A genetic pathway to reduce the impact of eosinophilic myositis in French cattle breeds

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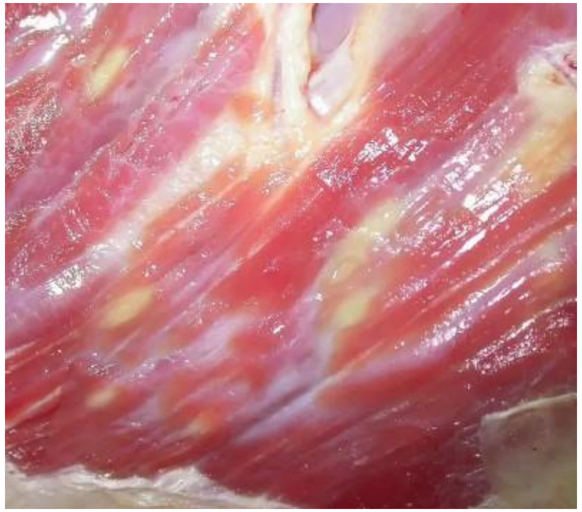
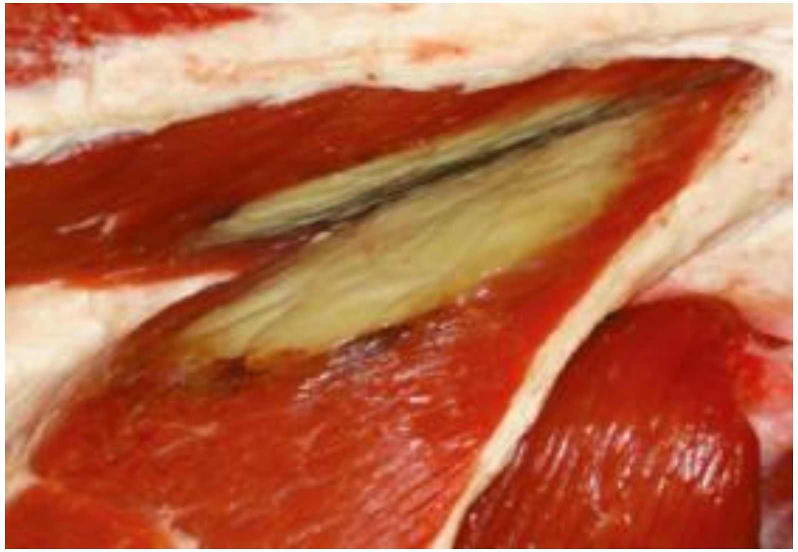
Bovine Eosinophilic Myositis (BEM): What's that?

- **BEM** is an **eosinophilic inflammation with myofiber degeneration / necrosis**
- **No clinical symptom** ⇨ only observed after slaughter
- BEM is characterized by **multifocal** or **diffuse** grey to green discolorations in striated muscles.
- Severity of affection is variable :
  Most active muscles are more affected (tongue, masseter, myocard, diaphragm…)
- **Large economic cost** : total **carcass condemnation** most of the time; BEM frequently occurs among the highest-quality carcasses



Source : Nicol

Multifocal lesions of BEM



Source : Cappelier et Honoré

Diffuse lesions of BEM

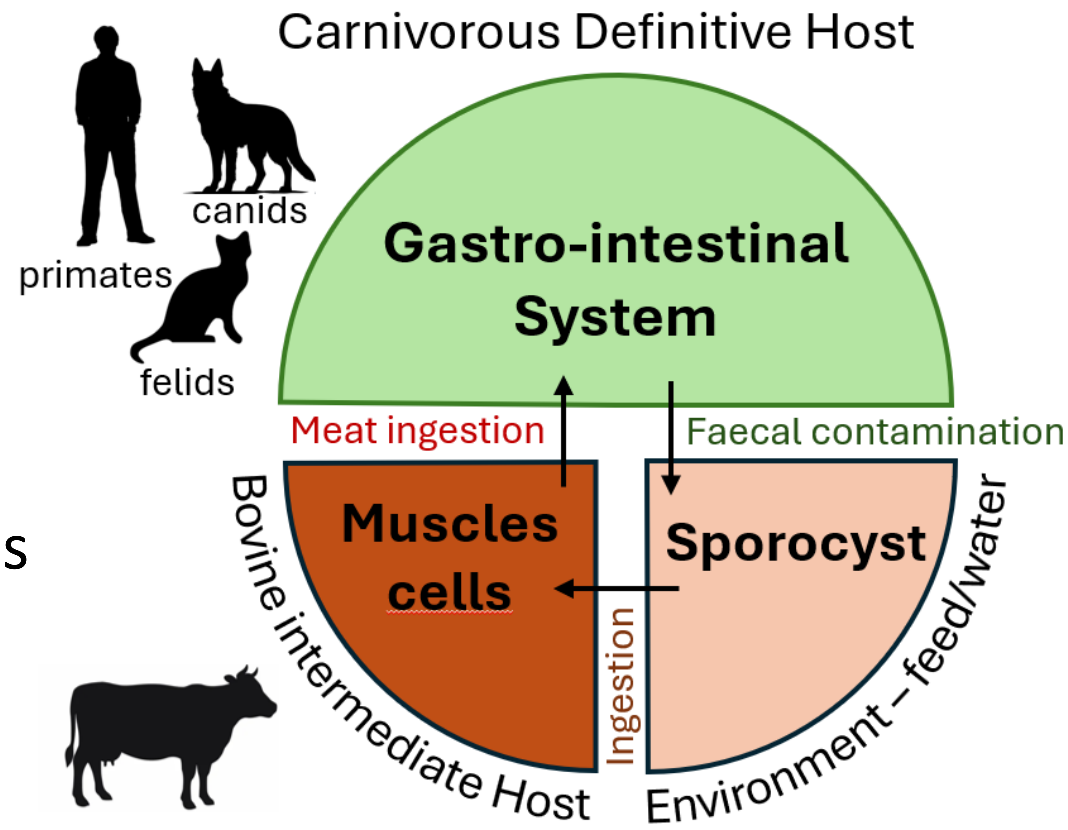
BEM: Link with bovine *Sarcocystis* species?

Although the etiology is still uncertain, ***Sarcocystis* *species* may play a role in BEM**, because:

1. They are often found in the center of the lesions
2. Antigens of *Sarcocystis* species can induce an immune response with predominantly eosinophilic granulocytes

Sarcocystis sp. are intracellular protozoan parasites with a 2 hosts life cycle

The **prevalence of *Sarcocystis*** in bovine muscle **is close to 100%** in most regions of the world **while** the **prevalence of BEM is very low** (between 0.01% to 0.1% in litterature)

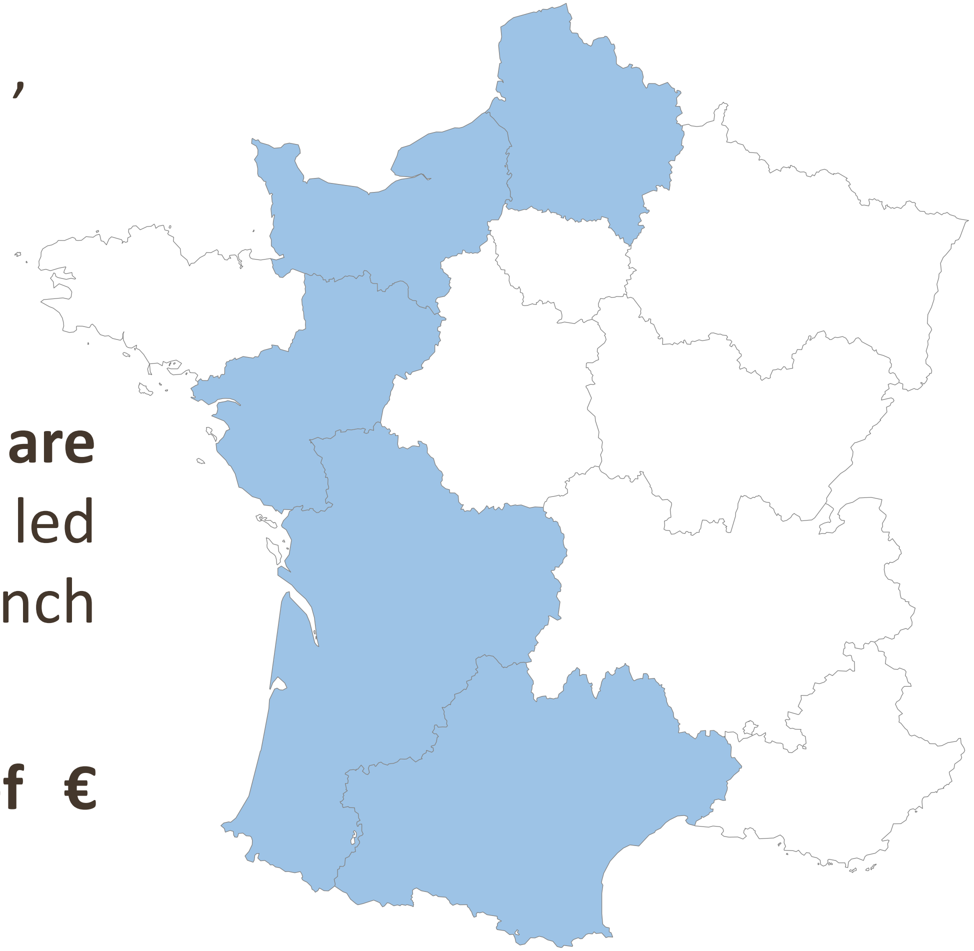


The situation in France

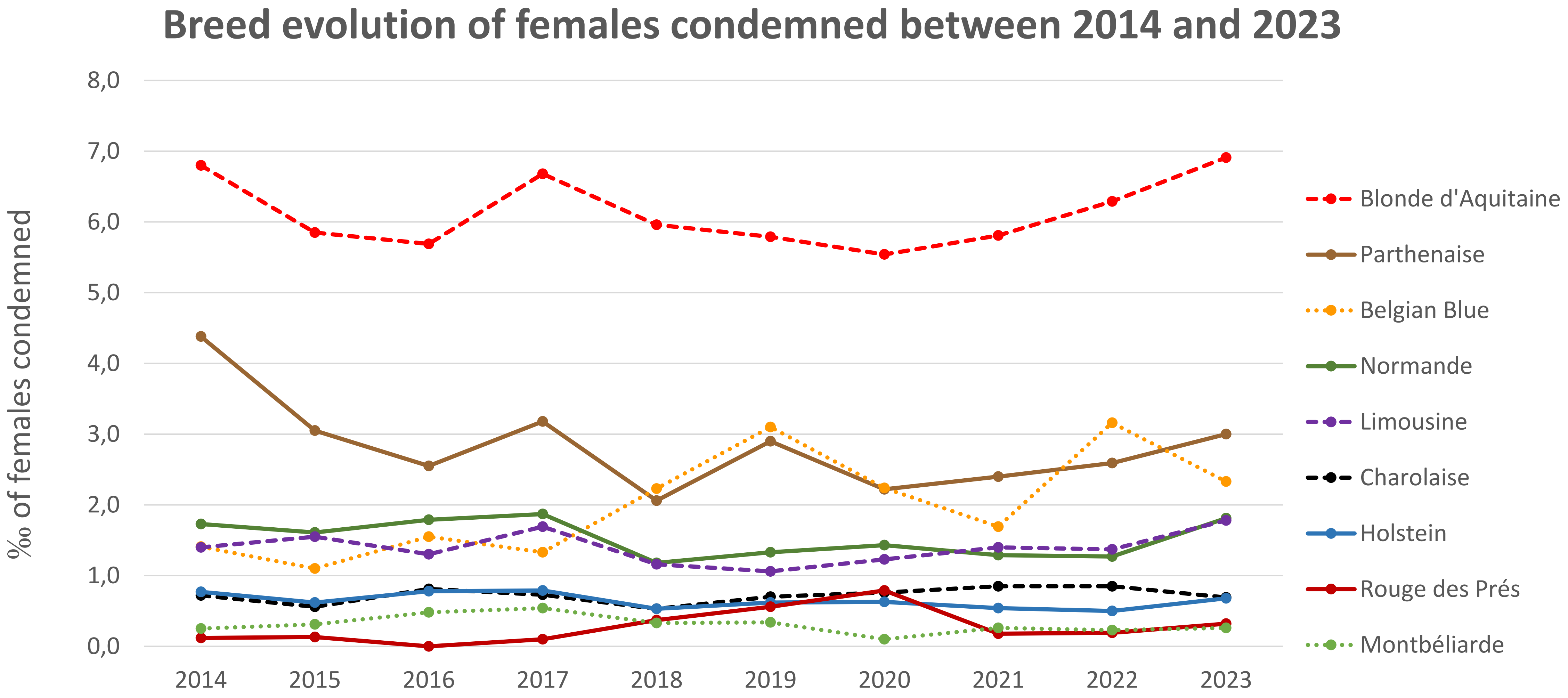
Through the **GMyosEo2 project**, funded by APIS-GENE Investir Innover Valoriser, the slaughterhouses of 5 french regions collected information on cattle with BEM affected carcasses

For French breeders, **condemned animals are compensated** through a Regional Action Fund (FAR), led by regional commitees of interbev INTERPROFESSION BÉTAIL & VIANDE (the French meat and cattle industry)

Annual cost is estimated around **4-5 millions of €** (≈ 2000 animals condemned per year)



A large breed predisposition



The data available

Breed	#cattle condemned	#females condemned (2-10 years)	#females slaughtered (2-10 years)	Prevalence of condemnation (‰)
Aubrac	29	17	63 769	0,27
Montbéliarde	126	114	374 724	0,30
Rouge des Prés	49	41	134 290	0,31
Brown Swiss	12	12	24 688	0,49
Holstein	3293	3056	4 593 813	0,67
Salers	110	65	83 361	0,78
Charolaise	1502	1291	1 631 457	0,79
Crossbred	1518	1237	1 181 510	1,05
Limousine	1673	1408	940 704	1,50
Normande	1940	1619	976 691	1,66
Belgian Blue	159	142	77 631	1,83
Parthenaise	453	415	143 697	2,89
Blonde d’Aquit.	**7135**	**6341**	**999 209**	**6,35**

Built a network of high-prevalence herds to create a specific reference population in Blonde d’Aquitaine

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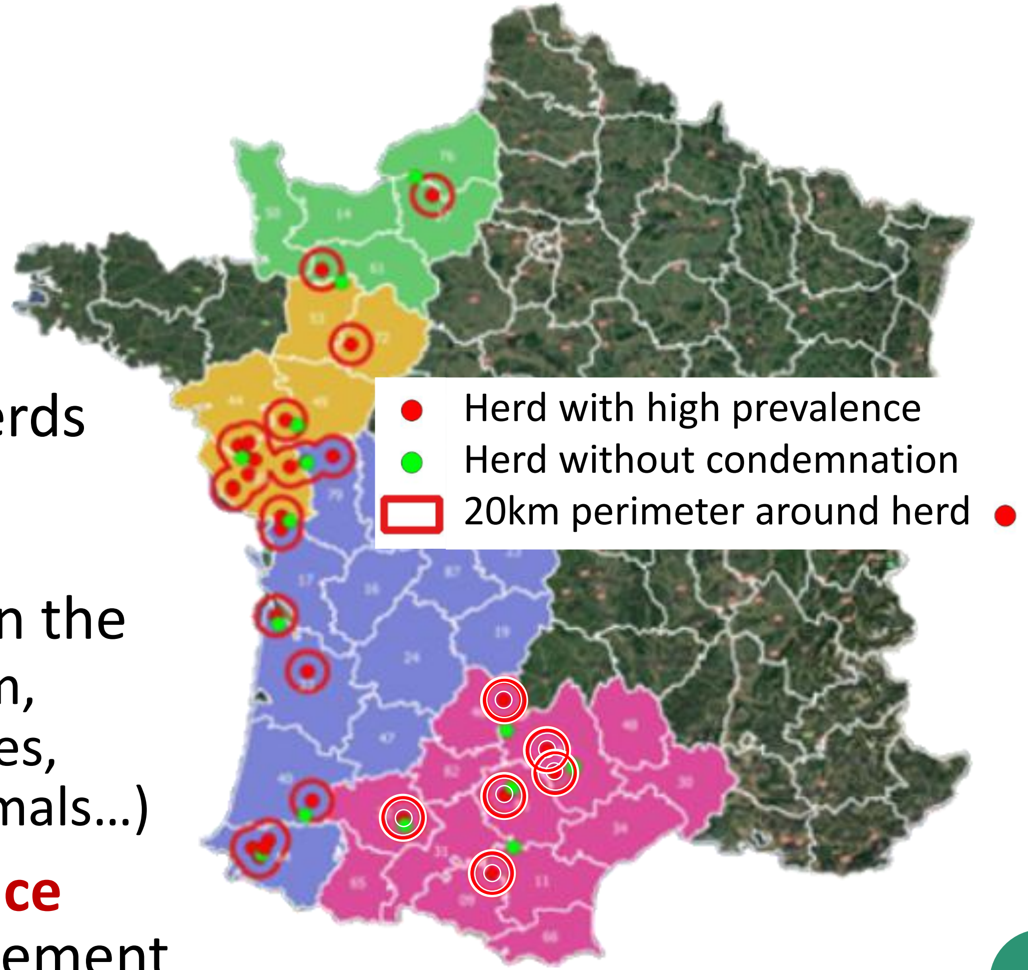
29 herds selected for **high-prevalence of BEM**

15 herds without case 20km around high prevalence herds

- A comprehensive survey (280 questions) on the herd environment was conducted to assess their impact on the development of BEM (on general description of the farm, feeding, watering, fattening, grazing, reproductive practices, sanitary elements, presence of dogs, cats and wildlife animals…)
- Shows only a few differences between **high-prevalence herds** and **no case herds**, just some in grazing management



Built a network of high-prevalence farms to create a specific reference population in Blonde d'Aquitaine

Crédit photo : Auriva Elevage

In high-prevalence of BEM herds

- Cartilage sampling before slaughtering on **2395 females**
- Only **37 condemnation due to BEM** (1,5%)

+ ≈ **400 samples of muscle tissue** were collected **from condemned carcasses** (various breeds) at slaughterhouses

Genotyping :

269 condemned females in Blonde d'Aquitaine

+ 1300 related or contemporary females

Sequencing (based on **trios** : father + 1 BEM daughter + 1 no-BEM one)

- 9 bulls
- **14 BEM females**
- 13 control half sisters

Study blood biomarkers to predict BEM

BEM is not detectable in vivo ⇨ study some possible **blood biomarkers to predict BEM**

4 herds among the **high-prevalence of BEM** participated

- **Protocol** = 3 blood samples at the beginning of fattening / middle / before slaughtering)
- 140 females – 262 blood analysis – 4 BEM female (2.9%)
- **4 blood biomarkers**:
  - Eosinophilic polymorphonuclear leukocytes (EPL)
  - Creatine Kinase (CK)
  - Aspartate Aminotransferase AST
  - Lactate Dehydrogenase (LDH)

The analysis of the 4 studied blood biomarkers **did not reveal any predictive factors for BEM lesions**.

It could be interesting to study other candidate biomarkers.

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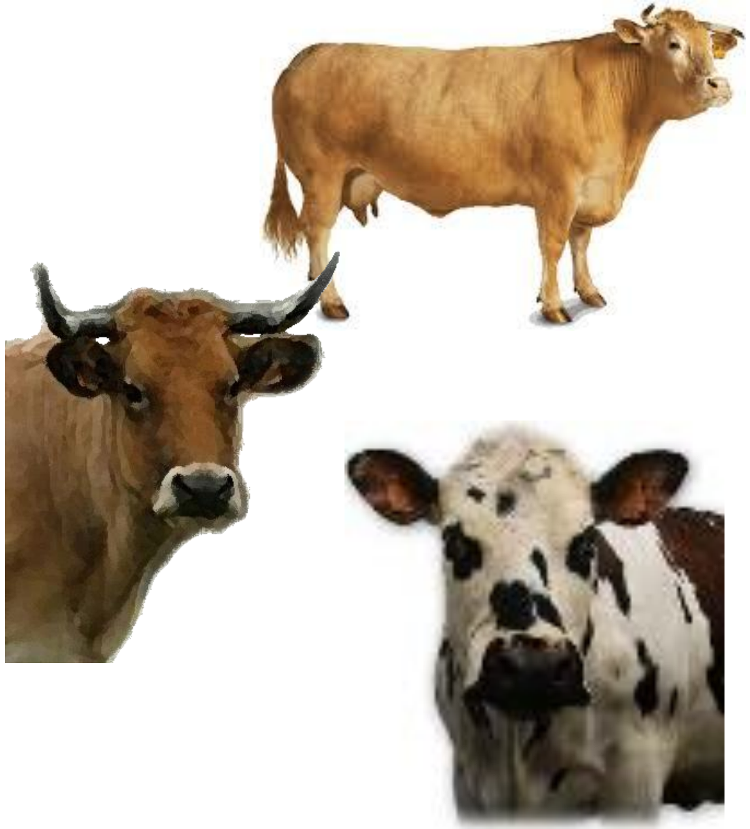
A genetic pathway to select cattle resistant to BEM

Genetic parameters (heritability) estimated for **Blonde d’Aquitaine**, **Parthenaise** and **Normande** breeds

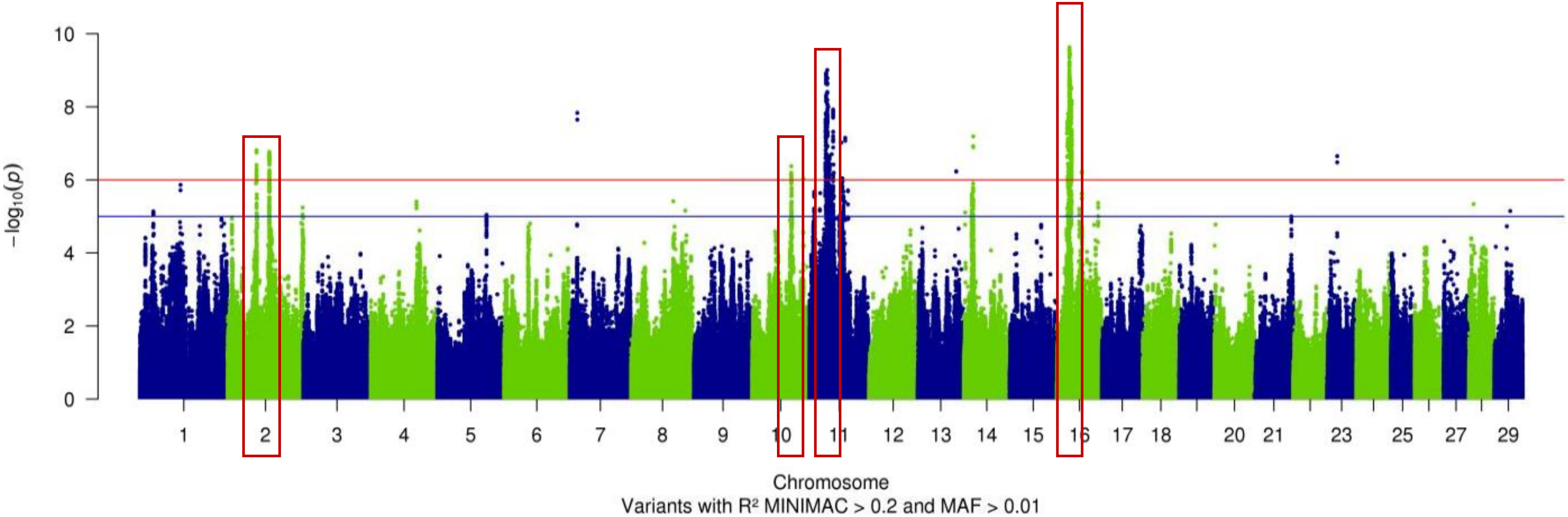


Data selection: **focus on female from herds with at least one female condemned**.

Blonde d’Aquitaine	h^2=4.4%
Parthenaise	h^2=2.3%
Normande	h^2=3.1%

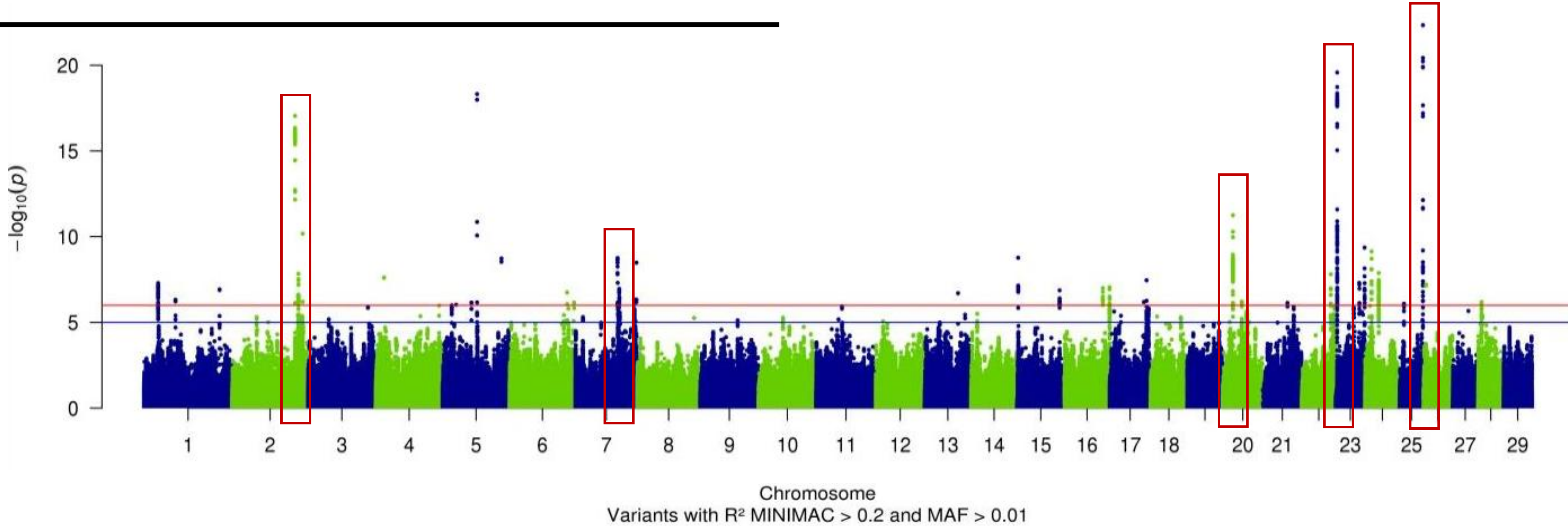
A **Single Step Genomic evaluation** was developped in **Blonde d’Aquitaine** and **Normande** breeds

Whole-genome sequence GWAS for BEM susceptibility/ resistance in Normande breed



Explore candidate genes on chromosomes 2, 10, 11 and 16

Whole-genome sequence GWAS for BEM susceptibility/ resistance in Blonde d'Aquitaine breed



Explore candidate genes on chromosomes **2**, 7, **20**, **23** et **25**

Take home message

- A **dedicated reference population** in Blonde d’Aquitaine
- The on-going **single step evaluation** of BEM resistance
- On blood biomarkers, we need to test another panel to detect BEM *in vivo*

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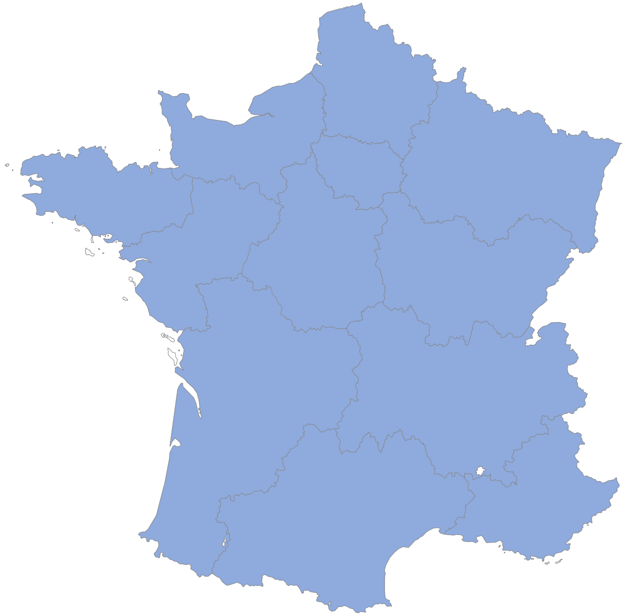
Further perspectives



- Extension of BEM condemnation data at the **national level**
- Incorporate **target SNPs into the upcoming BeadChip** and **investigate post-GWAS analysis**
- Develop a genomic management tool in Blonde d’Aquitaine with Auriva to **avoid mating with high BEM risk**

Thanks for your attention,
and to APIS-GENE for funding this GMyosEo2 project

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