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Multi-trait analysis of meat quality traits in Limousin, Charolais and Blonde d'Aquitaine breeds

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Introduction

Meat quality traits are key factor for
the final consumer and then the industry

Market advantage of beef breeds!
However, difficult and expensive traits to measure

Several research programs in France since 2000's
Genomic data → Better understanding of genetic architecture

⇒ "Pré-PILOTaGE" funded by APIS-GENE
Following Ramayo-Caldas et al. (2016) study

Objective: Perform multi-trait analysis of meat quality traits in 3 French breeds

Charolaise

Limousine

Blonde d'Aquitaine

Material

Dataset from QUALVIGENE project

1217 Limousine, 1059 Charolaise, 947 Blonde d'Aquitaine
young bulls (15 months) genotyped with the 50K chip
Progeny of 36, 48 and 30 AI bulls, respectively (HD genotyped)

Breed-specific imputation on HD chip (777K SNP)
(Fimpute, Sargolzaei et al., 2014)

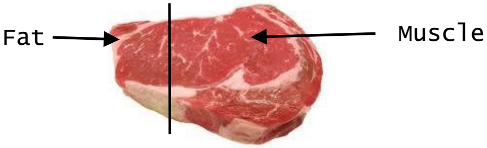
16 traits phenotyped on the carcass at the slaughterhouse:
- 4 scores for alive and carcass conformation
- 3 scores for meat quality
- 9 measures for meat proprieties and composition

Material

Description of traits and heritabilities

6 selected phenotypes

Trait	Description	Limousine	Charolaise	Blonde d'Aquitaine
FC	**Warner–Bratzler shear force (N/cm2)**	0.20	0.24	0.23
TEND	**Tenderness score (/100)**	0.11	0.50	0.19
JUIC	**Juiciness score (/100)**	0.08	0.06	0.09
FLAV	**Flavor score (/100)**	0.02	0.23	0.02
COUL	**Luminosity**	0.09	0.14	0.21
IMF	**Intramuscular lipid content (%)**	0.26	0.47	0.28
CI	Insoluble collagen content (%)	0.21	0.22	0.01
TAMF	Muscle fiber section mean area (10−6 mm2)	0.08	0.18	0.28
DM	Live muscle score (/100)	0.45	0.23	0.67
CONF	Carcass muscle score (/18)	0.70	0.16	0.53
REND	Carcass yield (/100)	0.66	0.59	0.29
RIBE	Rib eye area (cm2)	0.52	0.23	0.36
CIFW	Internal cavity fat weight (kg)	0.50	0.39	0.45
RIB6	Dissected 6th rib fat (%)	0.10	0.62	0.30
VOS	Velocity of sound (10−3s/cm)	0.12	0.40	0.13
TFIB	Rib eye area/muscle fiber area	0.21	0.29	0.39



Methods

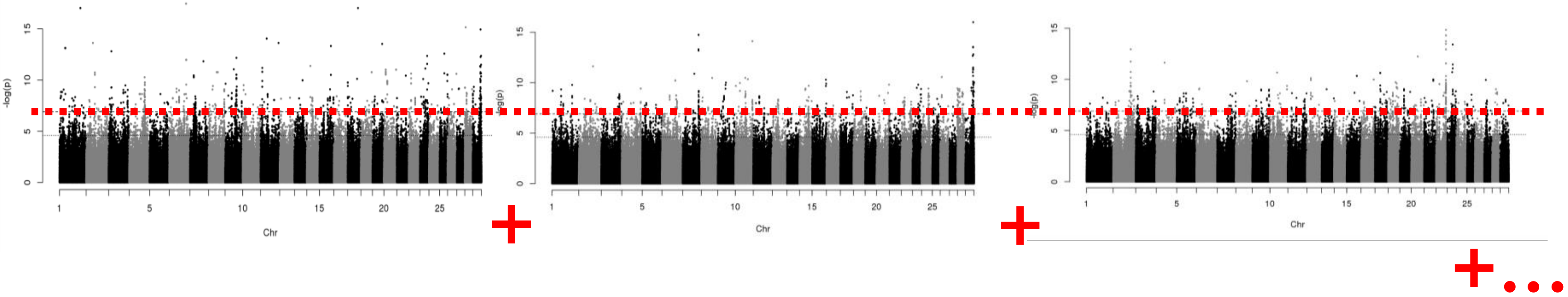
GWAS performed with GCTA (Yang et al., 2011) on HD imputed genotypes for 16 traits with a p-value threshold of 0.001

Shear Force

Tenderness

Flavor

(Charolaise breed)



Association Weight Matrix (AWM) method (Fortes et al., 2010)

3 categories of SNP:

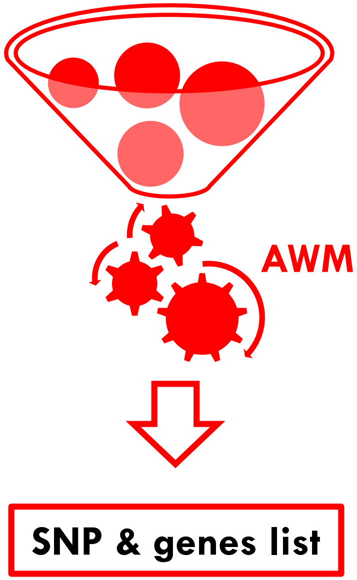
K : Detected for the key-phenotype only

K+O : Detected for the key-phenotype only and at least one other trait

O : Detected for several other traits (more than the average number of significant traits for the SNP of the key-phenotype)

Each of the 6 selected phenotypes considered as key-phenotype

Every trait with SNP effects correlation > 0.30 used in AWM

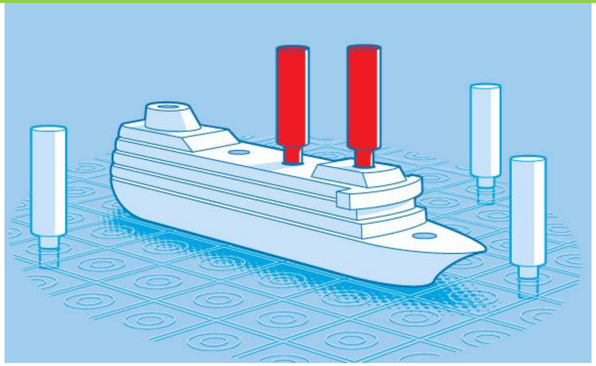


SNP & genes list

Methods

Difference between genomic and polygenic correlation

Threshold of 0.30



SNP effects correlation matrix in Limousine

	FC	**TEND**	**JUIC**	**FLAV**	**COUL**	**IMF**
TEND	-0.91					
JUIC	-0.22	0.11				
FLAV	-0.89	0.84	0.43			
COUL	-0.04	0	-0.01	-0.05		
IMF	-0.05	0	0.07	0.09	0.08	
CI	-0.04	-0.07	-0.02	0.03	-0.11	0.2
TAMF	0.13	-0.11	0.01	-0.04	-0.03	0.07
DM	0	0.02	0.06	0	0.1	-0.02
CONF	0.06	-0.07	0.05	-0.05	0.13	-0.01
REND	-0.01	-0.04	0.01	-0.1	0.05	-0.18
RIBE	0.01	0.04	0.12	-0.02	0.04	-0.08
CIFW	-0.06	0.06	0.1	0.1	0.09	0.28
RIB6	-0.05	0.14	0.07	0.13	0.09	0.31
VOS	-0.03	0.11	0.06	0.08	0.07	0.37
TFIB	-0.1	0.12	0.05	0.02	0.05	0.08

Genetic correlation matrix in Limousine (S. Allais thesis, 2011

	FC	**TEND**	**JUIC**	**FLAV**	**COUL**	**IMF**
TEND	-0.38					
JUIC	-0.09	0.48				
FLAV	-0.17	0.35	0.45			
COUL	-0.02	-0.01	-0.05	-0.11		
IMF	-0.04	0	0.07	0.1	0.08	
CI	-0.04	-0.09	-0.02	0.06	-0.16	0.07
TAMF	0.14	-0.13	0	-0.04	-0.02	0.08
DM	0	0.01	0.07	-0.02	0.11	-0.02
CONF	0.06	-0.05	0.06	-0.06	0.13	-0.02
REND	-0.02	-0.04	0.04	-0.09	0.05	-0.19
RIBE	0.02	0.03	0.13	-0.02	0.02	-0.08
CIFW	-0.06	0.05	0.08	0.1	0.09	0.31
RIB6	-0.05	0.14	0.06	0.13	0.1	0.33
VOS	-0.03	0.11	0.08	0.09	0.05	0.39
TFIB	-0.09	0.11	0.07	0.02	0.04	-0.1

|cor.gen.| > 0.30 & |cor.phen.| > 0.30

|cor.gen.| > 0.30 & |cor.phen.| < 0.30 or |cor.gen.| < 0.30 & |cor.phen.| > 0.30

Results

Correlated traits with 6 key-phenotypes

Trait	Limousine	Charolaise	Blonde d'Aquitaine
FC	TEND	TEND, FLAV	TEND
TEND	FC, JUIC, FLAV	FC, JUIC, FLAV	FC, JUIC, FLAV
JUIC	TEND, FLAV	TEND, FLAV	TEND, FLAV
FLAV	TEND, JUIC	FC, TEND, JUIC	TEND, JUIC
COUL	∅	∅	∅
IMF	CIFW, RIB6, VOS	RIBE, CIFW, RIB6, VOS	CIFW, RIB6, VOS

FC	Shear force	FLAV	Flavor score
TEND	Tenderness score	COUL	Luminosity
JUIC	Juiciness score	IMF	Intramuscular lipid content

Results

		Limousine	Charolaise	Blonde d'Aquitaine
FC	*SNP*	*567*	*668*	*718*
	Gene	84	122	118
TEND	*SNP*	*568*	*689*	*540*
	Gene	98	128	84
JUIC	*SNP*	*570*	*604*	*564*
	Gene	93	120	106
FLAV	*SNP*	*550*	*656*	*480*
	Gene	89	130	84
COUL	*SNP*	*537*	*626*	*546*
	Gene	85	116	98
IMF	*SNP*	*495*	*796*	*544*
	Gene	97	137	87

Results

		Limousine			Charolaise			Blonde d'Aquitaine		
		K	K+O	O	K	K+O	O	K	K+O	O
FC	*SNP*	*561*	*6*	*0*	*632*	*22*	*14*	*714*	*4*	*0*
	Gene	81	3	0	110	9	3	116	2	0
TEND	*SNP*	*508*	*37*	*23*	*610*	*40*	*39*	*484*	*34*	*22*
	Gene	84	11	3	104	13	11	72	11	1
JUIC	*SNP*	*517*	*51*	*2*	*561*	*44*	*9*	*512*	*52*	*0*
	Gene	82	11	0	105	14	1	96	10	0
FLAV	*SNP*	*496*	*31*	*22*	*577*	*49*	*30*	*428*	*22*	*30*
	Gene	78	4	7	106	14	10	74	1	9
COUL	*SNP*	*537*	*0*	*0*	*626*	*0*	*0*	*546*	*0*	*0*
	Gene	85	0	0	116	0	0	98	0	0
IMF	*SNP*	*450*	*25*	*20*	*535*	*82*	*129*	*477*	*33*	*34*
	Gene	81	7	9	107	16	14	71	8	8

K : Detected for the key-phenotype only

K+O : Detected for the key-phenotype only and at least one other trait

O : Detected for several other traits

(more than the average number of significant traits for the SNP of the key-phenotype)

Results

29 genes detected in at least 2 breeds for the same trait

Gene name	Trait	Trait-breed 1	Trait-breed 2
PLXNA4	FC	FC-CHA	FC-BLA
EXOC4	FC	FC-CHA	FC-BLA
SND1	FC	FC-LIM	FC-CHA
FAT3	FC	FC-LIM	FC-CHA
SPAG17	FC	FC-CHA	FC-BLA
ENSBTAG00000048061	FC	FC-CHA	FC-BLA
FBN1	TEND	TEND-CHA	TEND-BLA
FAM81B	TEND	TEND-CHA	TEND-BLA
F13A1	TEND	TEND-LIM	TEND-BLA
MBNL1	TEND	TEND_JUIC-LIM	TEND-BLA
RHOBTB3	TEND	TEND-CHA	TEND-BLA
APC	JUIC	JUIC-LIM	JUIC-CHA
CA12	FLAV	FLAV-CHA	FLAV-BLA
CDYL	FLAV	FLAV-LIM	FLAV-CHA
FARS2	FLAV	FLAV-LIM	FLAV-CHA
NTM	COUL	COUL-CHA	COUL-BLA
ENSBTAG00000038079	COUL	COUL-LIM	COUL-CHA
TEX10	COUL	COUL-LIM	COUL-BLA
PARK2	IMF	CIFW_RIB6-LIM	IMF-BLA
SMYD3	IMF	IMF-LIM	IMF-BLA
SYNPR	IMF	IMF-CHA	IMF-BLA
NEMP2	IMF	IMF_RIBE_CIFW_RIB6_VOS-CHA	IMF_CIFW_RIB6-BLA
HIBCH	IMF	CIFW_RIB6_VOS-CHA	CIFW_RIB6_VOS-BLA
CCDC6	IMF	IMF_CIFW-LIM	IMF-CHA
ATP2B2	IMF	IMF_CIFW-LIM	IMF-CHA
ABLIM1	IMF	IMF-CHA	IMF-BLA
RSU1	IMF	IMF-LIM	IMF-CHA
MFSD6	IMF	IMF_CIFW-CHA	IMF_CIFW_RIB6-BLA
SCG3	IMF	IMF-LIM	CIFW_RIB6-CHA

Results

Around 100 genes per trait were identified using AWM

AWM made it possible to detect new genes considering correlated traits

⇒ A total of 1,586 genes were found among the 3 breeds

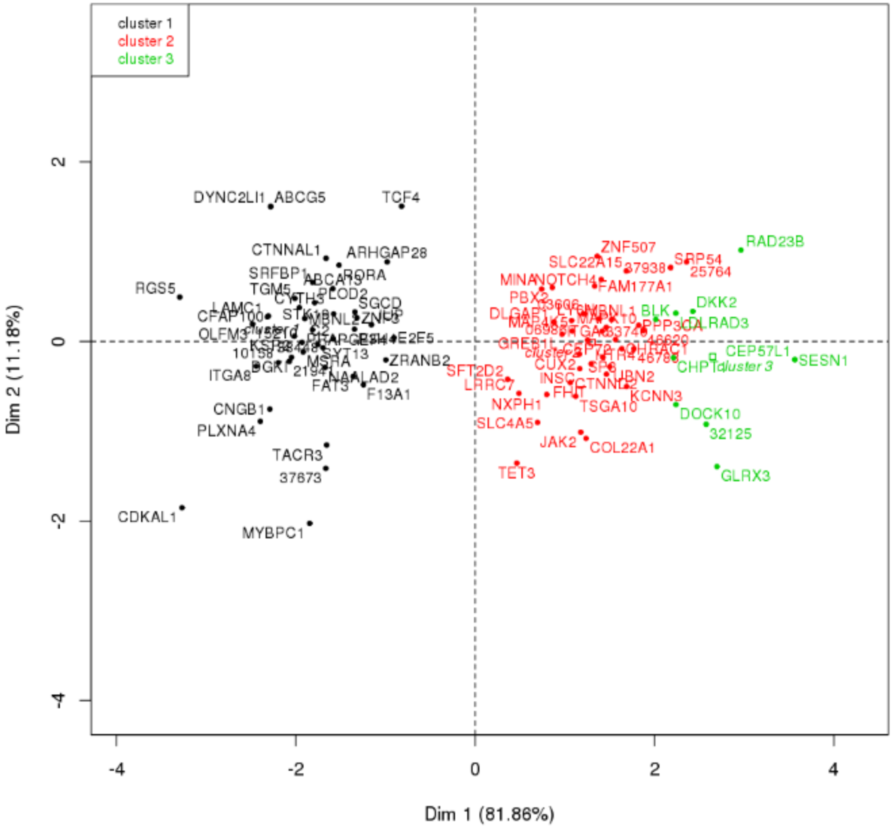
The effect associated to the lead SNP of the gene allow studying gene interactions

Principal component analyses (PCA) were performed with tenderness (TEND) trait for each breed

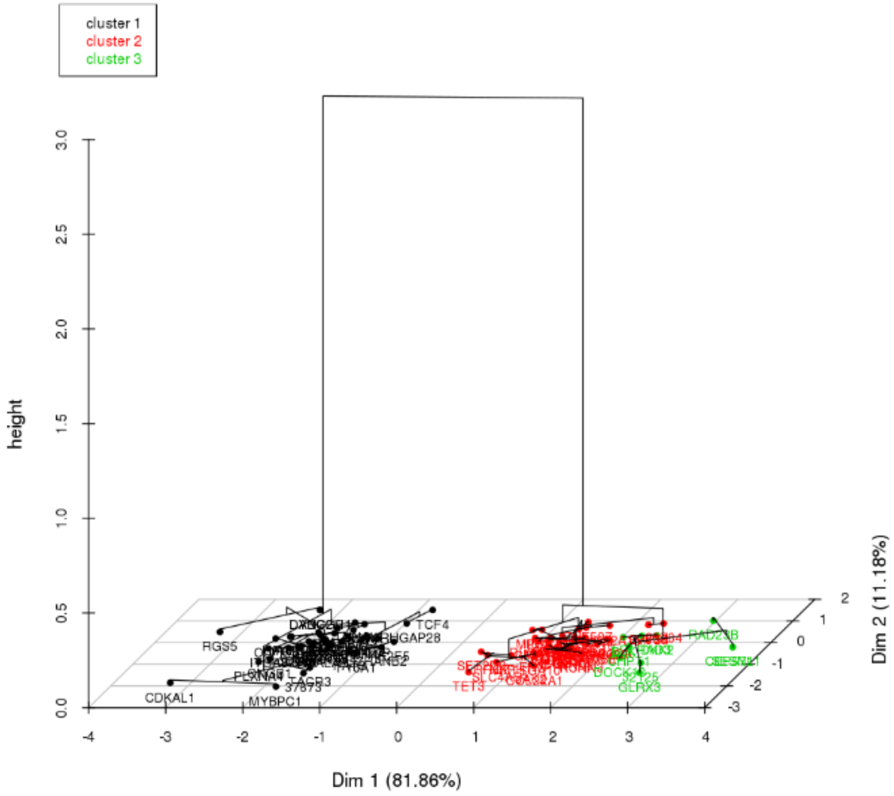
Results

PCA for tenderness in Limousine

Individual factor map



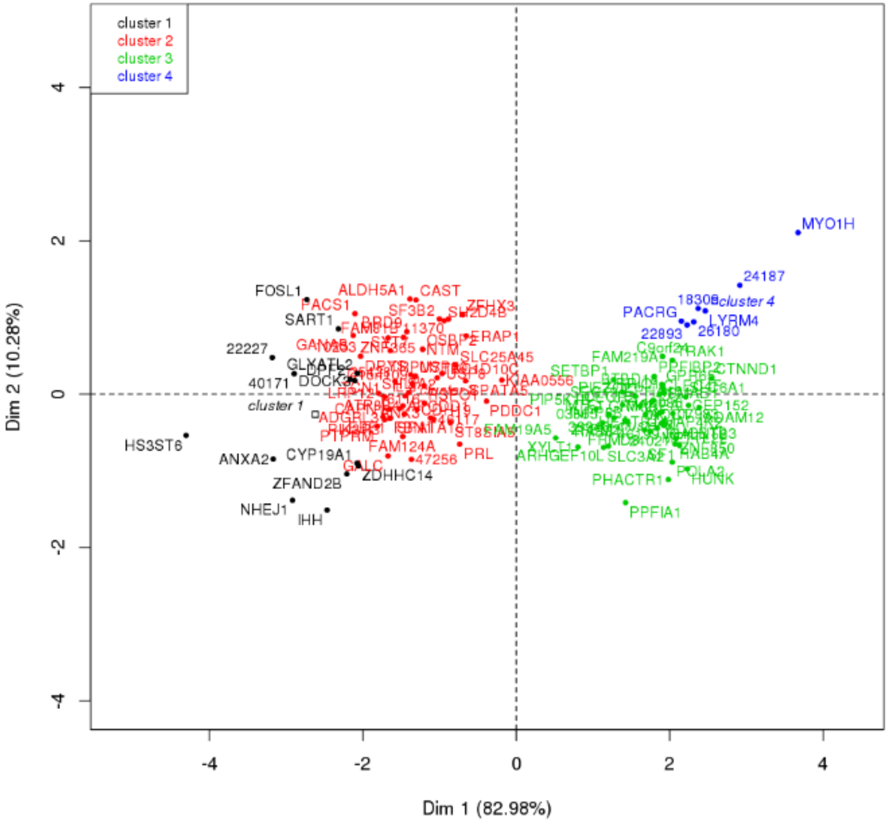
Hierarchical clustering on the factor map



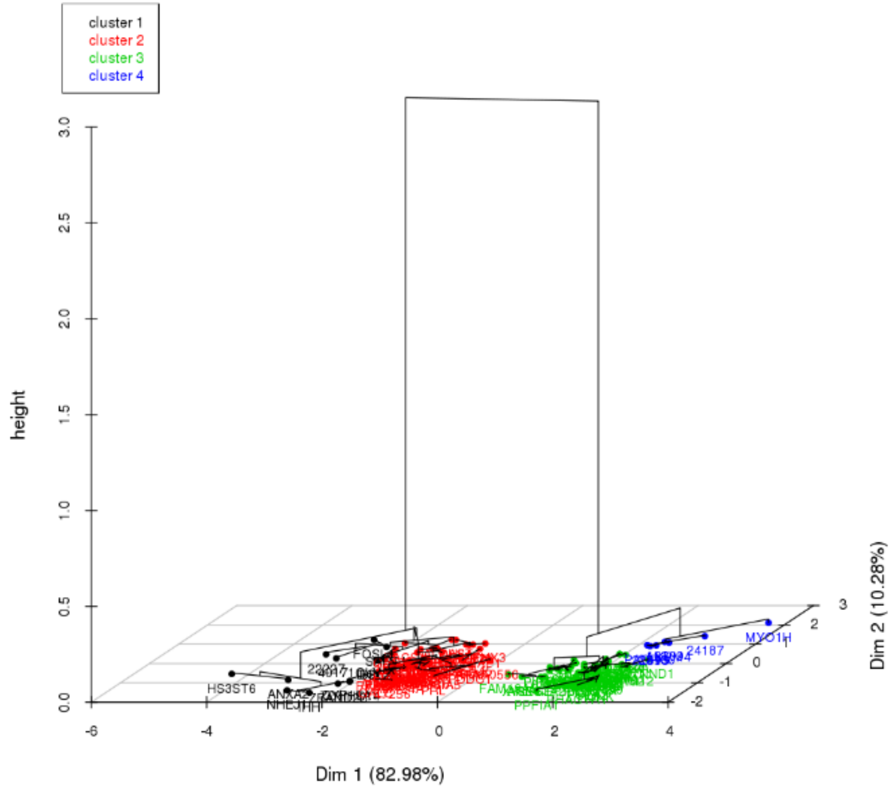
Results

PCA for tenderness in Charolaise

Individual factor map



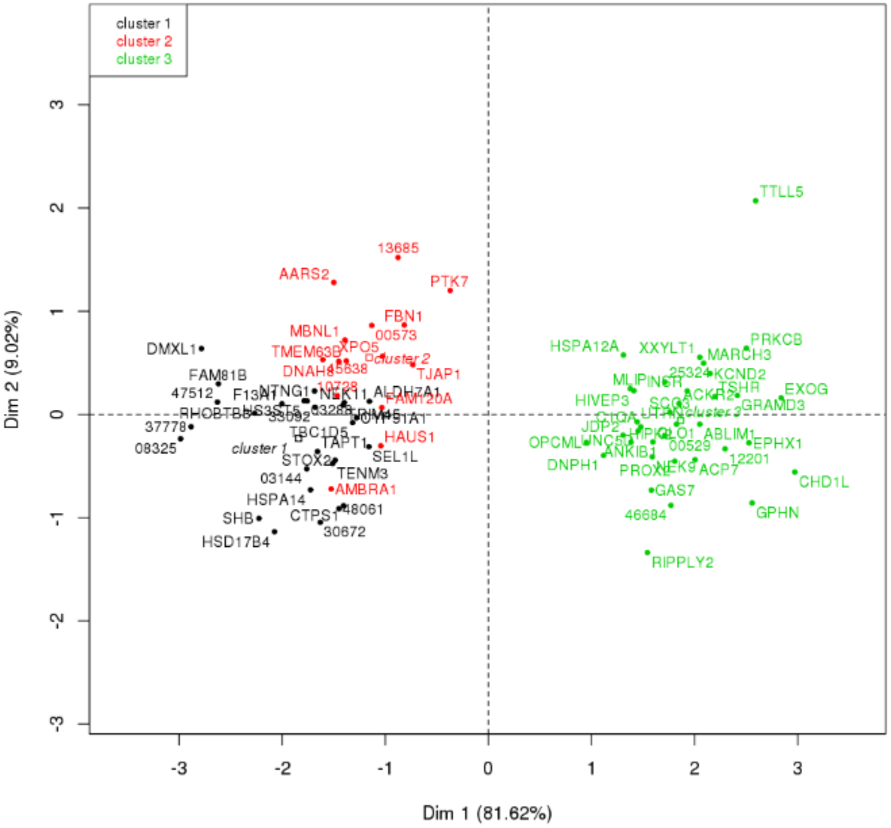
Hierarchical clustering on the factor map



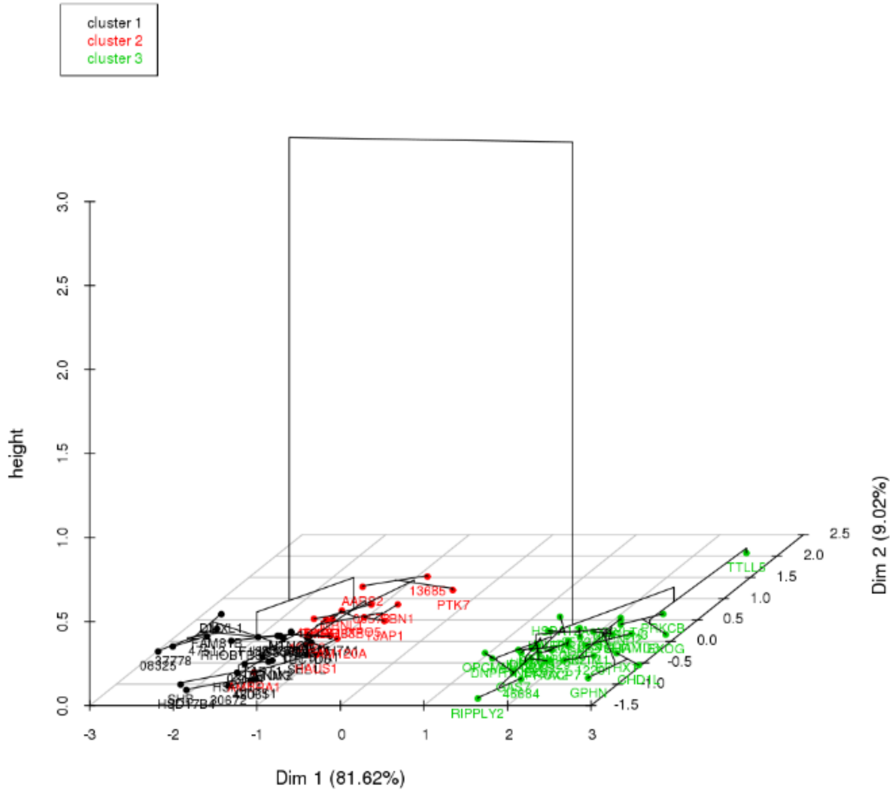
Results

PCA for tenderness in Blonde d'Aquitaine

Individual factor map



Hierarchical clustering on the factor map

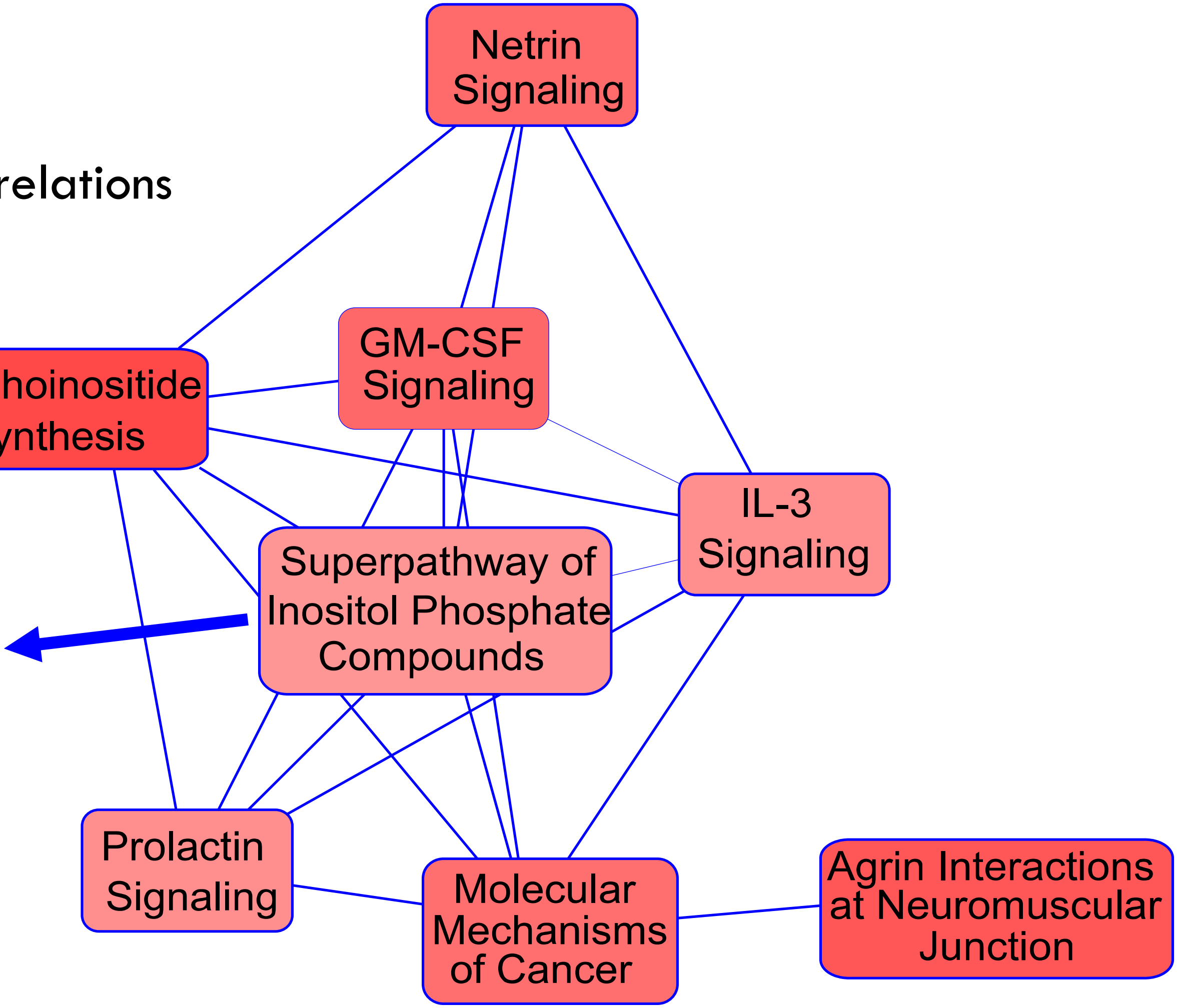


Results

Pathway Analysis (by Ingenuity Systems, Redwood City, CA)

318 genes detected for tenderness (TEND) in 3 breeds
242 genes mapped on IPA

⇒ Complex pathway
⇒ Several step and numerous relations



Netrin Signaling

GM-CSF Signaling

3-phosphoinositide Biosynthesis

IL-3 Signaling

Superpathway of Inositol Phosphate Compounds

Prolactin Signaling

Molecular Mechanisms of Cancer

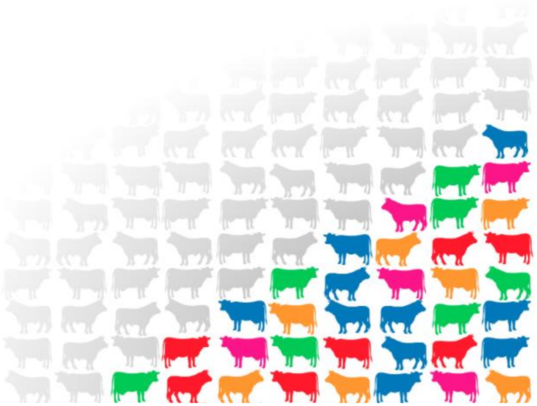
Agrin Interactions at Neuromuscular Junction

Crucial in metabolism : involved in the regulation of cellular events including growth, differentiation, vesicular sorting, glucose transport and platelet aggregation

Conclusion

Multi-trait analysis in the 3 French breeds provided:
-**numerous genes** affecting meat quality traits
-a better knowledge of their **genetic determinism**
Good perspectives for the implementation of **genomic selection**

Larger reference population is needed for **accurate** genomic predictions
⇒ Select the best performance!



THE FRENCH TOUCH
reliability & performance

Thank you for your attention

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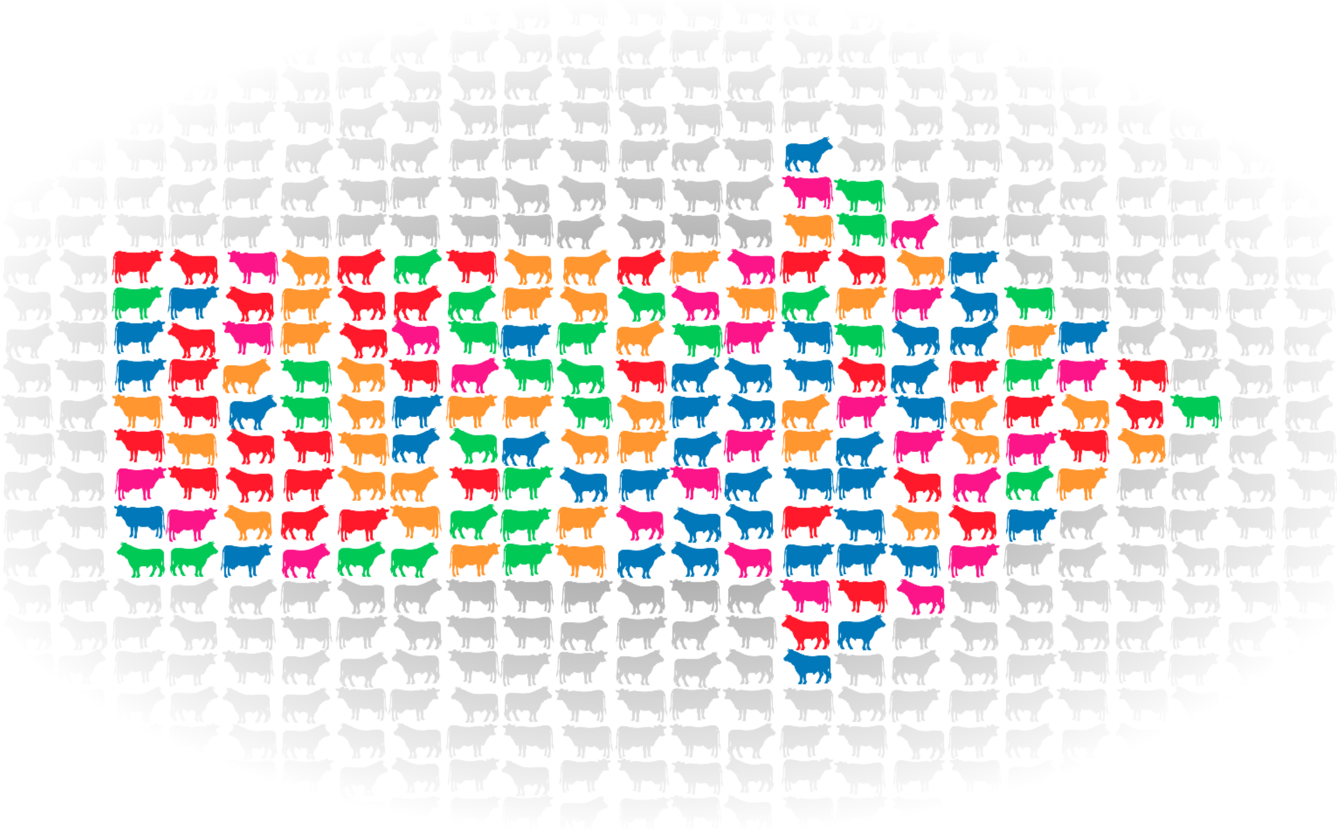

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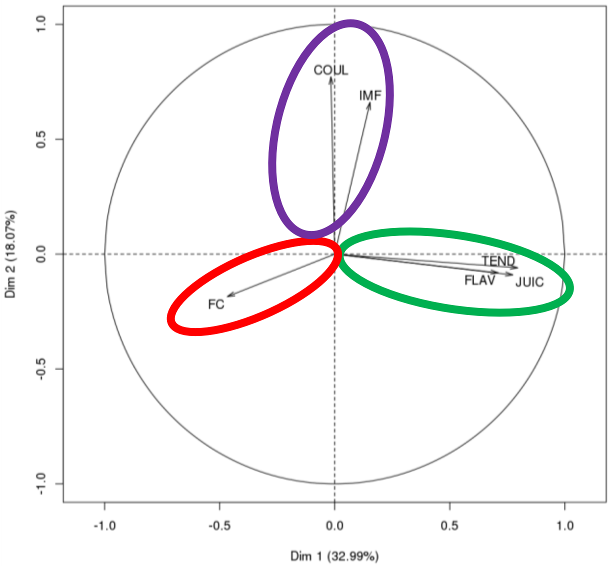
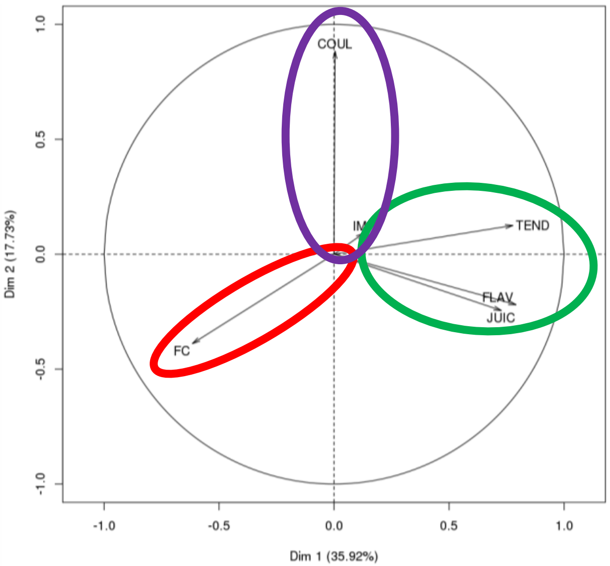
Appendix

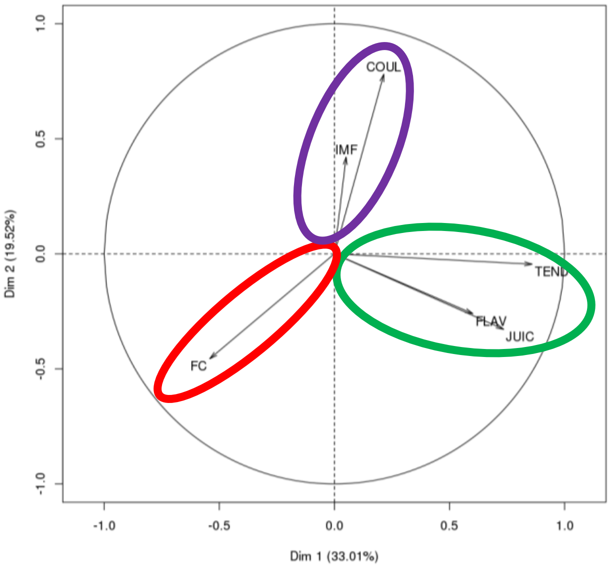
Principal component analysis based on individual phenotypes



Limousine



Charolaise



Blonde d'Aquitaine

Around 50% of variability explained on 2 dimensions

Opposition FC ***Vs*** TEND + FLAV + JUIC

COUL & IMF on the second dimension for Limousine and Blonde d'Aquitaine