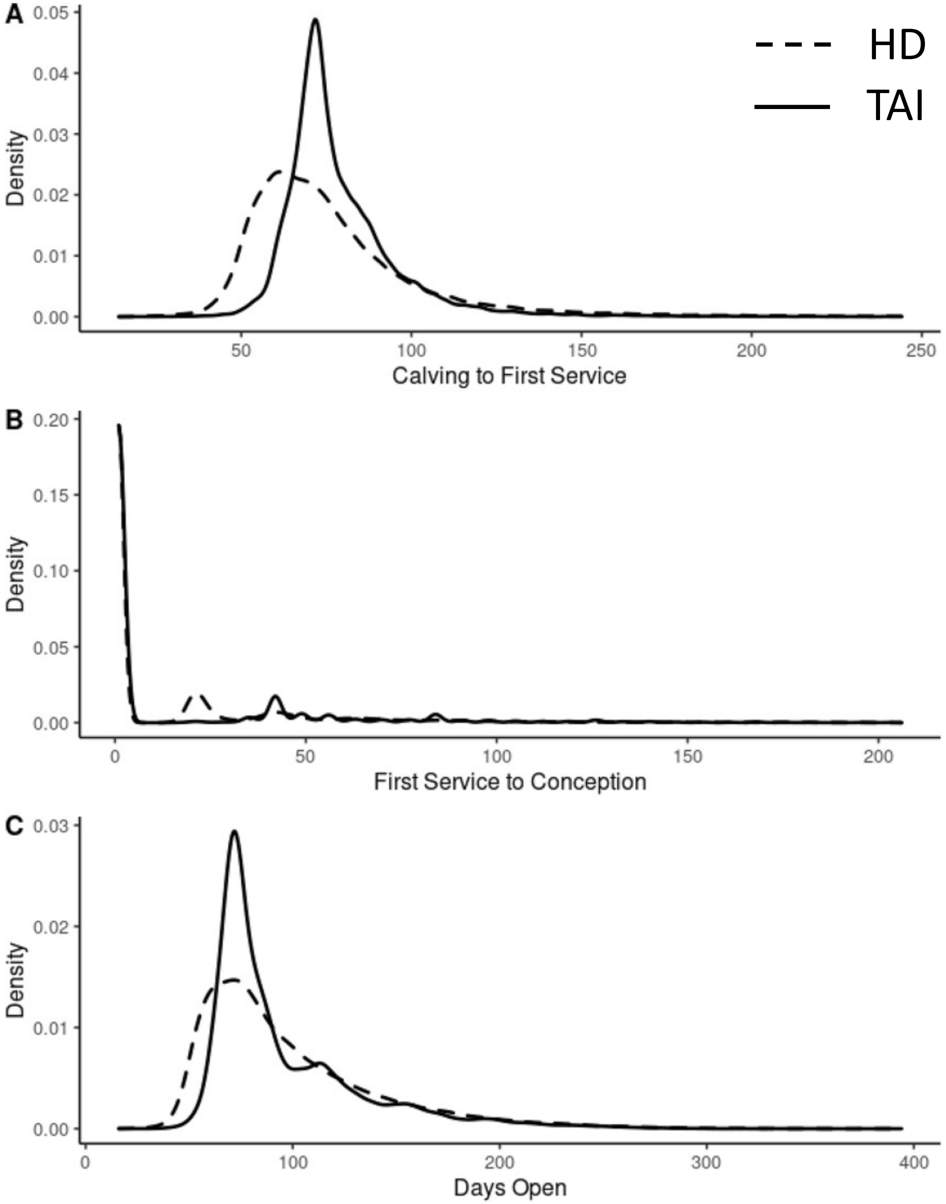
- Increases the efficiency of AI
- Increasingly popular management tool
- Can be used to reduce the interval between calving and conception

(MacMillan, 2010; Wiltbank et al., 2011)



Lynch et al., 2021

TAI affects the accuracy of genetic evaluations



- TAI allows genetically inferior animals to show similar fertility phenotypes as superior animals
- Accuracy of EBV decreased as the use of TAI increased in simulations (Oliveira Jr et al., 2021)
- Large re-ranking of bulls when using only TAI or heat detection (HD) records (Lynch et al., 2021)

Lynch et al., 2021

Objectives

1. Estimate the genetic correlation (r_g) between fertility traits measured on Canadian Holstein cows where HD and TAI were used

2. Identify different genomic regions associated with TAI and HD fertility traits using genome-wide association studies

Material and methods

- Data provided by Lactanet (Guelph, Ontario, Canada) containing 3842 breeding protocol descriptions:
  - 1840 HD
  - 2002 TAI

- Four traits for first parity cows:
  - Calving to first service (CTFS): 61,542 HD and 33,346 TAI
  - First service to conception (FSTC): 55,144 HD and 29,281 TAI
  - Days open (DO) : 55,144 HD and 29,281 TAI
  - 305-day milk yield (MILK)

- 50K SNP genotype data:
  - 6985 with FSTC and DO records
  - 7220 with CTFS records

Variance component estimation

$$y_{ijkl} = \mu + RYM_i + AM_j + H_k + a_i + e_{ijkl}$$

$\boldsymbol{y_{ijkl}}$ is the observed phenotype (e.g. CTFS HD, CTFS TAI, MILK) of the l^{th} cow

$\boldsymbol{RYM_i}$ is the fixed effect of region-year-month born

$\boldsymbol{AM_j}$ is the fixed effect of age previous calving-month (for DO and CTFS) or first service (for FSTC)

$\boldsymbol{H_k}$ is the random effect of herd-year born

$\boldsymbol{a_l}$ is the random additive genetic effect of the l^{th} cow

$\boldsymbol{e_{ijkl}}$ is the vector of random residuals

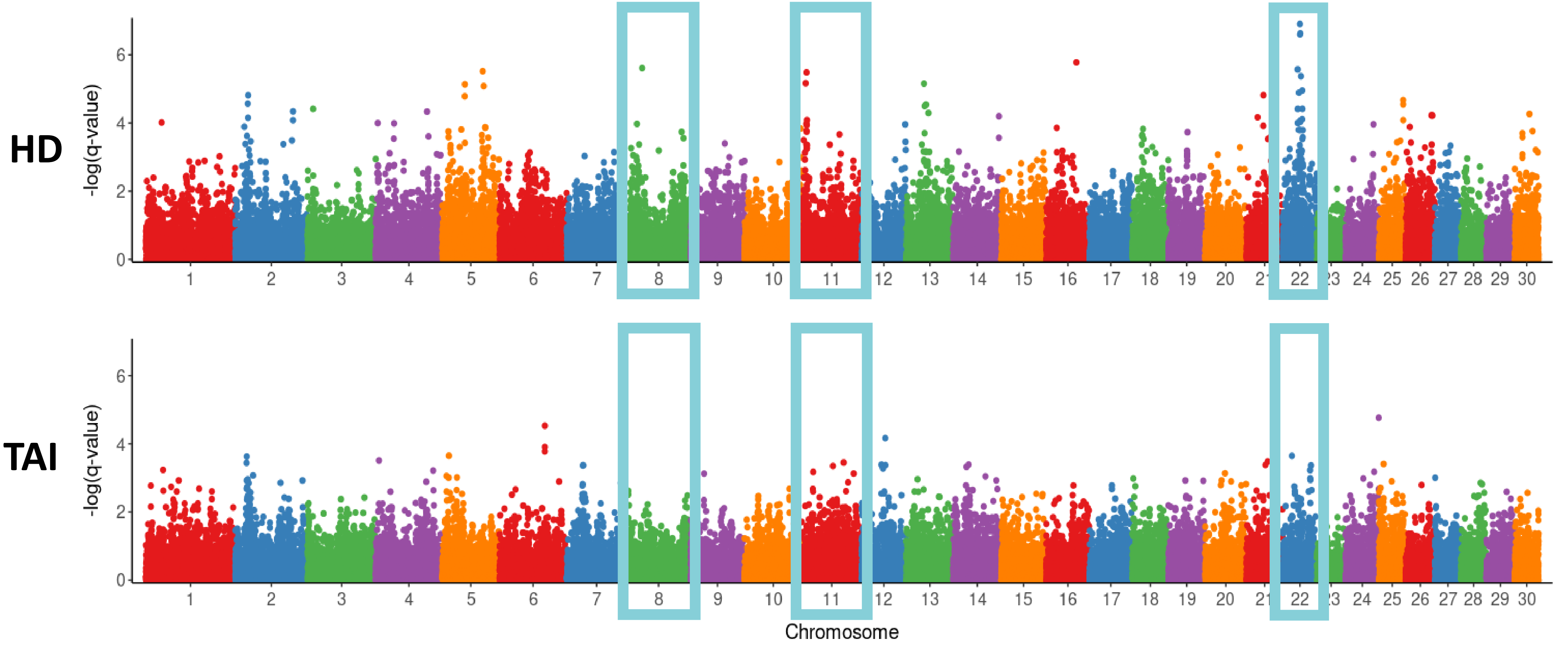
Genetic correlations and heritability for fertility traits

Heritabilities on the diagonal and genetic correlations above the diagonal (± SE)

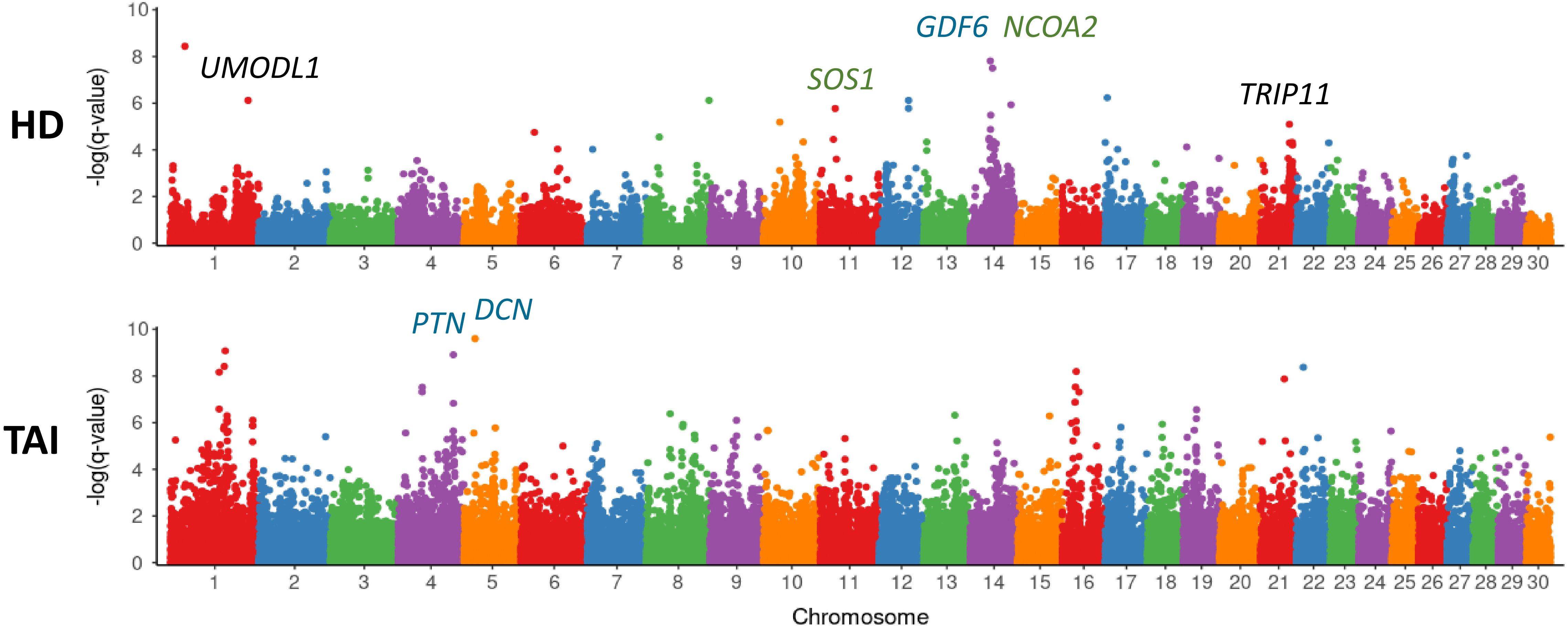
	FSTC HD	**FSTC TAI**	**CTFS HD**	**CTFS TAI**	**DO HD**	**DO TAI**	**MILK**
FSTC HD	0.02 ± 0.002	0.71 ± 0.04					0.36 ± 0.04
FSTC TAI		0.03 ± 0.002					0.37 ± 0.04
CTFS HD			0.02 ± 0.002	0.89 ± 0.03			0.36 ± 0.03
CTFS TAI				0.01 ± 0.001			0.34 ± 0.04
DO HD					0.03 ± 0.002	0.91 ± 0.01	0.42 ± 0.03
DO TAI						0.04 ± 0.003	0.41 ± 0.03
MILK							0.28[1]

[1] Average heritability from the three multi-trait analyses

Calving to first service

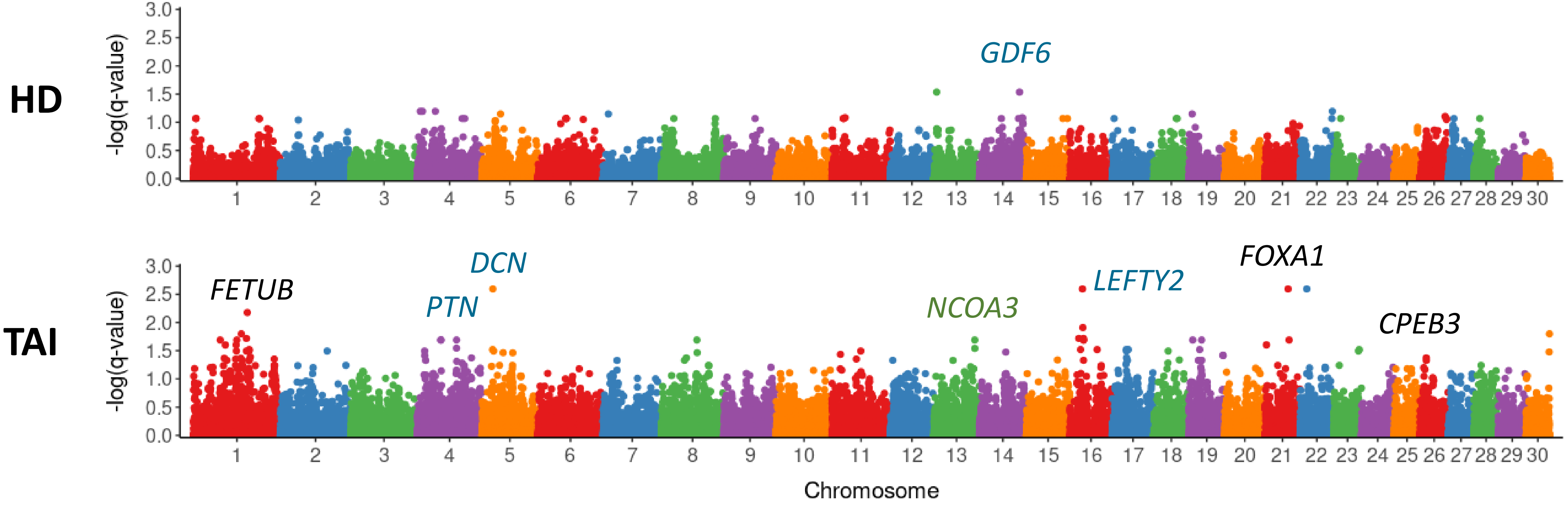


First service to conception: no overlapping significant peaks



TGF-beta signaling pathway
Estrogen signaling pathway

Days open: no overlapping significant peaks



TGF-beta signaling pathway
Estrogen signaling pathway

Shared significant peaks within HD and TAI fertility traits

HD
DO and FSTC

Chromosome	Position	Candidate gene	Candidate gene position
13	5,483,393		
14	68,228,943	*GDF6*	14:68,058,424-68,075,722

TAI
DO and FSTC

Chromosome	Position	Candidate gene	Candidate gene position
1	90,545,947-101,780,022		
4	100,990,430	*PTN*	4:100,885,905-100,995,239
5	21,048,868	*DCN*	5:21,014,376-21,053,400
16	30,505,468		
21	46,169,637		
22	11,209,744		

TGF-beta signaling pathway

Conclusions

- Genetic correlations between HD and TAI fertility traits (FSTC, CTFS, and DO) < 1 suggesting different traits

- Genome-wide association studies revealed different genetic backgrounds between HD and TAI fertility traits

Dr. Christina Rochus | crochus@uoguelph.ca