

**26/08/2013: 2nd Symposium on SUSTAINABLE ANIMAL PRODUCTION IN THE TROPICS (SAPT2) and high constraint areas**



# Genetic evaluations for crossbred Holstein x bos indicus cattle in India

## Use of a test day model



**Patry C.<sup>1</sup>, Gokhale S.<sup>2</sup>, Ducrocq V.<sup>1</sup>,**

# Content



- **BAIF and INRA collaboration**
- **Interest of the project**
- **How to predict breeding values for milk yield?**
- **Strategies for data analyses**
- **The data**
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# The GENOSOUTH project



- A 2 years project (September 2012 – September 2014) of international coordination
- Aiming at developing collaborations on methodological and applied aspects of genomic selection in cattle
- 4 targeted countries: **India, Brazil, South Africa and Kazakhstan**, with contrasted advances regarding methods for genetic evaluations and strategies of genetic improvement

# Partnership in India

- BAIF = **B**haratiya **A**gro **I**ndustries **F**oundation
  - An NGO founded in 1967, aiming at developing and improving livestock activities in India
  - Based on a Holstein/Jersey x zebu breeding program
  - BAIF activities (Central Research station):
    - ✓ **Semen production**
    - ✓ **Insemination**
    - ✓ **Milk recording**
    - ✓ **Progeny testing program** => *Estimation of the sire breeding value*
    - ✓ **Research**
- ⇒ **A large database (pedigree and phenotypes) in Holstein crossbred cattle**

# INRA –BAIF Collaboration



- A global topic: development of genomic tools for the improvement of crossbred dairy cattle under harsh environment
- 3 sub-topics:
  - *More robust and diversified genetic analyses of BAIF field performances*
  - *Detection of large genome areas (QTL) responsible for fat quantity in milk*
  - *Determination of the breed composition among crossbreds*

# Interest of the project

*“More robust and diversified genetic analyses of BAIF field performances”*

- More confidence in the breeding value estimation, with impact on breeding schemes

*Observed performances (milk yield)*

*= sire breeding value + environmental effects + residuals*

- Considering country specific constraints:
  - ✓ Very diverse management and production systems
  - ✓ Stressful and changing environment along the lactation (temperature, hygrometry, diseases, parasites, etc...)
  - ✓ Limited number of data:
    - ✓ Few pedigree information
    - ✓ Few animals / herd (to characterize the environment)
    - ✓ Number of observations / costs for milk recording

# Interest of the project

*“More robust and diversified genetic analyses of BAIF field performances”*

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*Observed performances (milk yield)*

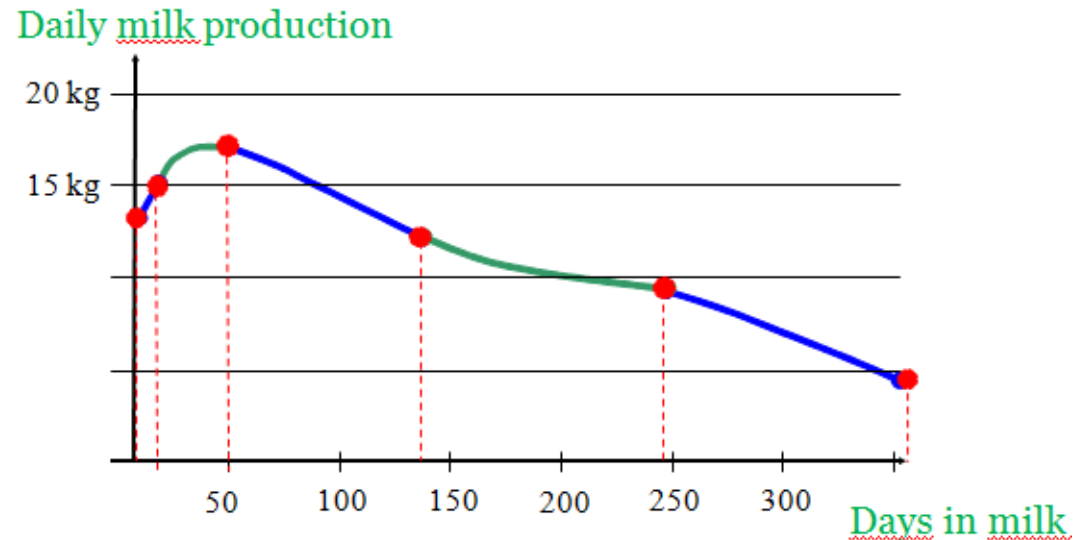
**Choose the most appropriate model for milk yield prediction and optimisation of the data recording**

- ✓ Limited number of data:
  - ✓ Few pedigree information
  - ✓ Few animals / herd (to characterize the environment)
  - ✓ Number of observations / costs for milk recording

# How to predict breeding values for milk yield?



1. Modeling the lactation curve from the discrete milk yield observations (milk recording)



2. Removing appropriately the environmental effects:  
*lactation model, multi-trait model, **test-day model***

⇒ for one lactation, each milk record is considered as a separate observation of each individual animal



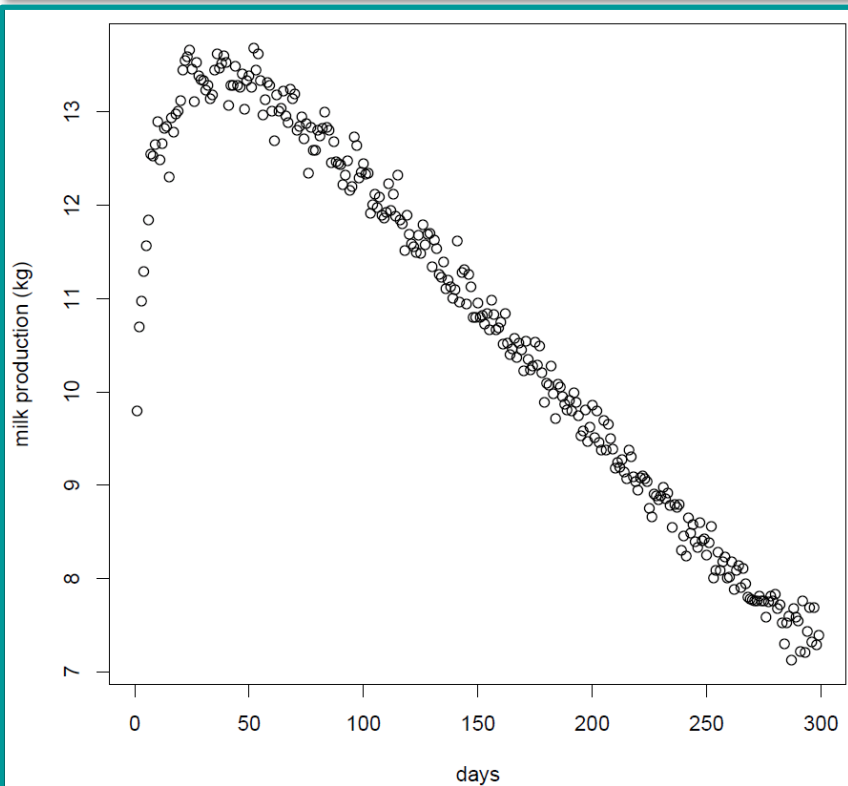
# The strategy chosen for data analyses



- For flexibility: **semi-parametric model**
  - lactation curve partitioned into 10 lactation stages, described using splines
- To account for environmental effects through the entire lactation: **test day model**
  - model accounting for repeated observation / animal (accounting for time)  
⇒ Changing  $h^2$  across the lactation length : more accurate
- To account for the lack of pedigree information: **a 2 step analysis**
  - Estimate the environmental effects (including the permanent one / lactation rank) based on all records available
  - Estimate the breeding values ONLY based on cows with pedigree information

# Data available

## Average milk production per day



Mean = 10.5 kg / day

Range: from 1 to 34 kg / day

- BAIF field data (milk recording, editing)
- **(STEP 1)** Performances for 6,675 crossbred cows
  - ✓ Recorded from 1994 to 2010
  - ✓ >120,000 observations
  - ✓ Up to the 6th lactation rank (mostly 1st or 2nd lactation)
- **(STEP 2)** Data set reduced: ~2, 000 COWS:
  - ✓ 38,000 adjusted performances
  - ✓ from cows with known sires
  - ✓ at least 5 recorded daughters

# Results and benefits



- **WOMBAT software (Karin Meyer)**
  - ⇒ Free of costs, friendly using
- **Breeding values for 193 bulls and 2404 cows**
  - ⇒ ranking the sires of interest
  - ⇒ ranking the dams to better benefit from the local genetic diversity in their crossbreeding scheme
- **Genetic parameters:  $h^2 = 0.12$  on the whole lactation**
  - ⇒ Low level explained by tiny herds, missing information
  - ⇒ Study the impact of less records / sire or less accurate records to mimick a simplified recording scheme (Duclos et al., 2008)

# Conclusions and perspectives

- India, crossbreds: limited number of data with complex factors to consider (data structure, changing environment): *Specific model & tools*
- Improvement of the genetic evaluation model, with perspective
  - for additional traits (e.g., fertility)
  - of including molecular data
- Improvement of the **recording** design:
  - ✓ AI technician
  - ✓ Smartphone: less data lost, centralized data base
  - ⇒ *More data for R&D & Evaluations for a larger number of animals: genetic trend*
- Genetic improvement is a long-term process, where recording is a key: **even if genomic selection tend to speed up breeding improvement programs, it is still a slow process**

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**THANK YOU !**



**Patry C.<sup>1</sup>, Gokhale S.<sup>2</sup>, Ducrocq V.<sup>1</sup>,**

**INRA, 78350 Jouy-en-Josas, France, <sup>2</sup>BAIF CRS, 412202 Uruli Kanchan, India**