

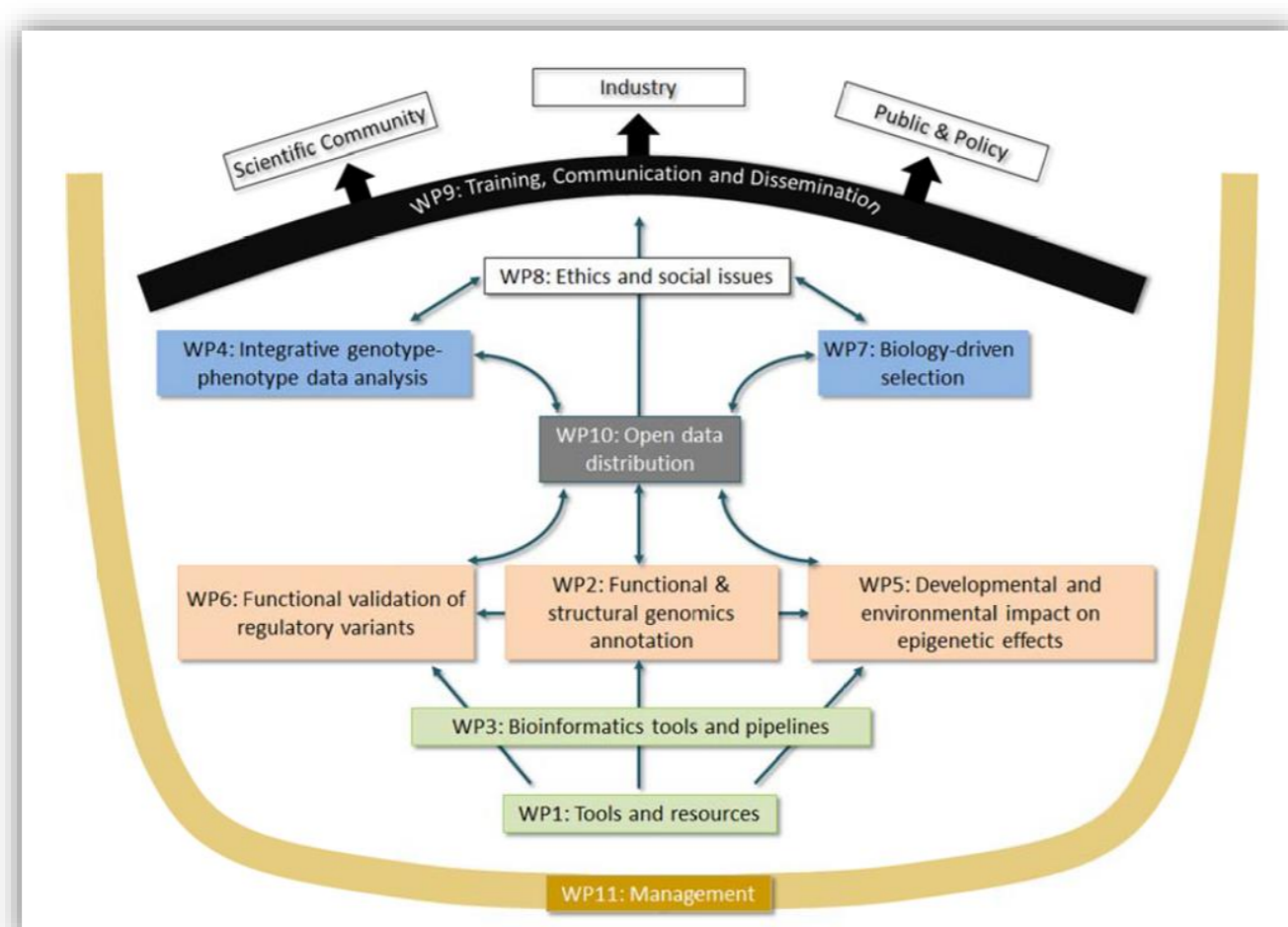
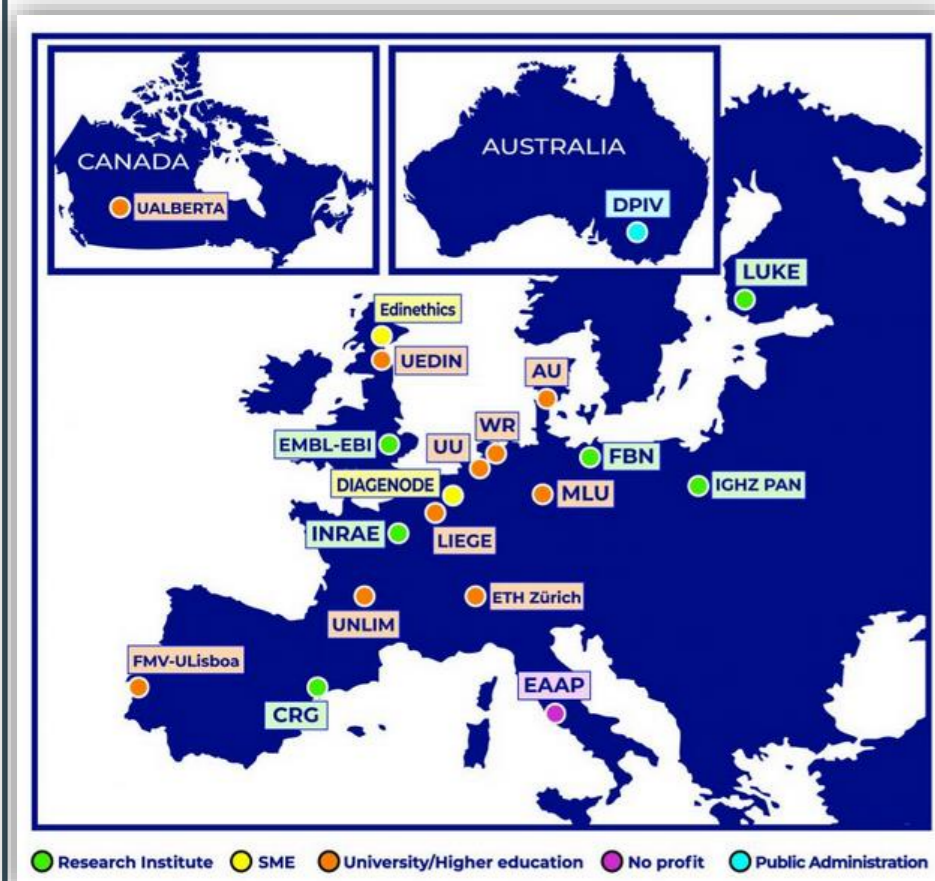
Sequence-based GWAS meta-analyses for beef production traits

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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)



2 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)

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/THIGHS/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/LMV/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

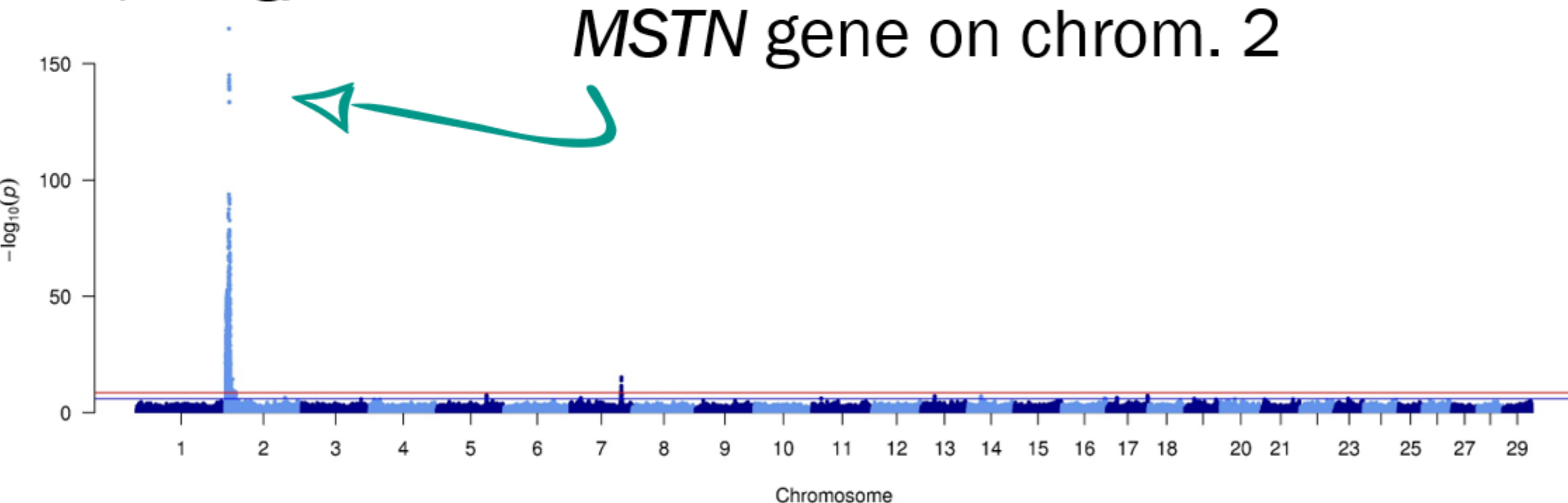
Grouping of traits in 16 MA

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

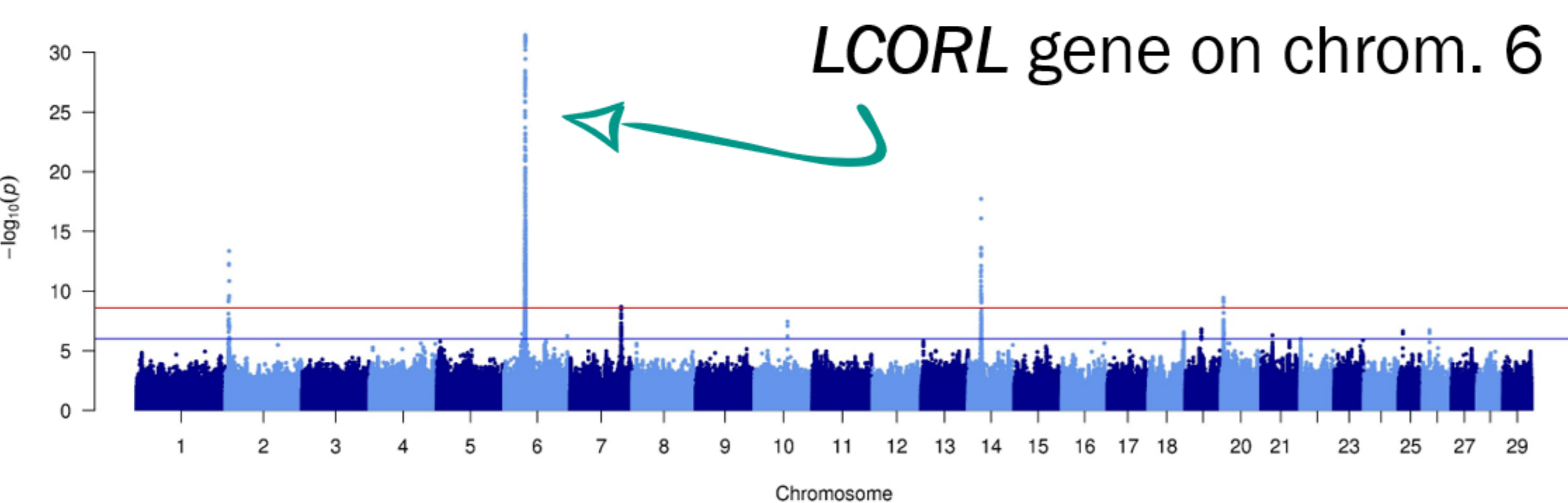
Results

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