Health recording systems: French experience on potential new valorizations of events recorded by farmers

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New traits in the Genomic selection era: French situation

- **Genomic evaluations in dairy cattle implemented in France in 2009**
- **Big interest in new traits :**
  - possible to implement an evaluation from a reference population of reasonable size
  - accurate GEBVs, even for animals without performances
- **Review among FGE partners : « which new trait you would like to get »?**
  - N°1 : new health traits

France Génétique Elevage

- **How to get phenotypes?**
  - ✓ Claw traits → records from trimmers
  - ✓ MIR spectra
  - ✓ **Health events recorded by breeders**
  - ✓ …

Recording health in France (ruminants)

- **Recording veterinary treatments has been mandatory since 2000**
  - Many forms (paper, softwares developped by private or collective initiatives…)
  - Breeders are encouraged to record health events (disease, observation of a symptom)

Potential use of health events for new valorizations (management, genomics)?

The health information systems of this study:

- **8 systems**
  - 7 developped by collective organisations of breeders (by MRO & herd support organisations and/or sanitary support associations)
    - ✓ Located in different regions
  - 1 developped by vets

Study: 2 parts

- **Presentation of general charasteristics (questionnaire)**
  - Owner, data model, recorded data, present enhancement…
- **Quantitative study (7 tools)**
  - Volume of data?
  - Quality of data?
    - ✓ Are events harmonized (between herds, between tools)?
    - ✓ Are records exhaustive within herd?
  - Confidentiality of data
    - ✓ No agreement from the breeders
    - ✓ → re-numbering each cow ID, each herd ID within tool
    - ✓ Only sire of animals with events were not re-numbered (→ connections between tools)

Volume of data

- **7 tools, data from 2007 to 2012:**
  - 18 300 herds, 7 Mo events
  - 1.8 Mo animals, 76% dairy
  - Treatments: curative or preventive
    - from 50 to 516 different types of events according to the tool
      - ✓Total of 7 tools = 898 different types!
      - → Needs for clusturing !

Classification of health events and animals

20 classes of Health events:

- ✓ Using ICAR guidelines
- ✓ 16 curative, 4 preventive
- ✓ Some ICAR classes were splitted into several classes

9 classes of Animals

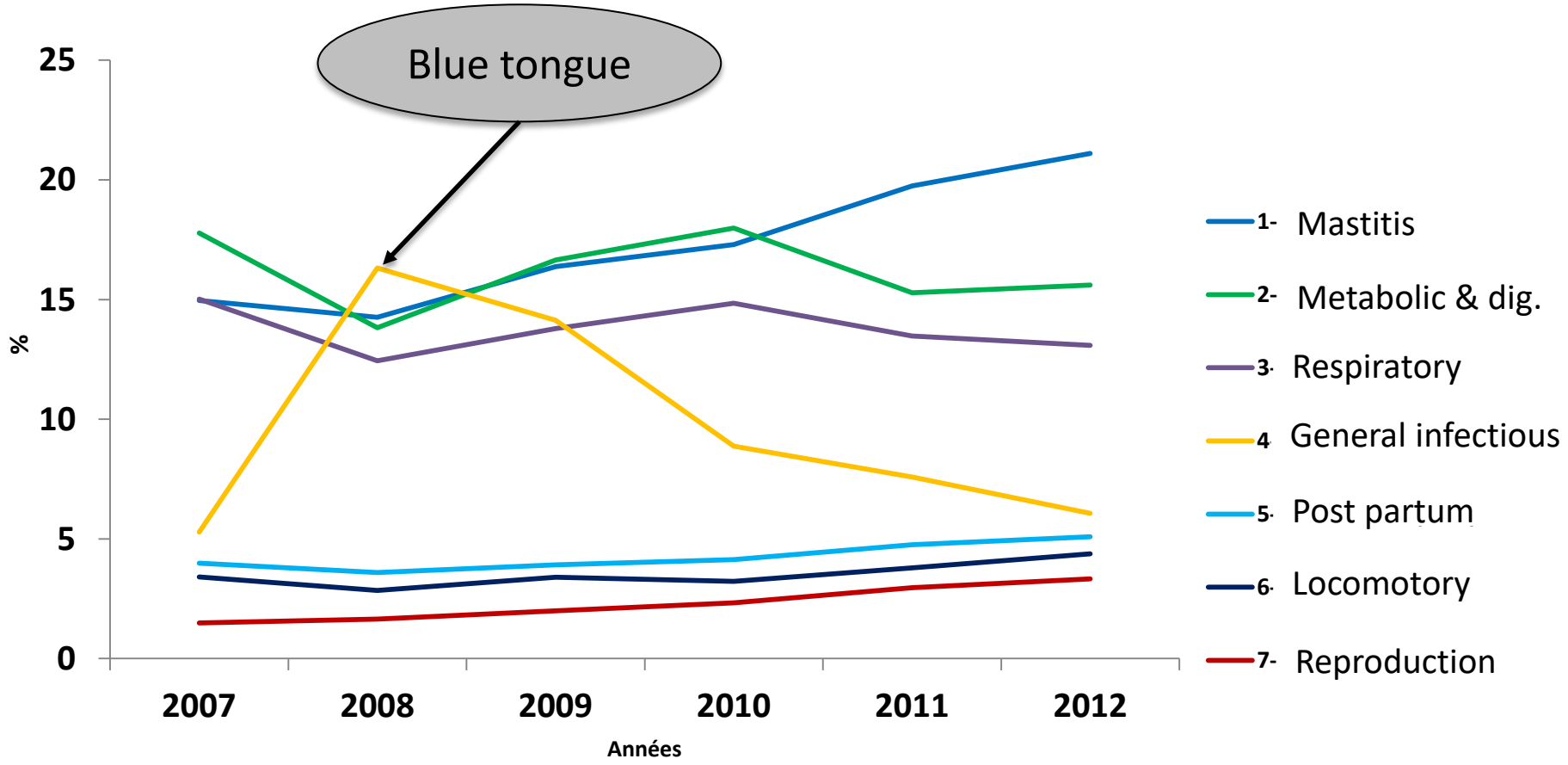
4 for dairy breeds

- ✓ Cows, heifers, calves less than 2 months old, bulls

5 for beef breeds

- ✓ Cows, heifers, calves, bulls + young bulls (<9 months)

Yearly proportion of events of each group of disease among all events (whole data, curative treatments)

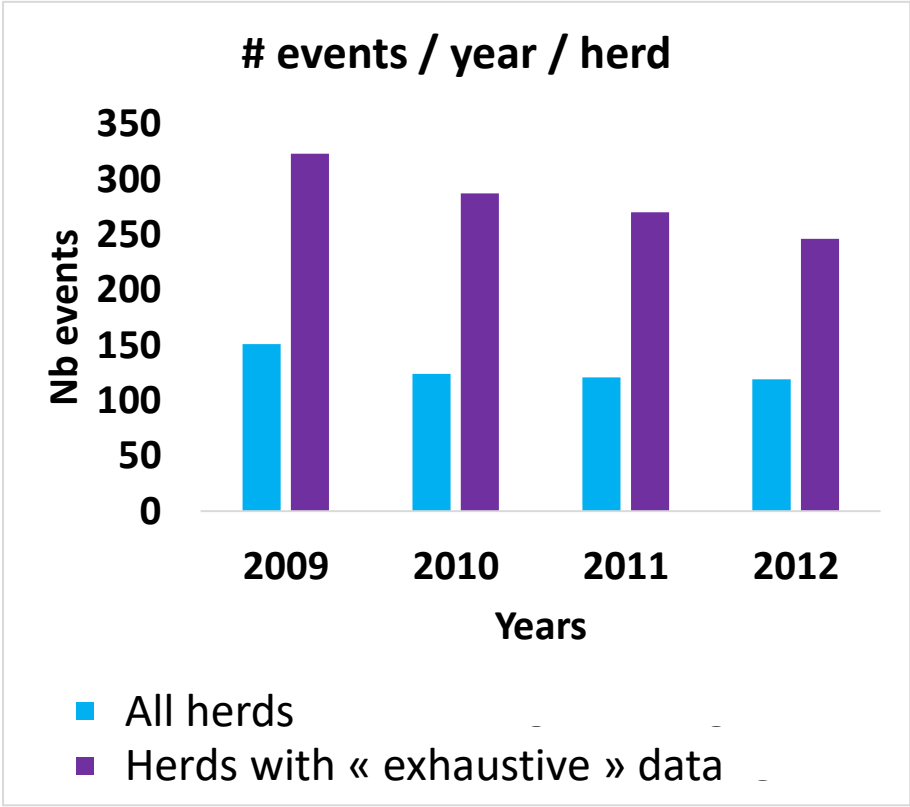


Selection of herds with « exhaustive data »

Empirical criteria:

- diversity & regularity of records: at least 3 ≠ categories each year between 2009 and 2012

- 15.6 % of the total nb herds
- 56.3 % of total nb events
- 80.5 % are dairy cattle

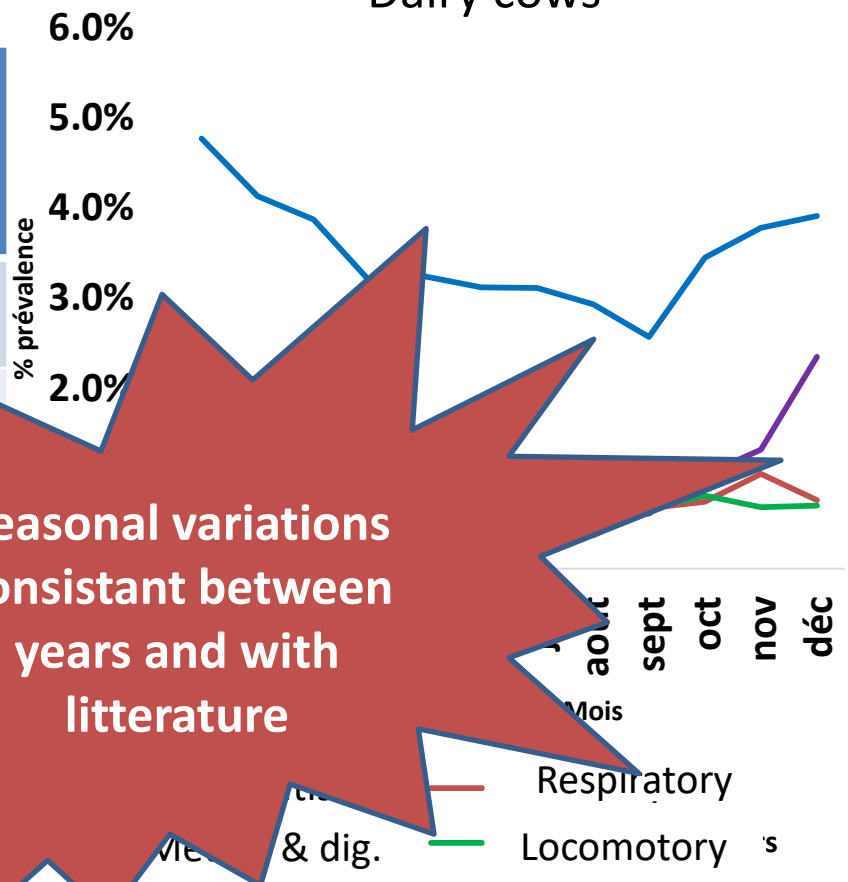


Monthly and yearly prevalence of main disorders

Yearly prevalence (in %) of main disorders according to the type of animals
Dairy animals only

Type of disorder / Type of animals	Cows 143278	Heifers 119228	Calf. 21428
Mastitis	29.1		
Metabolic & digestive	9.1	8.0	
Post partum	9.1		
Locomotory disorders	7.1	0.6	
Infectious	4.3		
Respiratory	5.4	8.6	
Reproduction disorders	4.5	1.2	

Monthly Prevalence in 2012 (en %)
Dairy cows



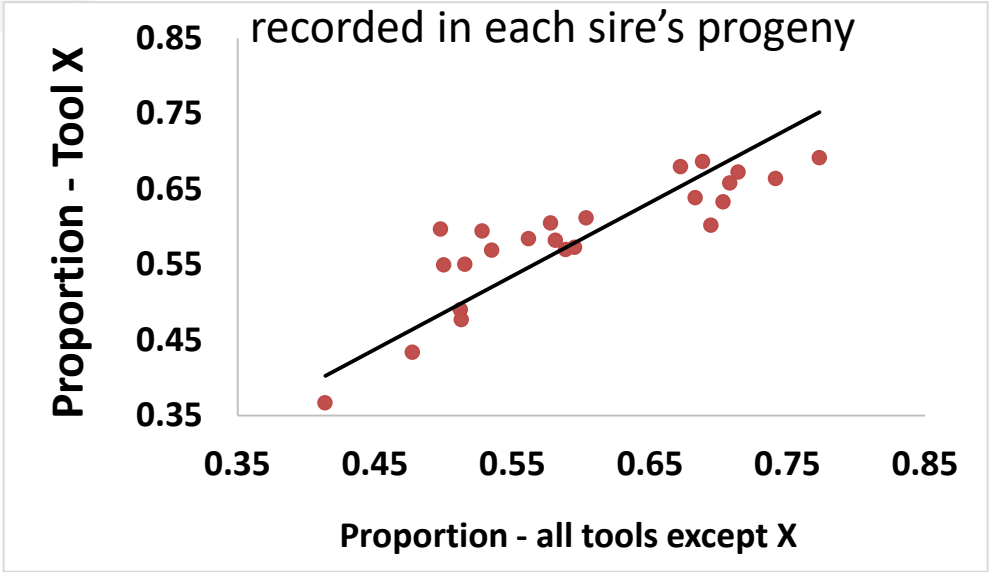
Seasonal variations consistant between years and with litterature

Analysis of sire progeny

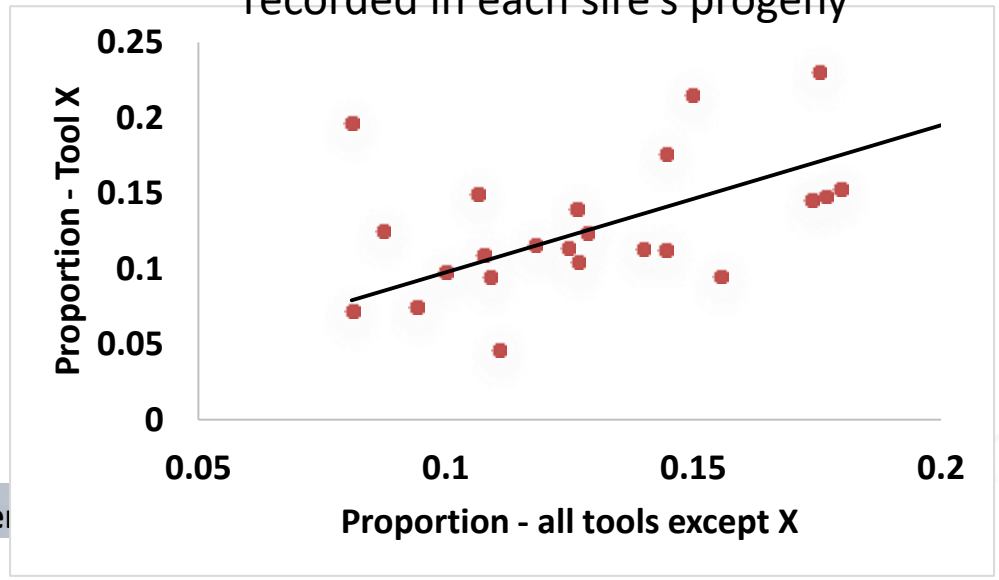
- **Re-numbering Ids of cows:**
  - Only sires of cows with disorders present in the files
- **→Prevalence replaced by proportion of a disorders of each category within each sire**
- **Selection of bulls:**
  - ≥ 500 daughters (cows)
  - ≥ 2 tools
- **Compare proportion of a given disorder within 1 tool to the proportion within the 6 others together**

Result – example with one tool (X)

Proportion of mastitis within all disorders recorded in each sire's progeny



Proportion of locomotory disorders within all disorders recorded in each sire's progeny



Conclusion

- **Large volume of recorded events**
- **Selecting herds with « exhaustive » data is possible**
- **Grouping disorders into categories → using different tools together is possible**
  - Enhancement is limited to reports within herd
  - No national reference / breed, year etc…
    - → **Interest both for genomics and for herd management**
- **Health data = sensitive**
  - agreement of the breeders is necessary

Thank you for your attention!