

Genome-wide association studies in purebred and crossbred entire male pigs



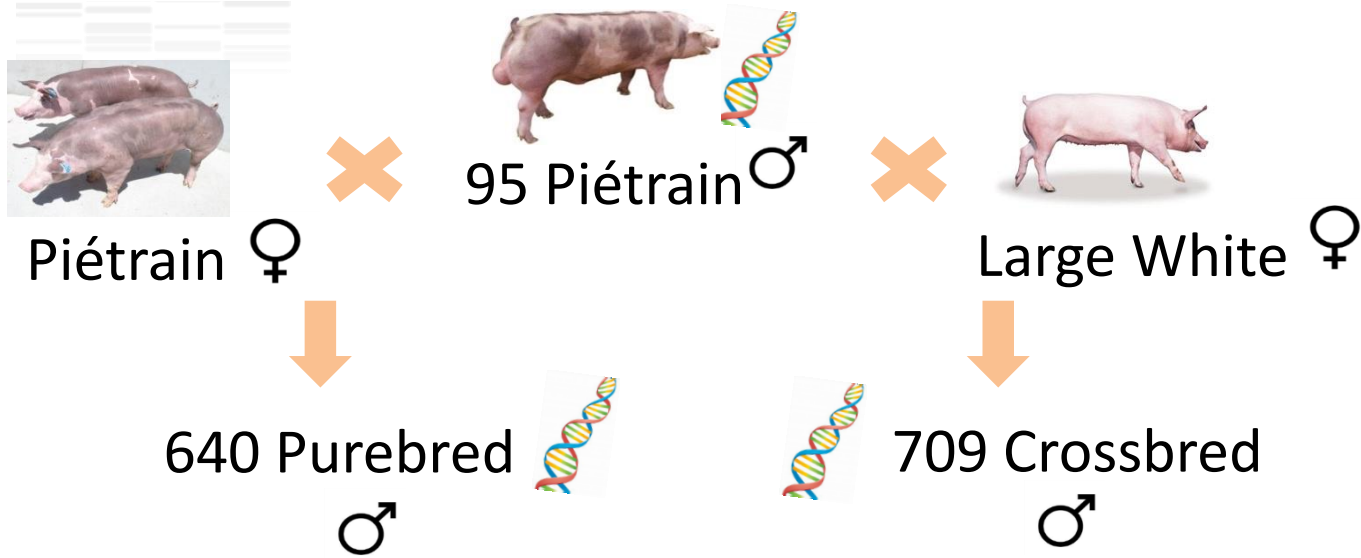
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**Labrune Y, Chassier M, Muller N, Parois S, Mercat MJ,
Prunier A, Larzul C, Riquet J**

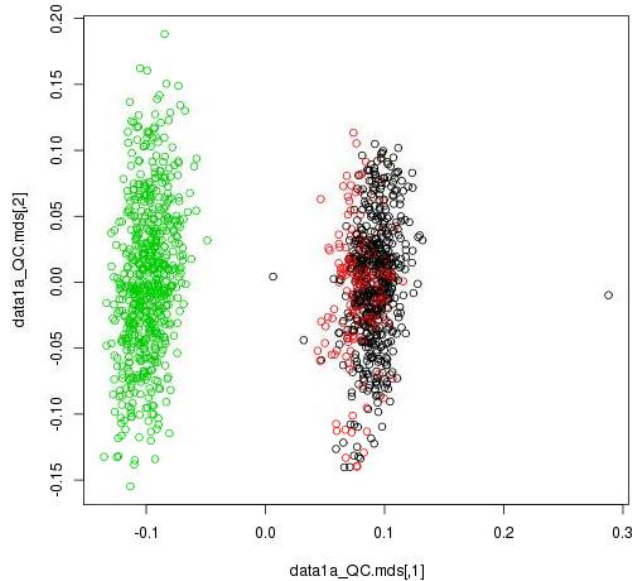
Objective



Genome wide association studies in purebreds and crossbreds
Are they common regions?
What could explain the differences?

Population structure and genotyping

Purebreds
Piétrain



Crossbred

Piétrain x LW mat

Piétrain x LW pat

Quality control



Illumina SNP chip
62 626 markers

42 379
purebred

47 247
crossbred

**41 450 common
markers**

Traits

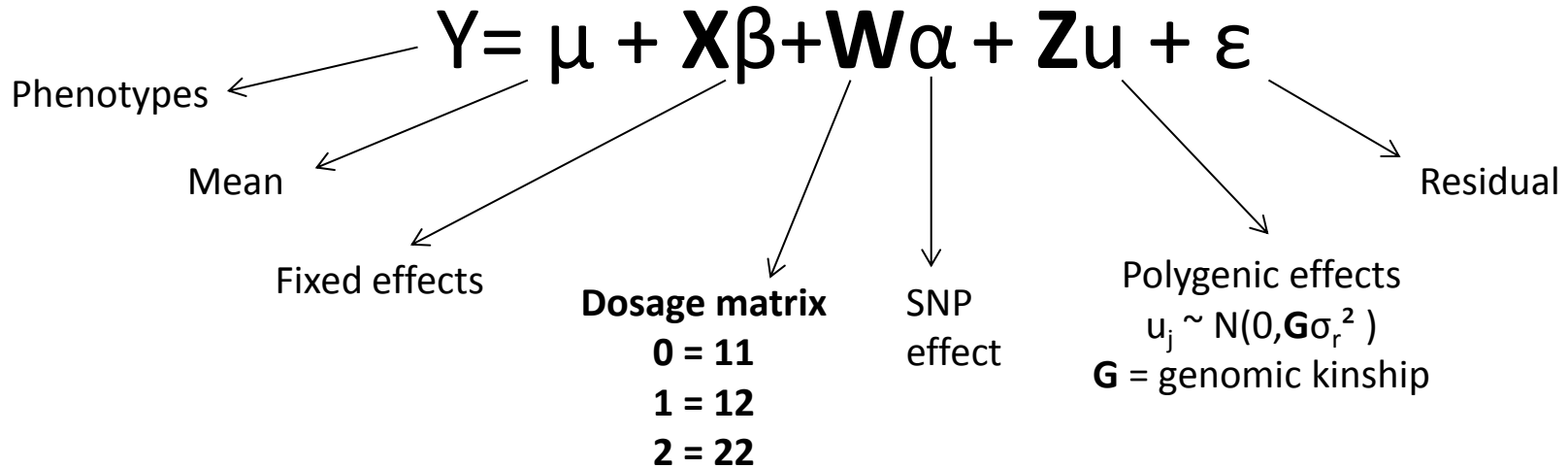
- ❖ **Production:** feed intake and growth (DFI, FCR , RFI, ADG), BW
- ❖ **Carcass composition:** Carcass yield, lean meat content, tomograph, ...
- ❖ **Meat quality:** a*, b*, L*, drip loss, ultimate pH
- ❖ **Lesions:** at mixing, before slaughter, on the carcass
- ❖ **Boar taint/sex hormones:** androstenone, skatole, indole, testosterone, oestradiol
- ❖ **Health parameters:** leucocytes, CRP, Pig-MAP,...
- ❖ **Lameness**



78 traits

Genome wide analyses

Linear mixed model

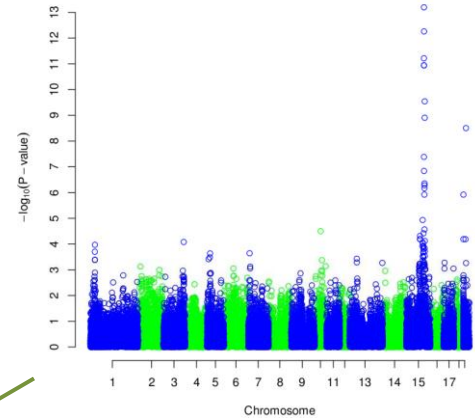
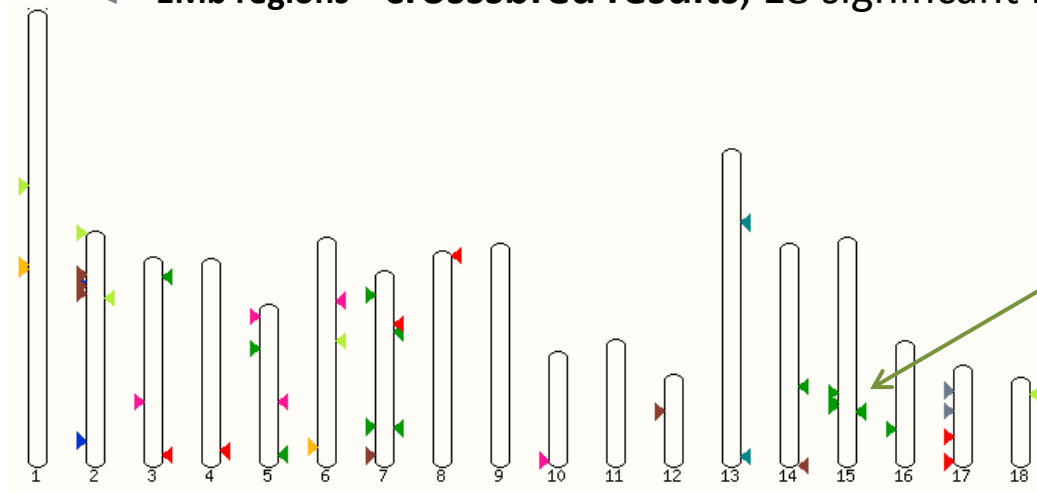


Applied to purebreds and crossbreds separately

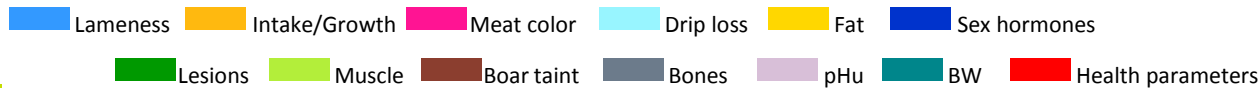
GWAS (2) $-\log_{10}(\text{p.value}) > 5$, traits

▶ 1Mb regions – purebred results, 24 significant regions

◀ 1Mb regions – crossbred results, 18 significant regions



Lesions, posterior part, crossbreds





GWAS (3) common regions, trait families

For all SNP with $-\log_{10}(\text{p.value}) > 4$

In the 1 Mb-region surrounding the marker, look for $-\log_{10}(\text{p.value}) > 3$ in the trait family

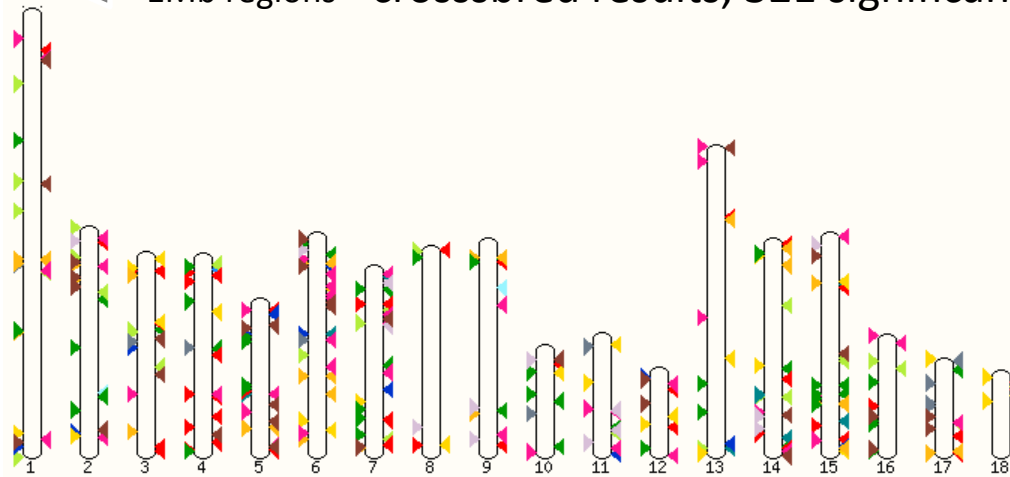
GWAS (3) common regions, trait families

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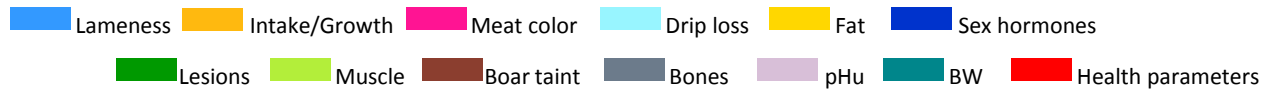
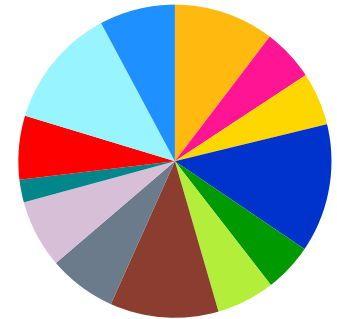
In the 1 Mb-region surrounding the marker, look for $-\log_{10}(p.value) > 3$ in the trait family

▶ 1Mb regions – purebred results, 325 significant regions

◀ 1Mb regions – crossbred results, 321 significant regions



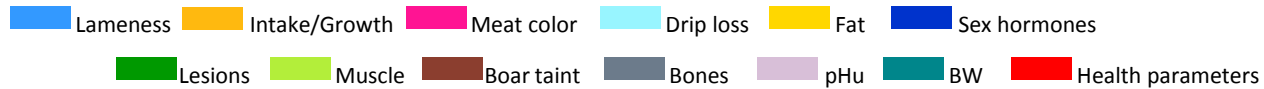
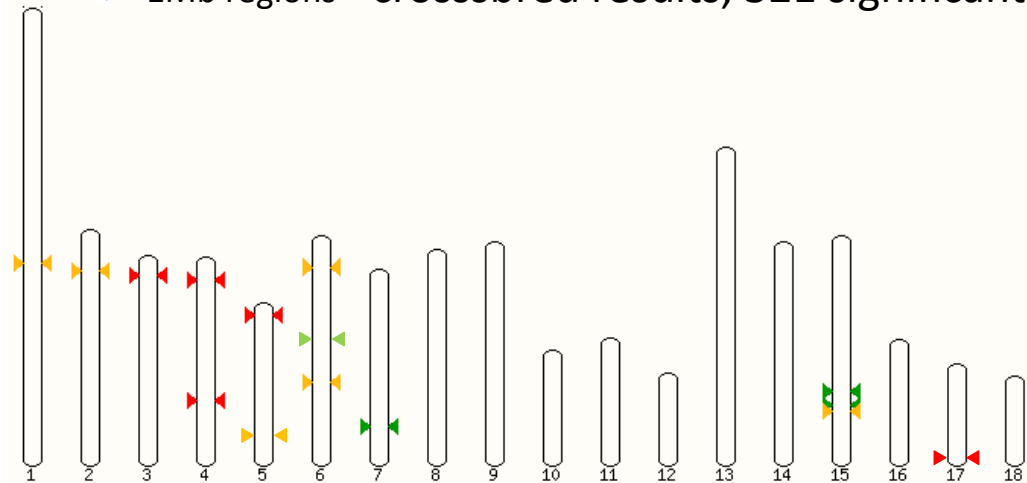
3 to 17 regions per trait



GWAS (3) common regions, trait families

▶ 1Mb regions – purebred results, 325 significant regions

◀ 1Mb regions – crossbred results, 321 significant regions



Only 15 common regions





GWAS - summary

1. Similar number of regions detected in purebreds and crossbreds

2. Only few common regions in the two populations
 - a. Different allelic frequencies between breeds
 - b. Different linkage disequilibrium (opposite marker/QTL phases)
 - c. Different genomic background effect
 - d. Limited power

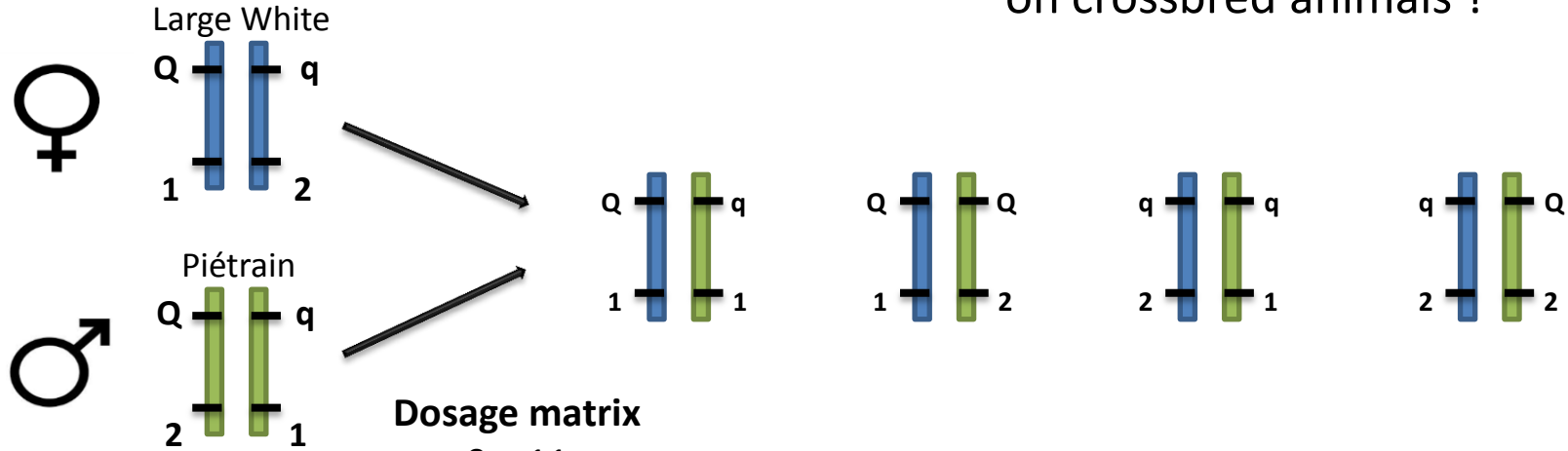


Allelic breed effects

Breed origin of the alleles  Are allelic effects different depending on the breed on crossbred animals ?

Allelic breed effects

Breed origin of the alleles \longrightarrow Are allelic effects different depending on the breed on crossbred animals ?



Dosage matrix

0 = 11

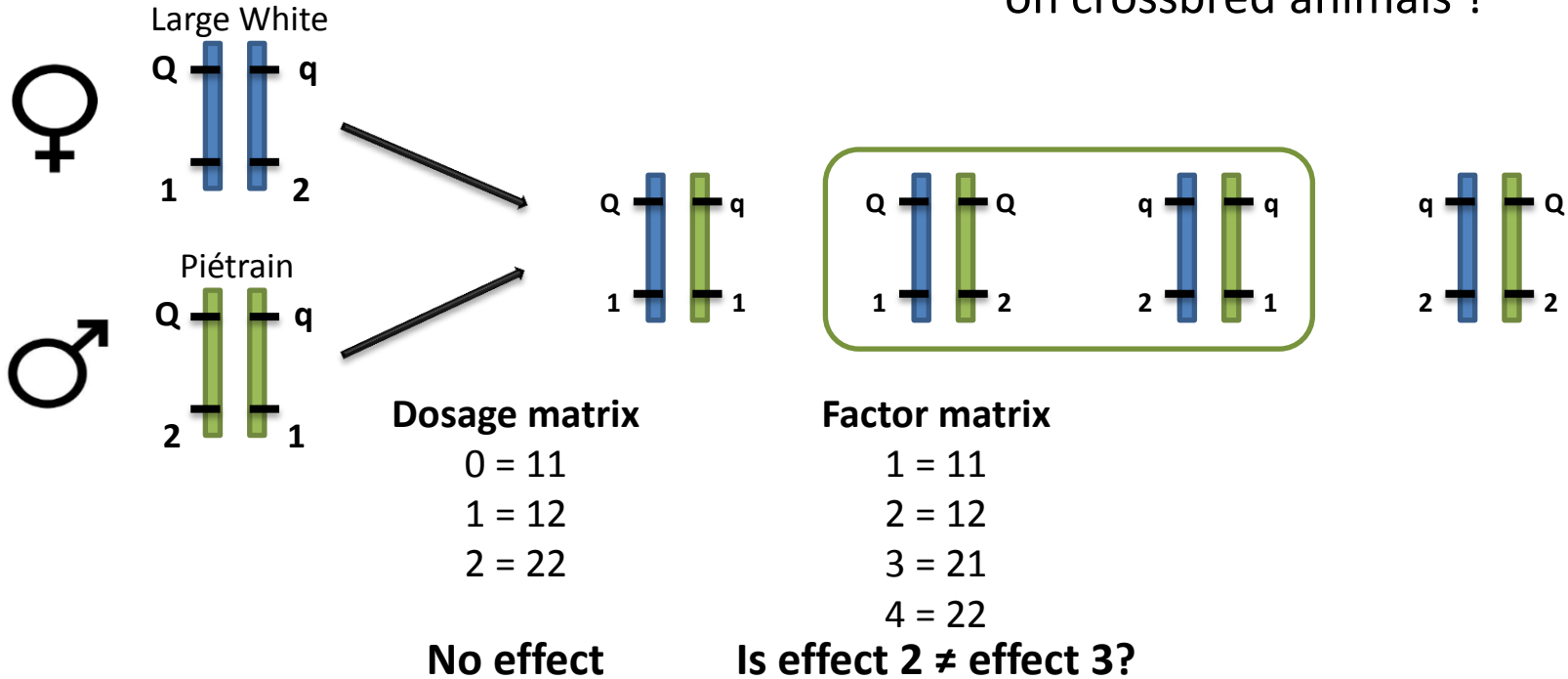
1 = 12

2 = 22

No effect

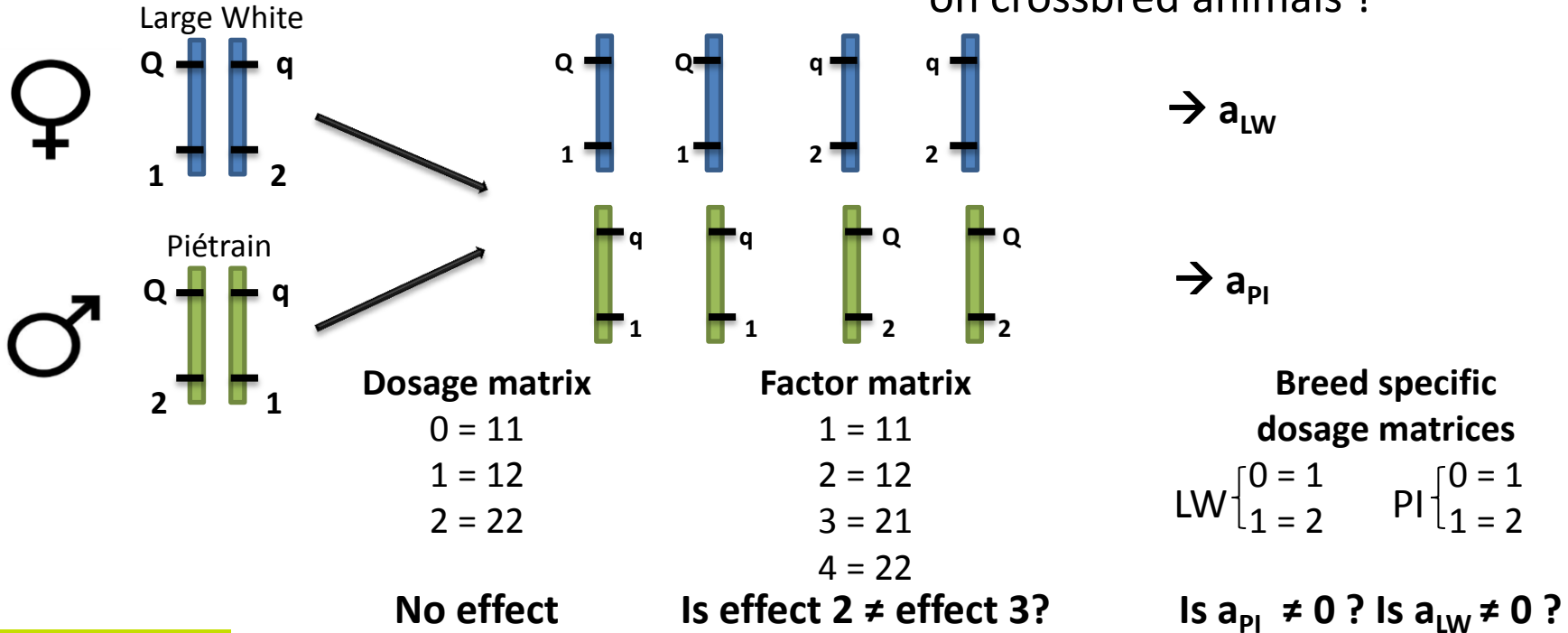
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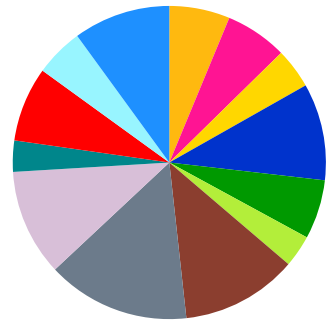
Allelic breed effects, 1Mb regions

Factor matrix

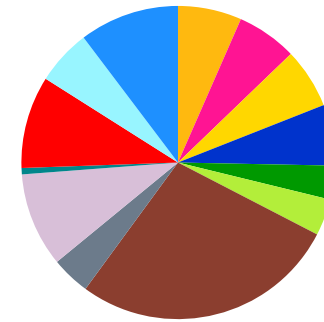
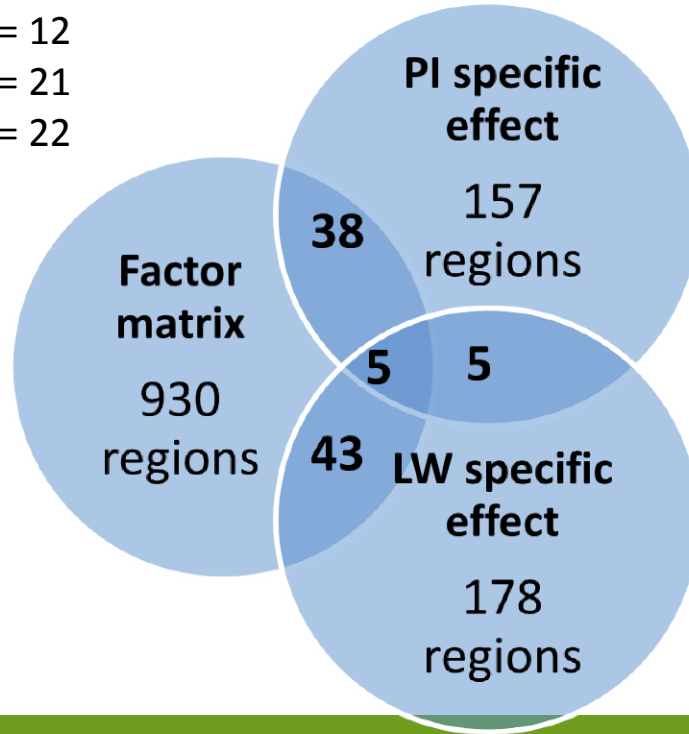
- 1 = 11
- 2 = 12
- 3 = 21
- 4 = 22

Breed specific dosage matrices

$$LW \begin{cases} 0 = 1 \\ 1 = 2 \end{cases} \quad PI \begin{cases} 0 = 1 \\ 1 = 2 \end{cases}$$



6 to 29 regions
per trait



1 to 24 regions
per trait

- Intake/Growth
- Meat color
- Fat
- Sex hormones
- Lesions
- Muscle
- Boar taint
- Bones
- pHu
- BW
- Health parameters
- Drip loss
- Lameness

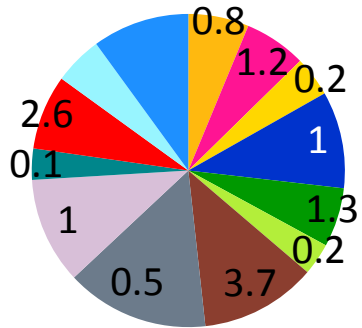
Allelic breed effects, 1Mb regions

Factor matrix

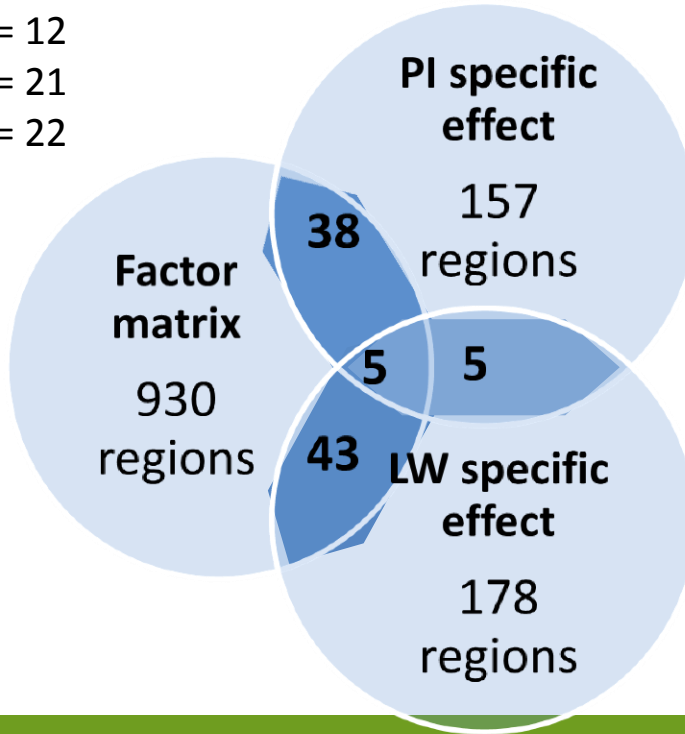
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6 to 29 regions per trait



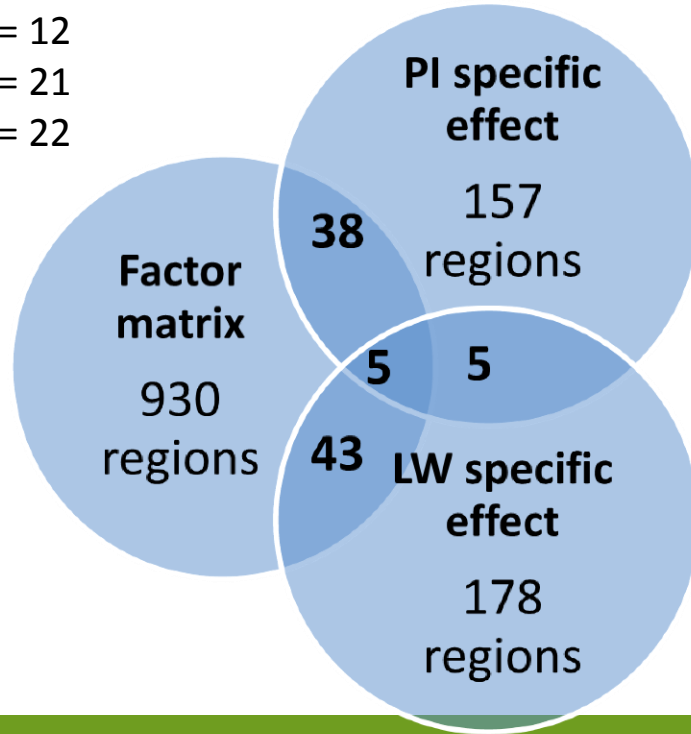
1 to 24 regions per trait

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Allelic breed effects, 1Mb regions

Factor matrix

1 = 11
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Breed specific dosage matrices

$$LW \begin{cases} 0 = 1 \\ 1 = 2 \end{cases} \quad PI \begin{cases} 0 = 1 \\ 1 = 2 \end{cases}$$

30% with different MAF
in LW and PI

$$(\text{MAF in LW}) - (\text{MAF in PI}) > 0.2$$

42% with different MAF
in LW and PI

Common regions across models

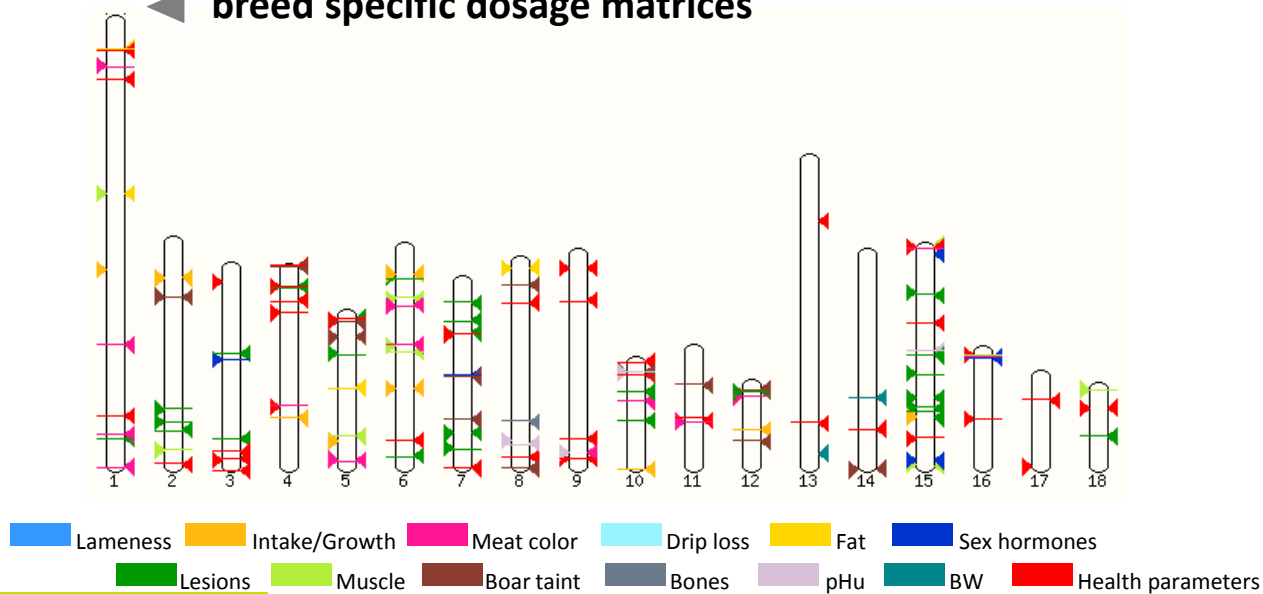
► purebreds and/or crossbreds

— factor matrix

◄ breed specific dosage matrices

Total of 2154 1Mb-regions detected with one model

291 were detected in at least two analyses



Common regions across models

► purebreds and/or crossbreds

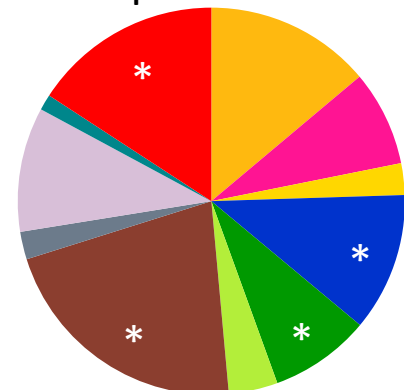
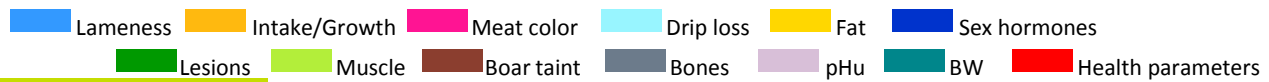
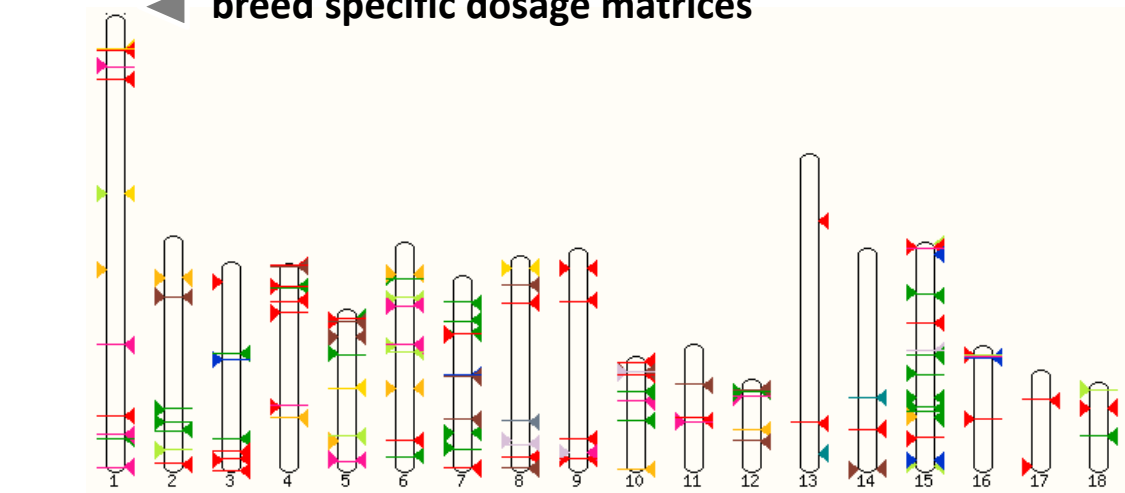
— factor matrix

◄ breed specific dosage matrices

Total of 2154 1Mb-regions detected with one model

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0 to 7 common regions per trait



* Genetic correlations different from 1 between crossbreds and purebreds



Conclusions

- Not many regions detected in common between purebreds and crossbreds: about 40% of the traits had genetic correlations between purebreds and crossbreds different from 1
- Quite a lot of breed specific effects:
 - ~1/3 might be due to different allelic frequencies between breeds
 - What about the 2/3 left?
 - Show unequal distribution across trait families
 - Could relate to genetic correlations magnitudes between purebreds and crossbreds



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