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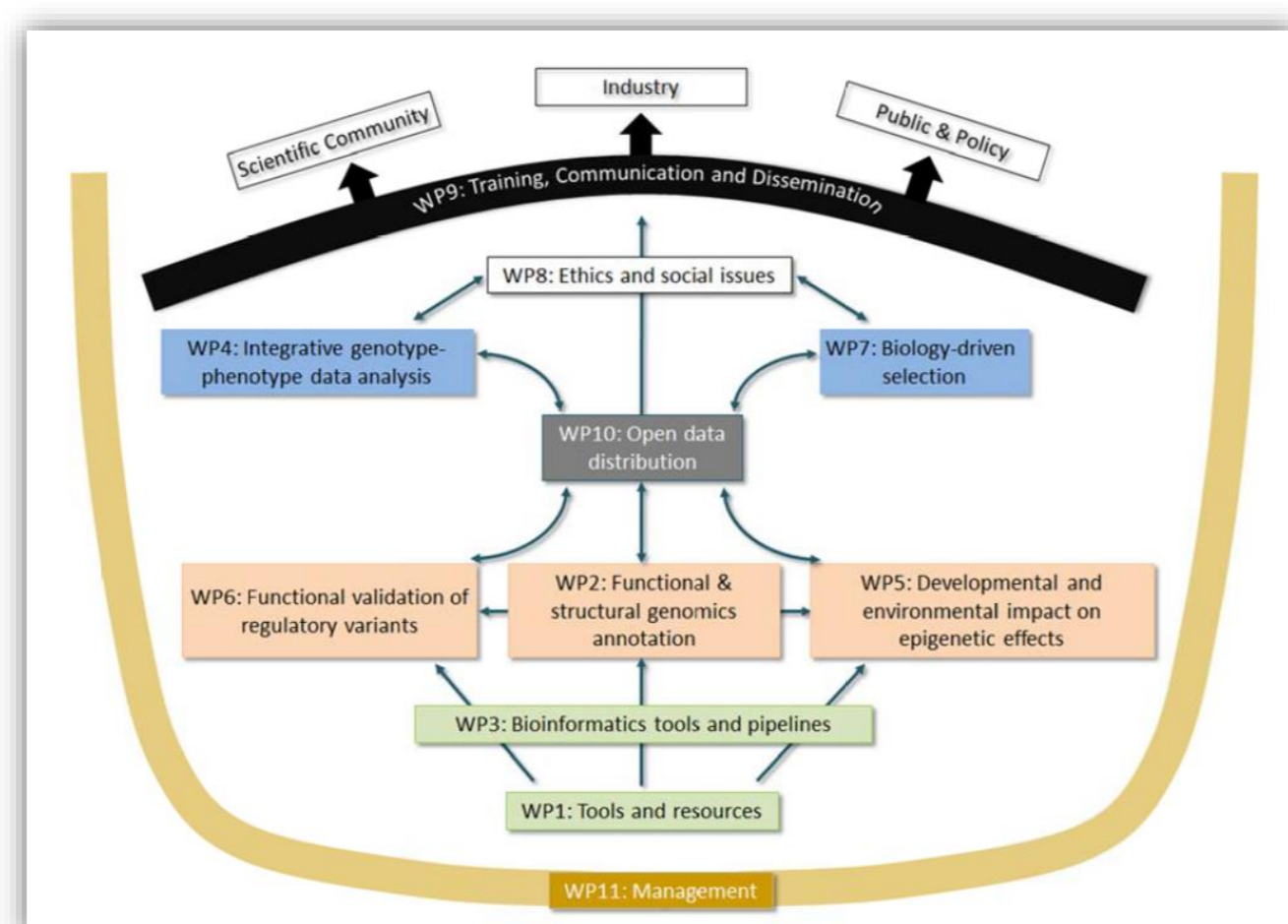
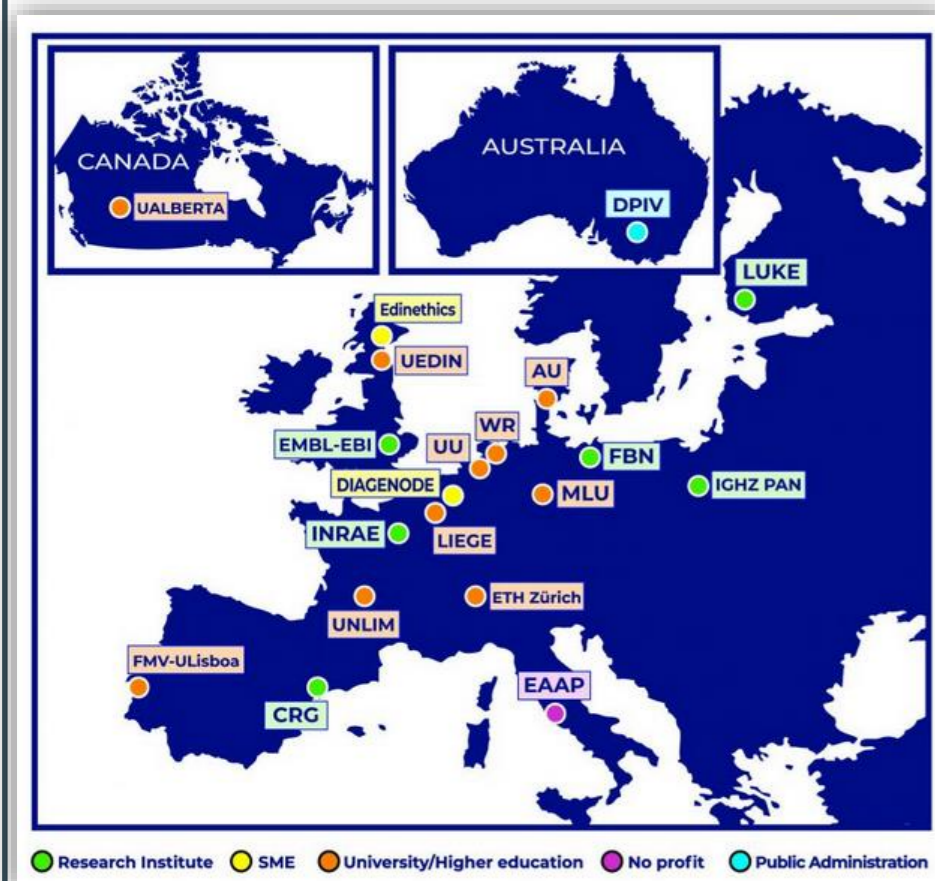
Sequence-based GWAS meta-analyses for beef production traits

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The H2020 BovReg project



20 partners from 14 countries

11 WP incl. WP4: Integrative analysis of genotype-phenotype

Objectives of the present study

GWAS and meta-analyses from whole-genome sequences (WGS) for beef traits

Material & Methods

A large number of various populations

8 purebred populations from France (NOR, MON, CHA, LIM, BLA)



4 populations from Swiss breeds (BSW, OBR)



2 crossbred populations from Germany (HOL x CHA)



1 composite line from Canada (ANG, CHA, beef)



Sequence-based GWAS meta-analyses (METAL)

1 GWAS by each partner from imputed WGS (GCTA)

A large number and a large diversity of traits

Growth (6)
Morphology (6)
Carcass (21)

1	Growth	Birth Weight	BW
2	Growth	weight at month 15	W15
3	Growth	weight at 18 months	W18
4	Growth	weight at 24 months	W24
5	Growth	average daily gain	ADG
6	Growth	average daily gain during fattening	ADG
7	Morphology	muscularity score	MS30
8	Morphology	skeletal score	SS30
9	Morphology	thickness of bones	TE30
10	Morphology	Thighs	THIGH
11	Morphology	Wither	WITHER
12	Morphology	Fat score	FS
13	Carcass	carcass weight	CW
14	Carcass	fat coverage	CF
15	Carcass	meatiness	MT
16	Carcass	Area of longissimus thoracis	ALT
17	Carcass	Carcass conformation	CC
18	Carcass	carcass fat score	FS
19	Carcass	carcass yield	CY
20	Carcass	Internal fat weight	IFW
21	Carcass	length of the leg	LL
22	Carcass	Rib Eye Area	REA
23	Carcass	Weight at slaughter	WS
24	Carcass	Maximum width of the thigh	WT
25	Carcass	age at slaughter	AS
26	Carcass	carcass grade	CG
27	Carcass	average back-fat thickness	ABT
28	Carcass	hot carcass weight	CW
29	Carcass	lean meat yield	LMY
30	Carcass	fat content of 6th rib	FC6
31	Carcass	fat content measured by ultrasound	FCU
32	Carcass	muscular development	MD
33	Carcass	skeletal development	SD

Grouping of traits in 16 MA

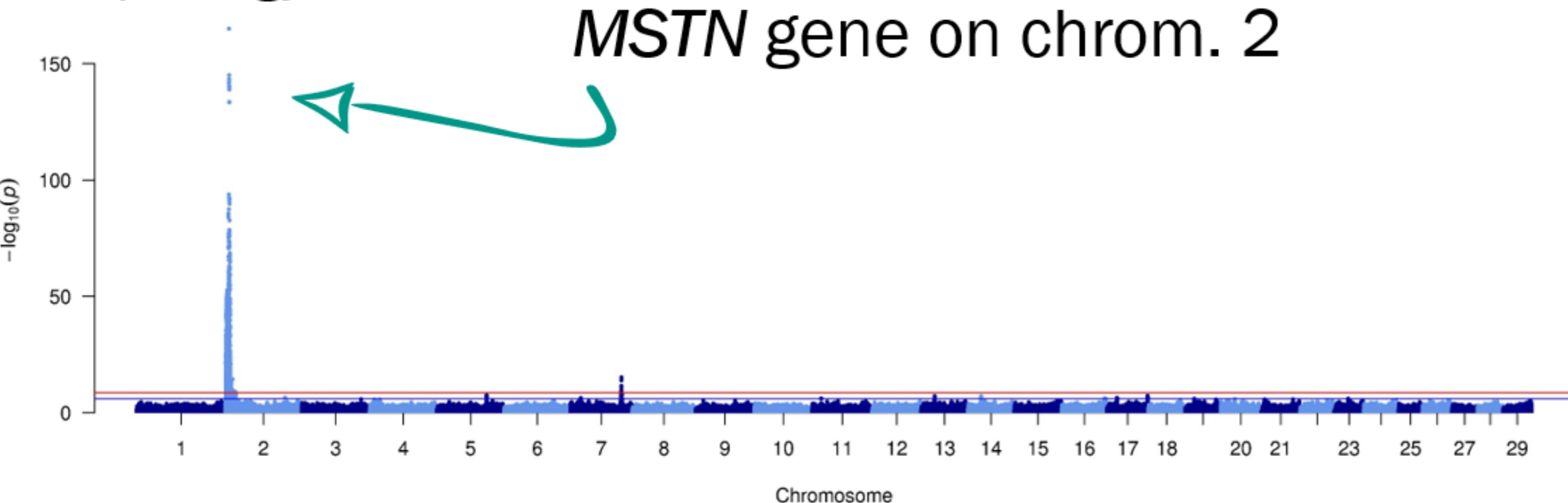
MA	Trait type	Traits	# traits	# pop.	# partners	# anim.
1	Growth	W15/W18/ADG	3	7	4	18774
2	Growth	BW	1	5	2	2720
3	Morphology	MS30/THIGH/CC	3	6	2	17418
4	Morphology	MS30/WITHER/CC	3	6	2	17418
5	Morphology	LL	1	5	2	3695
6	Morphology	WT	1	5	2	3695
7	Morphology	SS30/SD	2	4	2	12140
8	Carcass	CW	1	7	4	19989
9	Carcass	AS	1	6	2	12208
10	Carcass	CF	1	5	2	3694
11	Carcass	GG/LMY/MT/CC	4	10	5	25367
12	Carcass	FS/ABT/FC6/FCU/CF	5	8	5	14622
13	Carcass	WS	1	5	2	2636
14	Carcass	ALT	1	5	2	3692
15	Carcass	IFW	1	5	2	3686
16	Carcass	REA	1	3	2	4453

- ☑ 1 to 5 traits / MA
- ☑ 3 to 10 populations / MA
- ☑ 2 to 5 partners / MA
- ☑ 2600 to 20,000 animals / MA

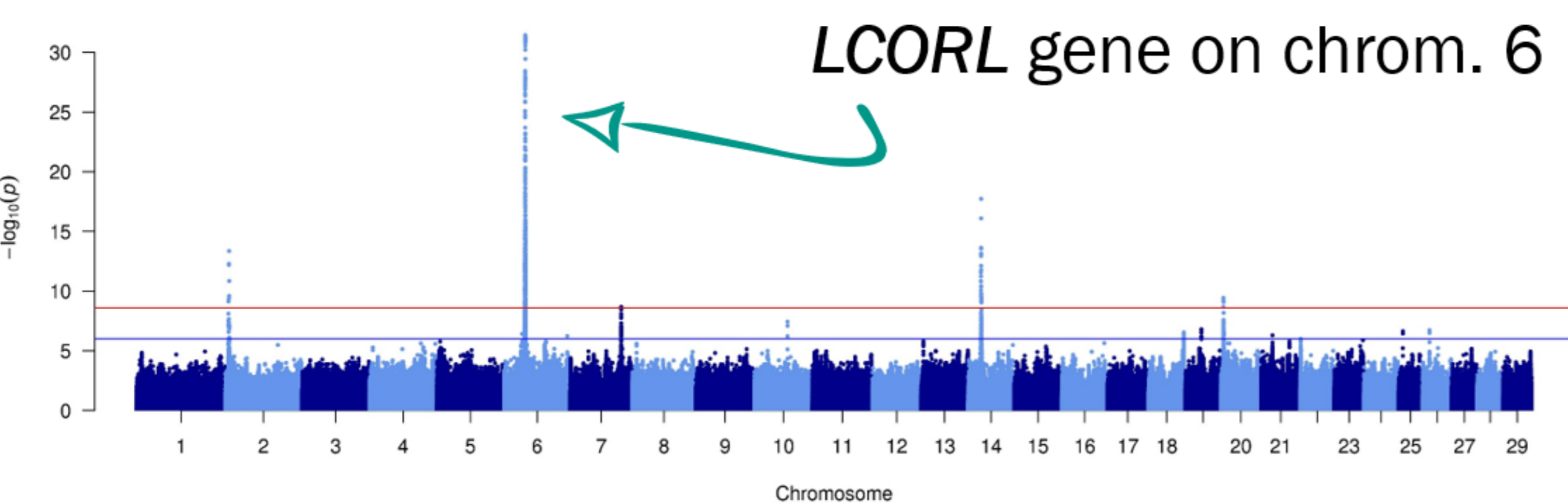
Results

Significant results (QTL) for 15 of the 16 MA

Morphology



Carcass



Compared to GWAS, meta-analyses highlights:

- 1) a larger number of QTL,
- 2) QTL more frequently located in genomic regions with effects on growth and meat/carcass traits reported in *CattleQTLdb*,
- 3) a smaller number of variants within the QTL,
- 4) variants more frequently located in genes.

Candidate variants located in genes including *MSTN*, *LCORL*, *PLAG1*, *HS6ST1*, *HERC2*, *WDR75*, *COL3A1*, *SLIT2*, *MED28*, and *ANKAR*

Some of these variants overlap with expression or splicing QTL reported in *CattleGTEx* and could therefore regulate gene expression.

Conclusions

By identifying candidate genes and potential causal variants associated with beef production traits in cattle, meta-analysis demonstrates great potential for investigating underlying biological mechanisms