New phenotypes for new breeding goals in cattle

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Introduction (1)

Cattle selection has been long oriented towards production, in a non sustainable way

Cattle have to face new challenges for sustainable production with its three pillars, economic, societal and environmental.

Breeding objectives should be adapted to efficiently account for all traits involved in sustainability

Introduction (2)

A critical situation in dairy cattle and in some beef cattle :

After a long period of selection on production, most functional traits have been deteriorated, sometimes up to a critical point, and need to be restored.

This is particularly the case for fertility, mastitis resistance, longevity, metabolic diseases

e.g. : -1% conception rate (CR) per year in Holstein

Most of these traits have a large genetic variability

(σ_g(CR)=5%, CV_g > 10% as for production)

… but a low heritability (h^2(CR) < 0.02) and are difficult to select.

New selection methods

Emergence of **Genomic Selection** (GS)

In GS, animals are evaluated from their DNA information, with markers covering the genome

GS is already applied in dairy cattle and will be extended to other situations in the near future

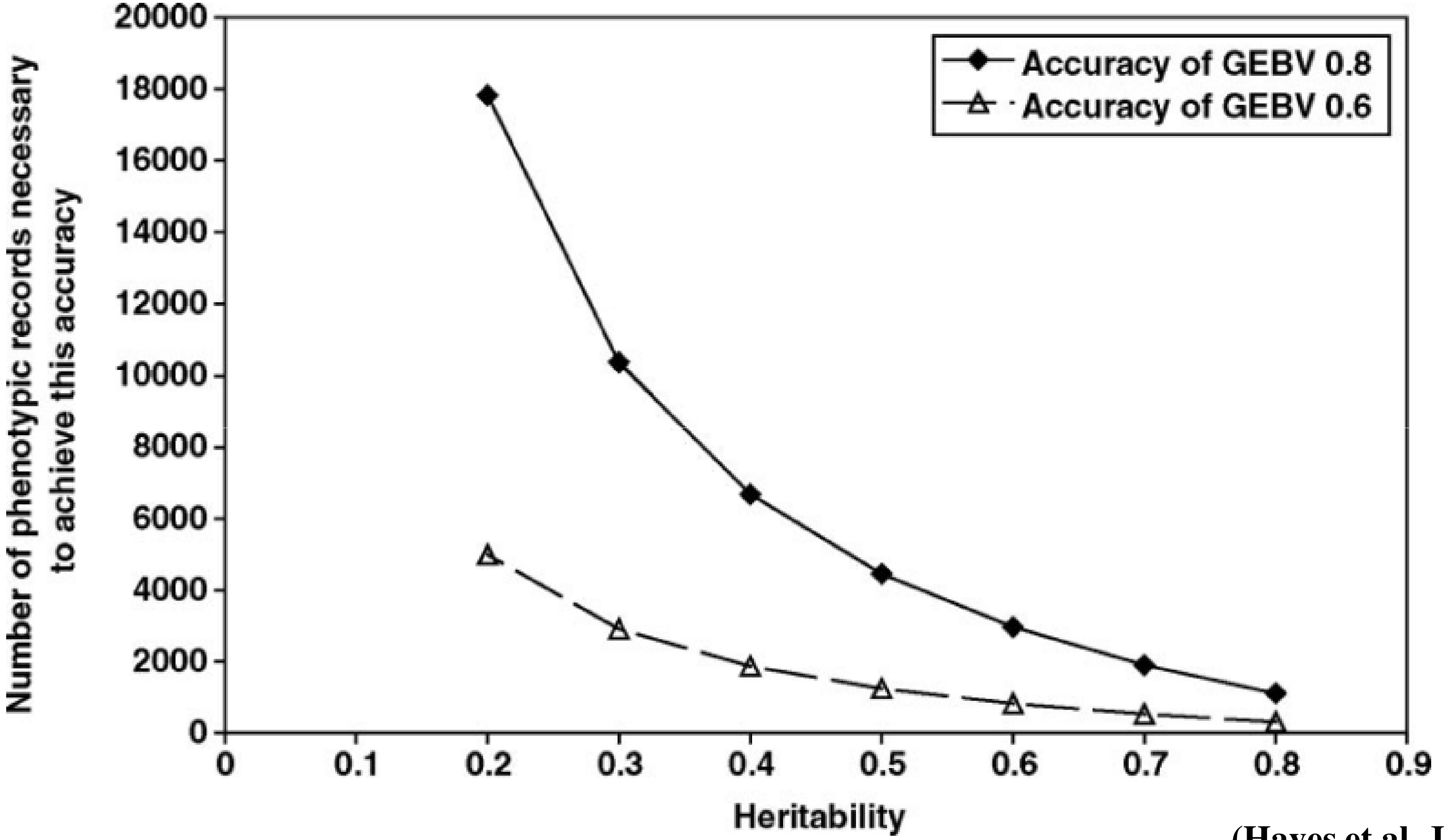
It is a unique opportunity to :

- have a more balanced genetic trend
- select for new traits considered as unachievable until recently

Properties of Genomic Selection

- Disconnection between performance recording (in a reference population) and selection (of candidates without performance) => Flexibility
- Genetic trend up to doubled ! => Opportunities for a more diversified objective
- Accuracy is the same for males and females
- For some traits recorded on a high scale, the accuracy is little dependent on heritability

Properties of Genomic Selection



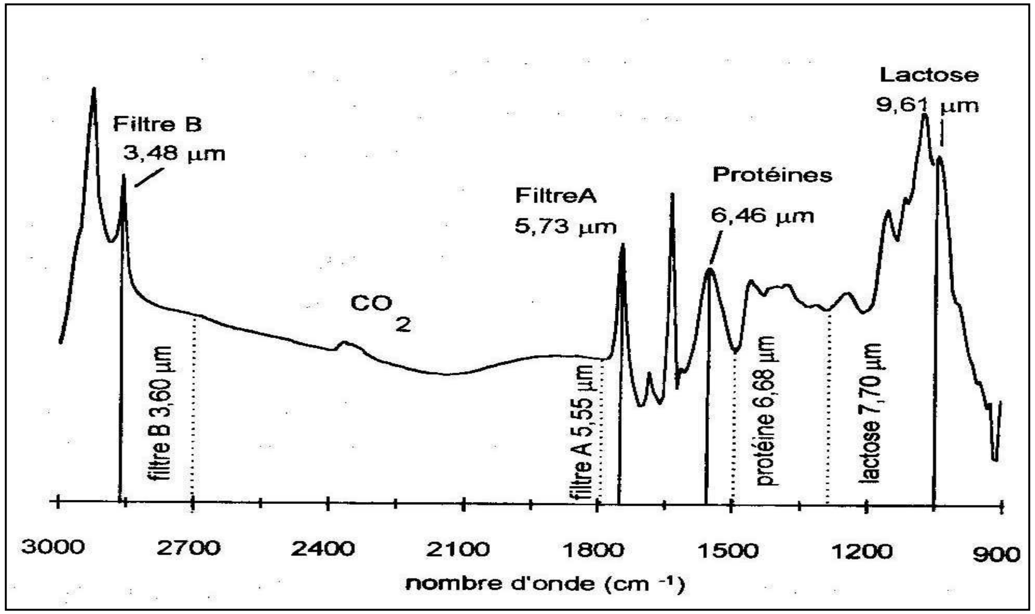
(Hayes et al, JDS, 2009)

Selection Objective

- It is time to revisit our selection objective
- What are “new” traits ?
  - already selected traits, with too small weights or little selection efficiency, such as fertility => not new but rediscovered !
  - already selected traits, with new recording systems, e.g. heat detection => not new but better characterized
  - not yet selected traits, with traditional but improved recording systems, e.g. metabolic diseases => previously neglected information
  - really new traits, with new recording systems
- Of course, new traits could be used in selection and in management system, focus will be put on selection in this talk

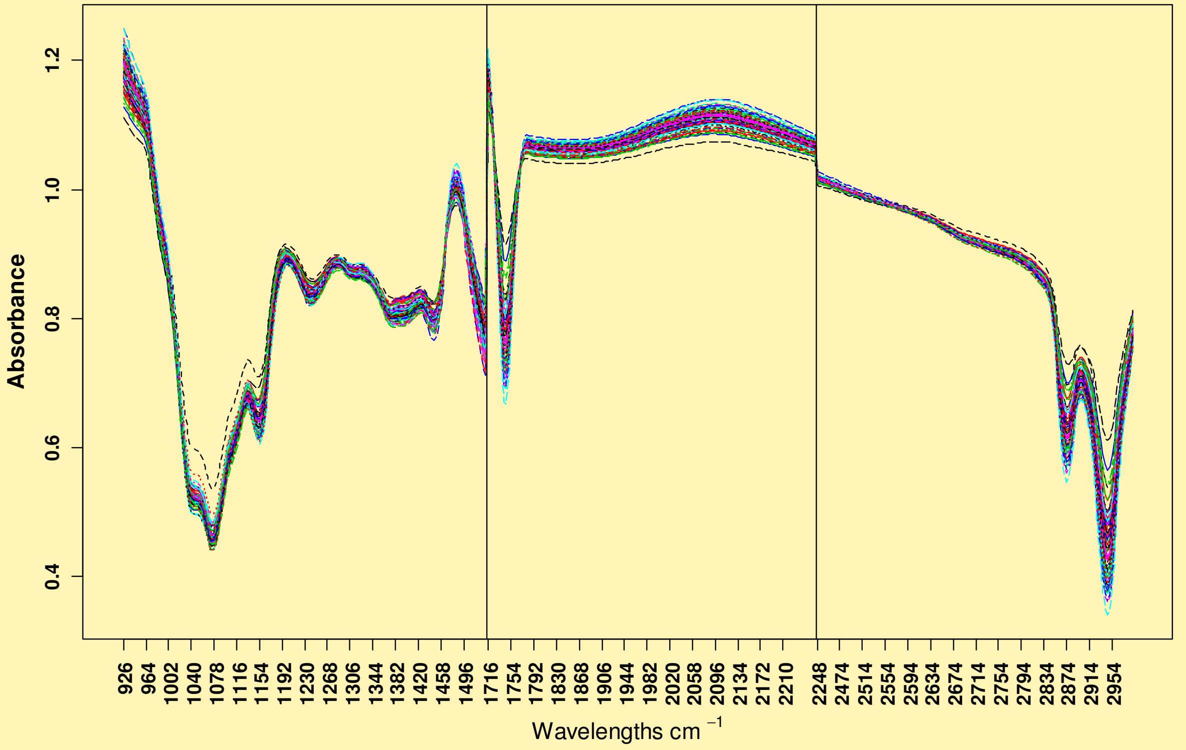
Milk composition

- Traditionally limited to fat and protein
- New methods based on Mid Infra Red (MIR) spectrometry



Milk composition

Variations in spectra in relationship with variations in milk composition


Spectrum from 75 cow milk samples (UE INRA Mirecourt + Domaine du Pin)
MilkoScan FT6000 (Foss Electric, Hillerod, Denmark)
LILANO (Milk recording laboratory)

Milk composition

- Equations to predict fatty acids and some proteins
- Initially developed by Gengler et al (Gembloux)
- Needs calibration samples (few 100s), with both spectra and reference records
- Accuracy depends on sample size, quality of reference data, statistical methods

Crossvalidation results in cow milk

	R^2
C6:0	0,95
C8:0	0,94
C14:0	0,91
C16:0	0,92
C18:1	0,93
Saturated	0,99
Monounsaturated	0,95
Polyunsaturated	0,80

From Ferrand et al, submitted

See presentation
of F Faucon et al, this meeting
for more details

Milk composition

- Easy to generalize in milk recording at the national level: just save the MIR data produced in the milk analysis laboratories !
- High throughput data : about 1,000 (x,y) points per sample to be stored in data bases
- But as soon as an equation is available or updated for a new component, predictions could be applied on an historical basis !

(assuming machine-dependent calibration is solved)

Milk composition

- This will offer new possibilities to select for individual components
- However, everything is not possible :
  - too many traits
  - saturated FA are highly correlated
  - and negatively correlated with unsaturated FA
  - unsaturated FA have limited h^2 and limited genetic variability

Milk composition

- Other indicators derived from milk :
- Fatty acids as indicators of body fat mobilization
- Other parameters useful to infer the reproductive or health status

Health

- Use of the information collected in the sanitary notebook of each herd
- Up to now **neglected and wasted** information !
- Readily available if encoded and standardized
- Mastitis, milk fever, ketosis, metritis, etc…
- Data from hoof trimming (second reason of culling)
- Some infectious diseases with relatively high prevalence and limited prophylaxy efficiency (e.g. paratuberculosis)

Carcass traits

- ➢ Little use of carcass and meat information
- ➢ Although a lot of information exists in the beef industry branch
- ➢ The main difficulty is often political : it requires an agreement between breeding and beef industries

e.g. after >10 years of negotiation, an agreement has been signed in France for slaughterhouse data use in genetic evaluation

Dehorning

- Dehorning is a painful practice
- An alternative genetic solution exists
- “pooled” gene = hornless gene, dominant, without any deleterious effect on the animals
- Use of pooled animals within breed or introgression (e.g. from Angus)
- In breeds without known pooled animals, a careful screening of pooled animals should be organized

Genetic defects

- Most cattle breeds are small genetic populations

  (e.g. Ne < 100 worldwide in Holstein)
- Inbreeding could not be avoided

  (+1% per generation in many breeds)
- Recessive defects are present in all populations
- Usually at low frequency, but potentially increasing by founder effect, when a carrier is widely spread
- Defects appear only in homozygous animals and should be detected early, to eradicate them through a genetic test
- **Specific observatories should be implemented**

Precision farming

- Very fast development ! -
- (a) Recording instrument (physical, chemical, optical…) on, in or close to the animal – (b) Data recovery – (c) Interpretation software and diagnostics
- During milking : milking speed, temperature, conductivity, composition of milk, biochemical markers…
- Podometers : heat detection, calving, lameness…
- Repeated weighting, for body weight change/energy balance
- Rumination sensor, for acidosis

=> health, reproduction, behaviour

Ecological footprints

- Increasing interest mainly since 2006 ("Livestock Long Shadow" FAO report)
- Improvement of longevity to decrease replacement cost and the number of non productive animals
- Adaptation to low quality feeding
- New emphasis on Feed efficiency, in relationship with methane production

Ecological footprints

- Methane production : is there a genetic variability ?
- Probably Yes, in relationship with feed efficiency, but to what extent ?
- If Yes, is selection one of the ways to go ?
- Preliminary steps : how to define and measure this trait ?
  - methane production ?
  - feed efficiency ?
  - rumen flora composition ?
- If a large reference population is required for genomic selection, an international collaboration is to set up !

Conclusion

- Past selection has been too much oriented towards production traits, in a non sustainable way, and should be partly reoriented
- Cattle selection will be easier than in the past, because of genomic selection potential
- More traits should be integrated in the breeding objectives
- A large amount of information already exists and is not well used => need for a better data recovery, overall management and coordination between actors
- Many technical opportunities to have access to new phenotypes