

Interest and limits of the bovine 50k chip to study *Bos taurus* x *Bos indicus* crossbred animals in an Indian bull stud



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**Bovine Genetics and
Genomics ,GABI, INRA
Jouy-en-Josas**



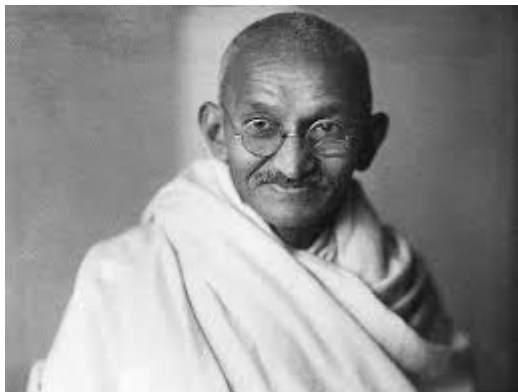
BAIF: Bharatiya Agro Industries Foundation

Largest Indian NGO in Agriculture, founded in 1967

... committed to sustainable development in rural India



Dr Manibhai Desai (1920-1993)



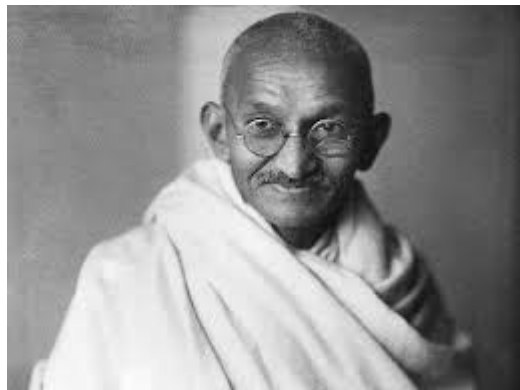
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<http://www.baif.org.in>

BAIF main activity: Livestock Development

Genetic improvement of local cattle through **AI** in tiny farms (< 2 cows)



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➔ 5.3 million families spread over 90,000 villages in 12 states

Semen production

- In the late 70's, a **nucleus herd** of ~200 pure Holstein and Jersey heifers from Denmark and Canada + some imported semen
→ a **bull stud** producing now > **8 millions doses a year** ...

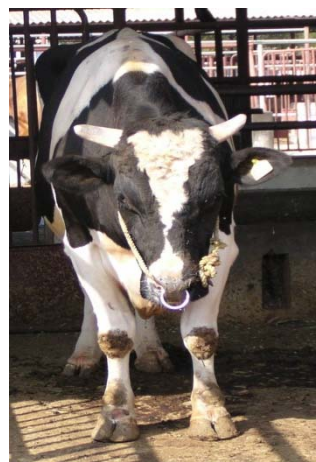
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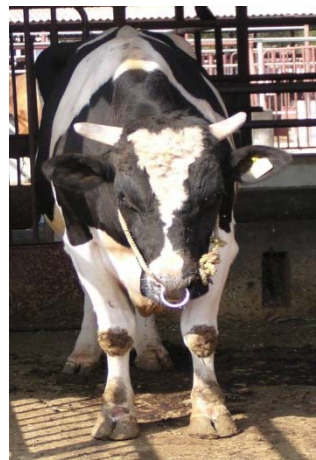
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= **pure « exotic »** (HF/J) and **crossbred** bulls
but also pure **indigenous** (*Bos Indicus*) as well as **buffaloes**



Joint BAIFF-INRA genomic project

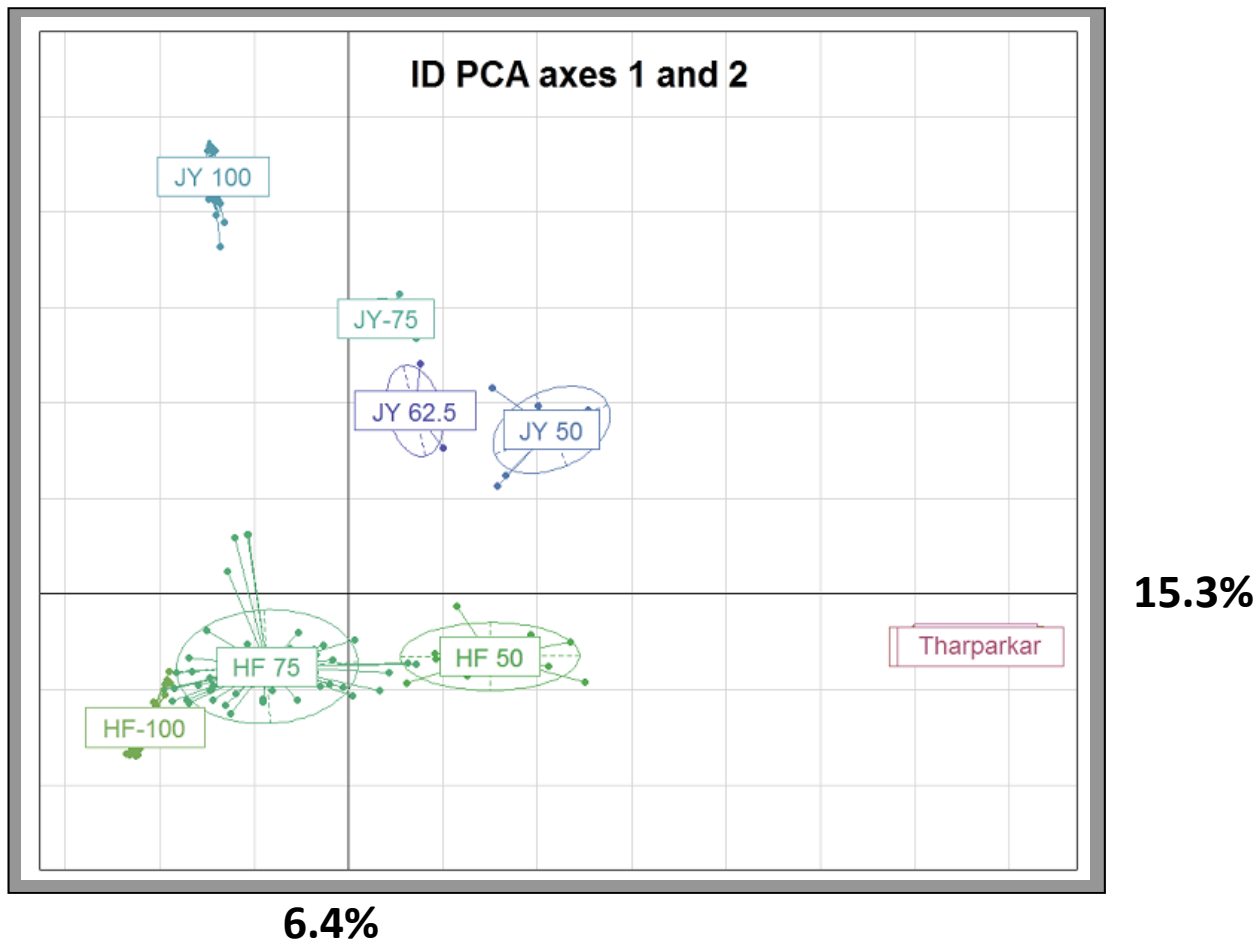
- 288 animals genotyped on Illumina Bovine SNP50 Beadchip®

	Bulls	Cows	
Indigenous	58		(8 breeds, <u>mainly Sahiwal and Gir</u>)
Holstein	59	22	
Holstein crossbreds	78	7	(71 HF75%, 13 HF 50%, 1 HF 62.5%)
Jersey	30	6	
Jersey crossbreds	28		(8 J 75%, 16 J 50%, 4 J 62.5%)

- Question: **how to use this genomic information to help the management of the bull stud?**

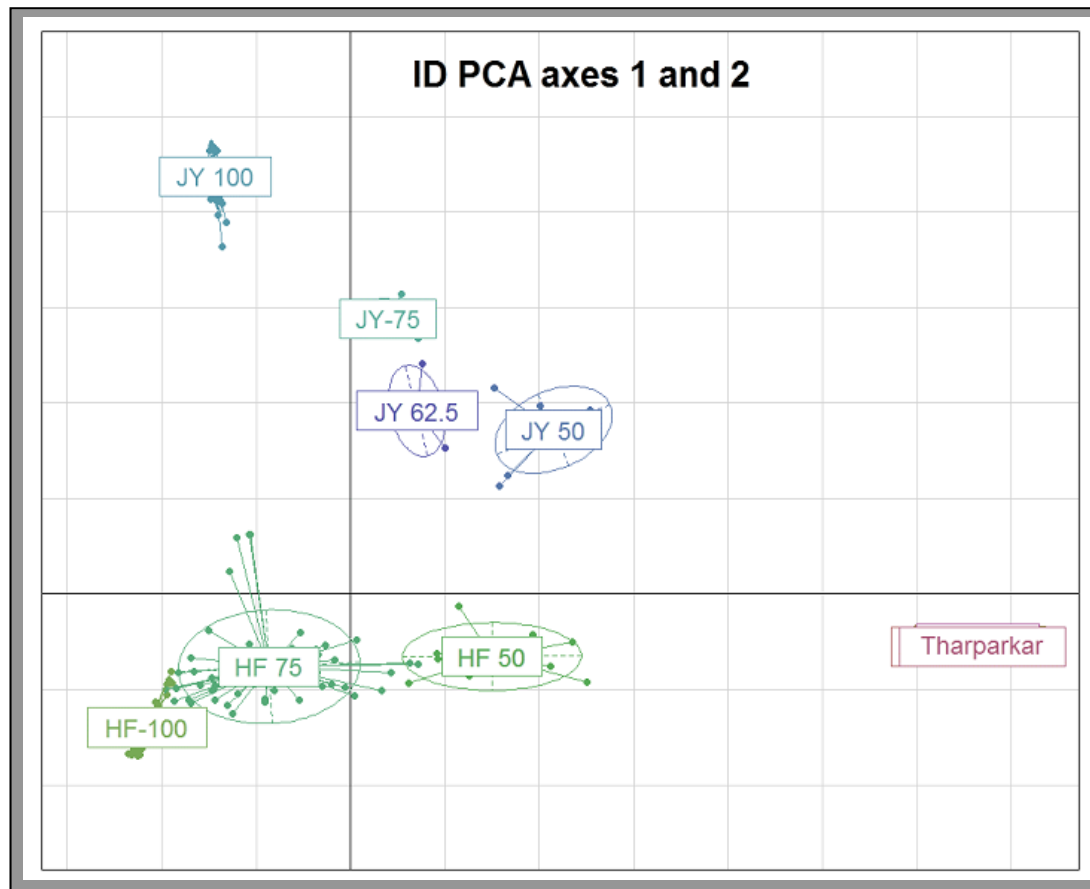
Principal Component Analysis (PCA)

1 animal = 1 point = (up to) 43,167 SNP

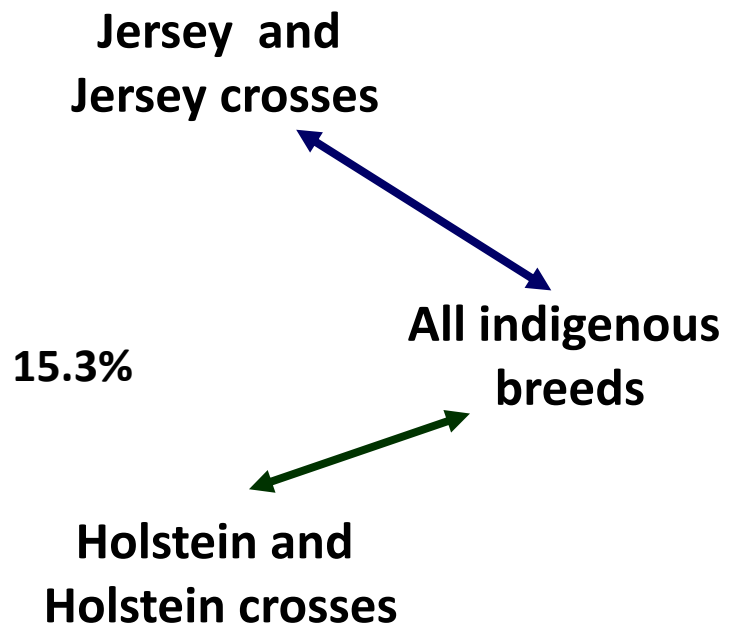


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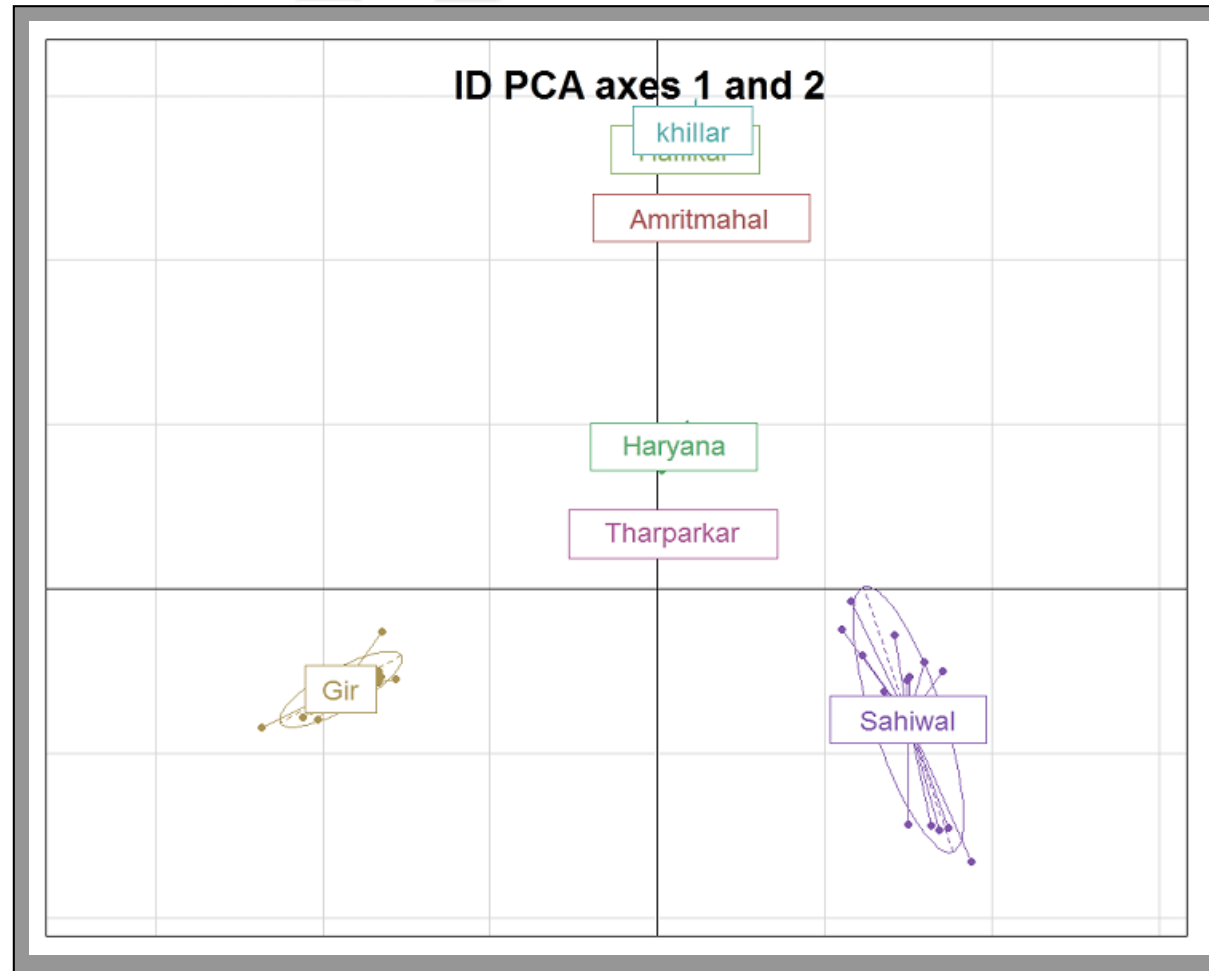
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6.4%



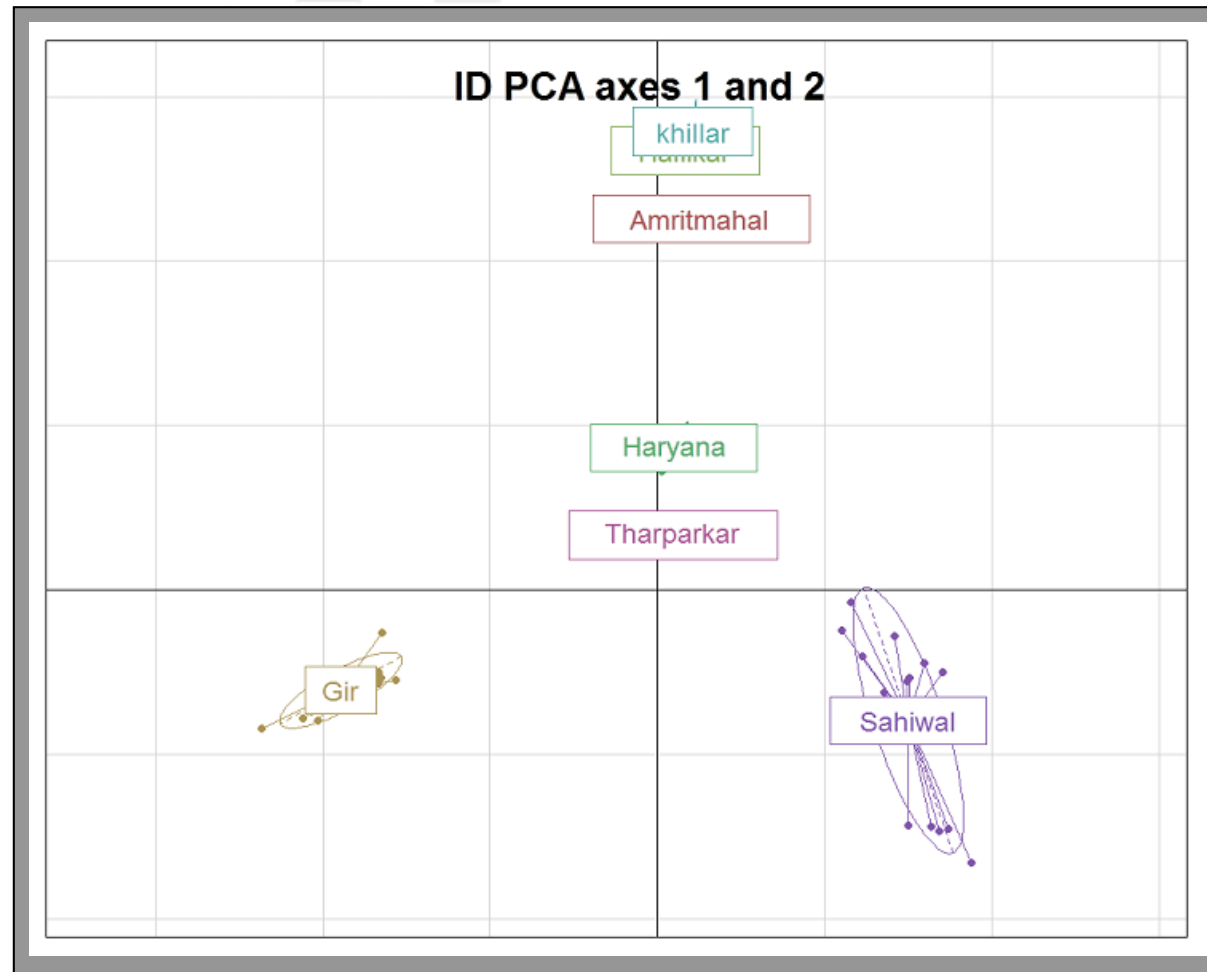
PCA for Indigenous breeds



4.2%

5.3%

PCA for Indigenous breeds



↑
**Draft
breeds**
↓

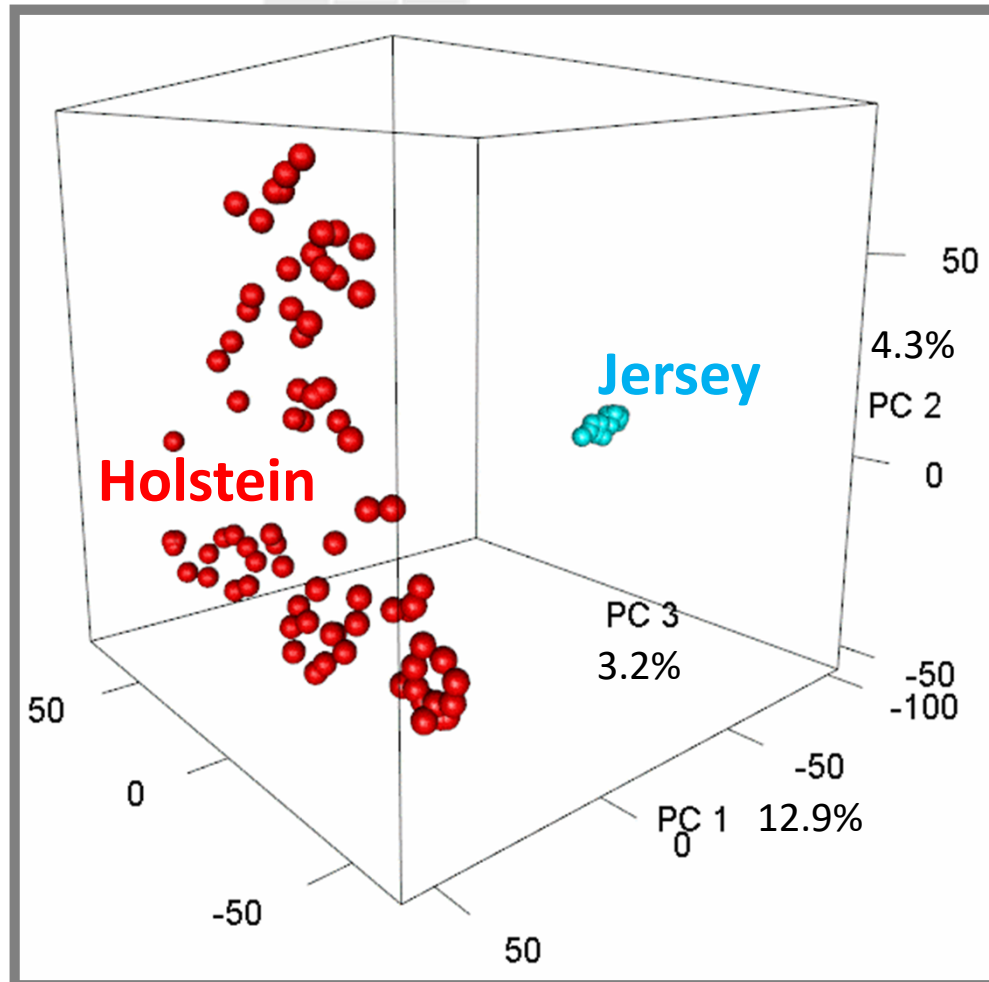
5.3%



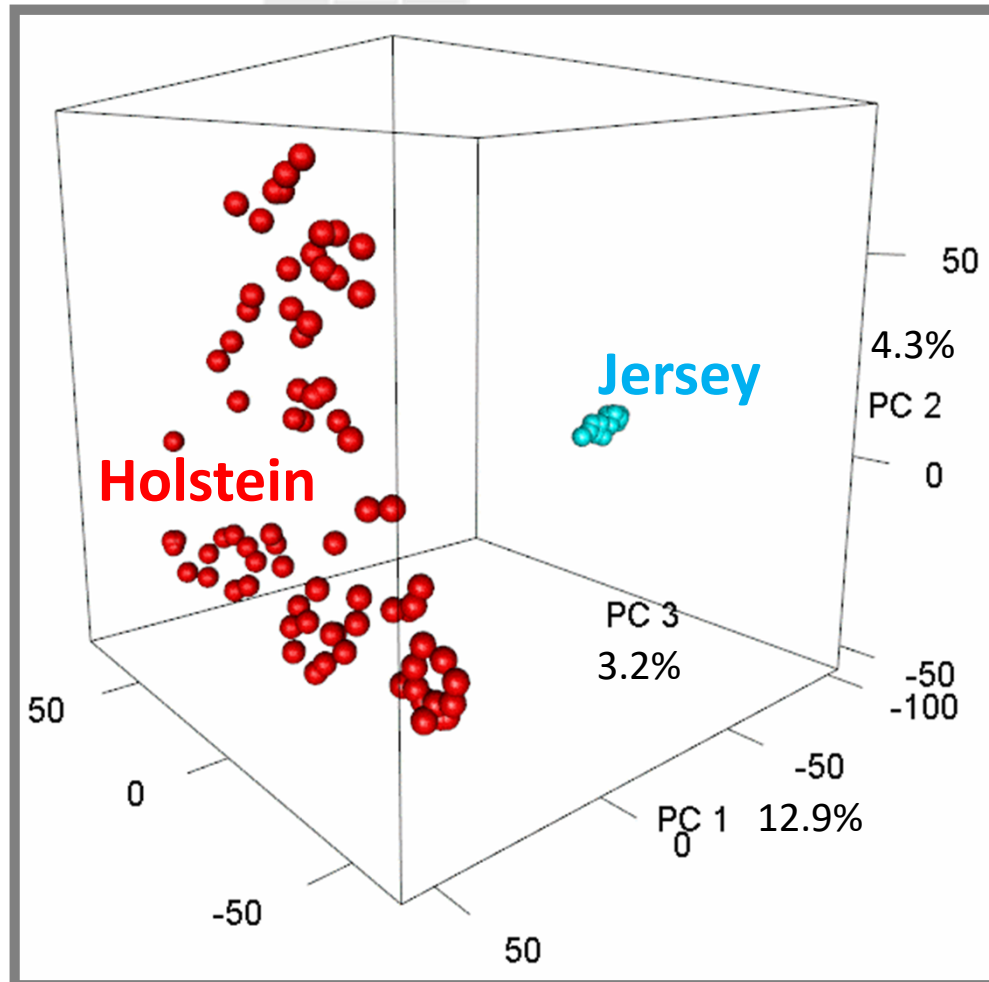
↔
**Dairy
Breeds**
(higher
heterogeneity
in Sahiwal)

4.2%

3D PCA for exotic purebreds

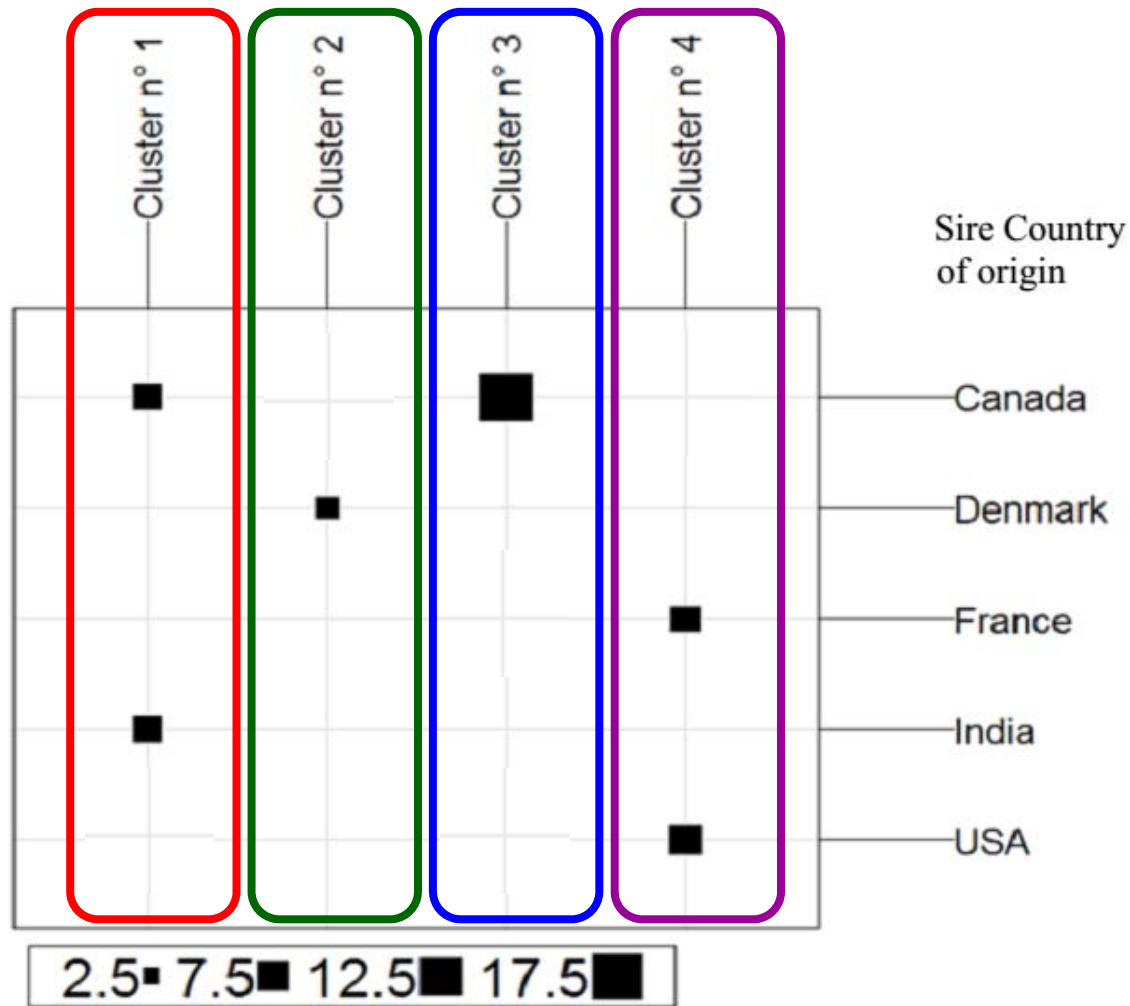


3D PCA for exotic purebreds

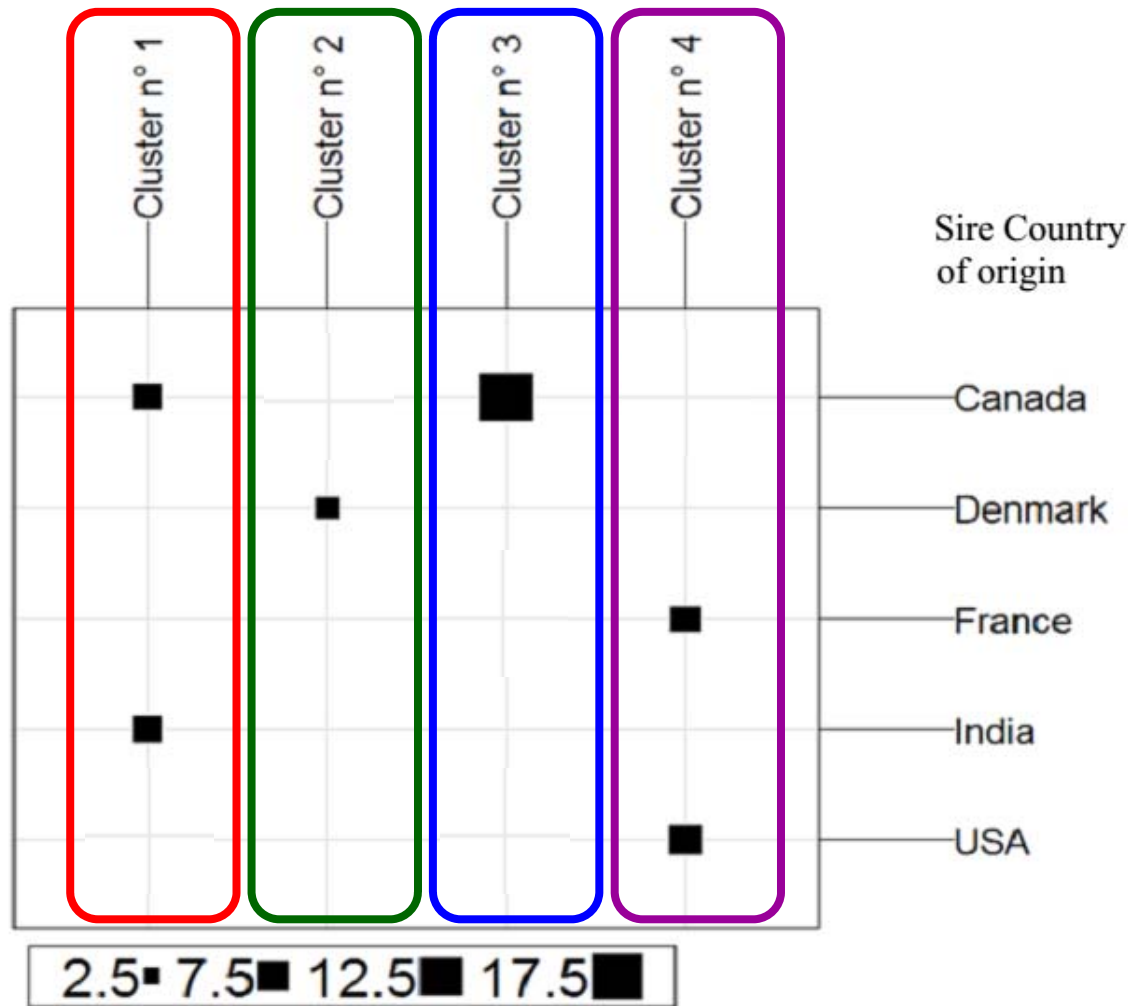


Much larger heterogeneity among Holstein animals !

Cluster analysis within pure Holsteins



Cluster analysis within pure Holsteins



Clusters: sons of ...

1. « recent » CD HF
2. « old » Danish
3. « old » Canadian
4. « recent » HF



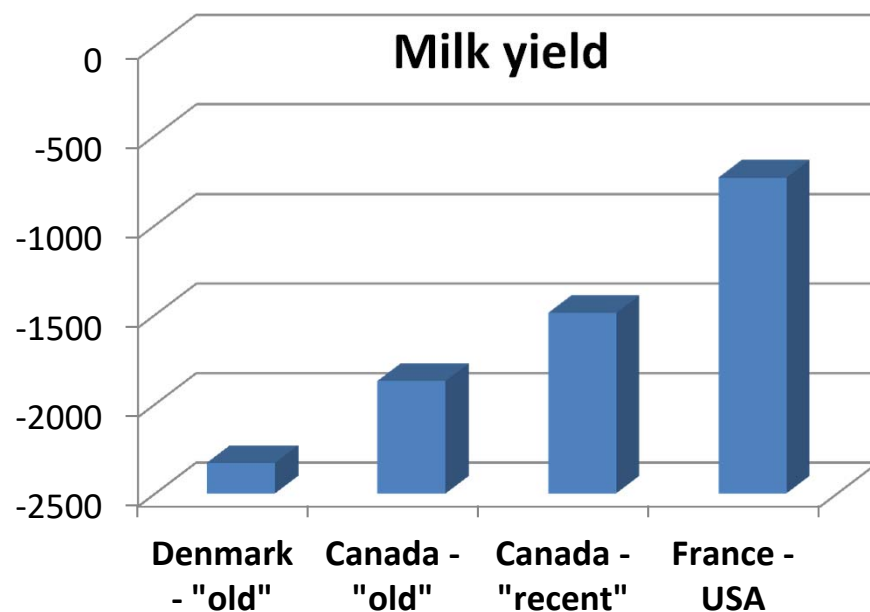
Why ?



- **Genomic evaluation** on ~40 traits on the **French scale**
(obviously not necessarily an adequate scale, given the huge Gx E)

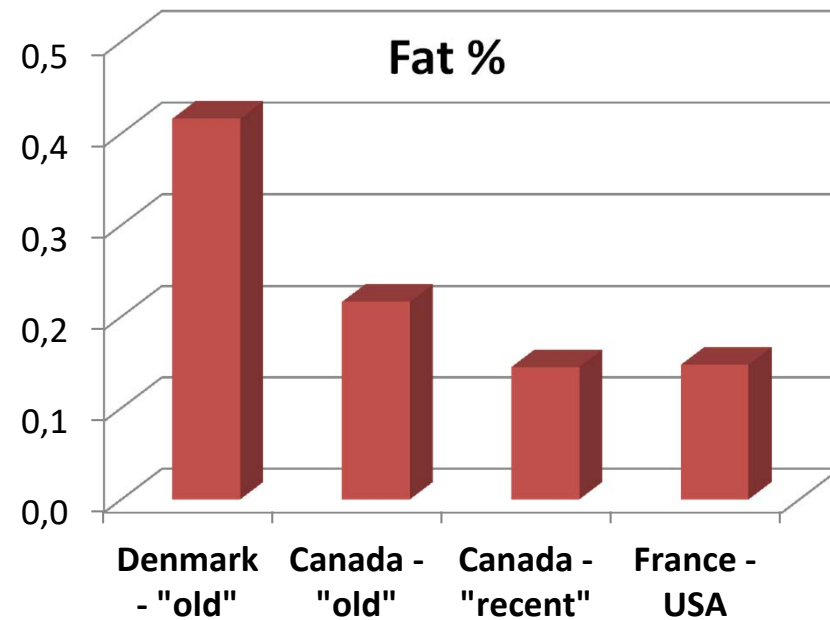
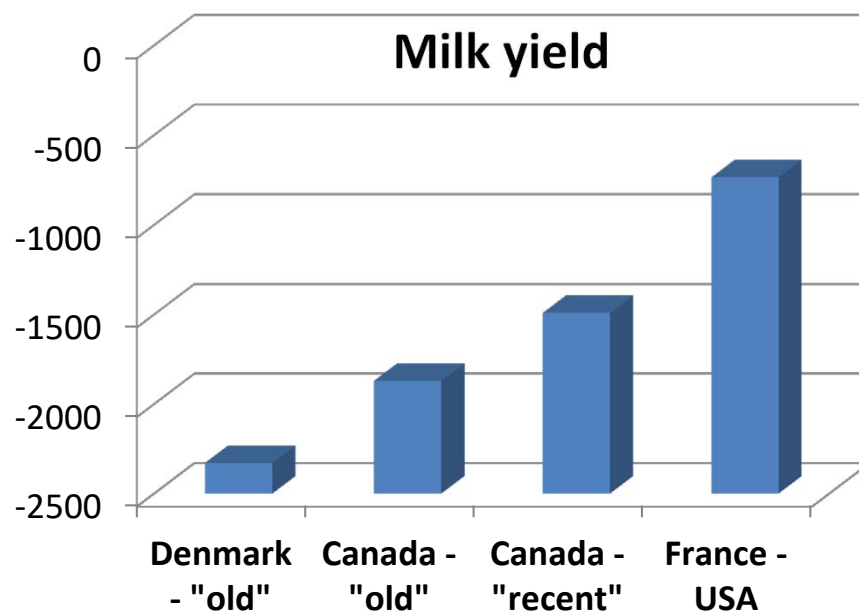
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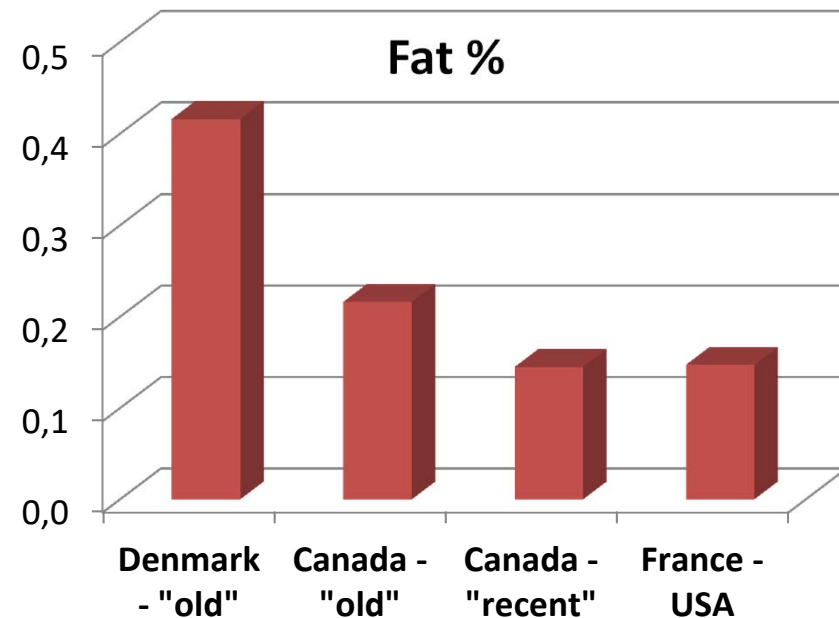
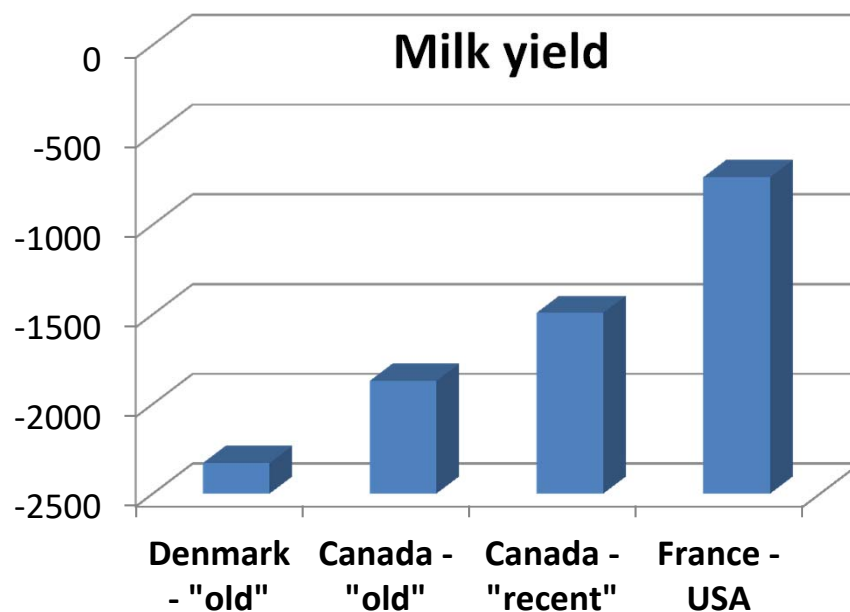
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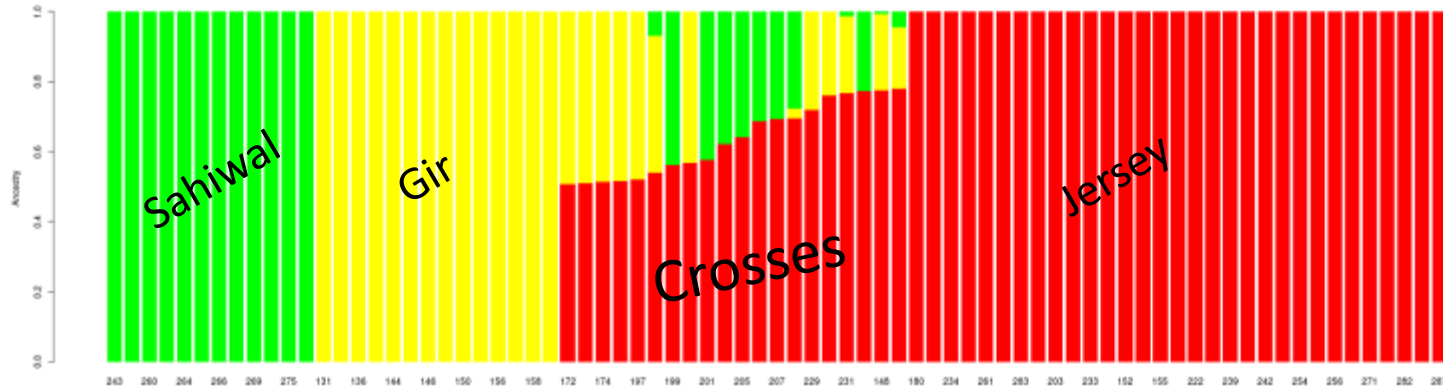
- **Genomic evaluation** on ~40 traits on the **French scale**
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→ Clearly reveals huge differences in genetic merit, **consistent with the history of semen procurement and use at BAIF**

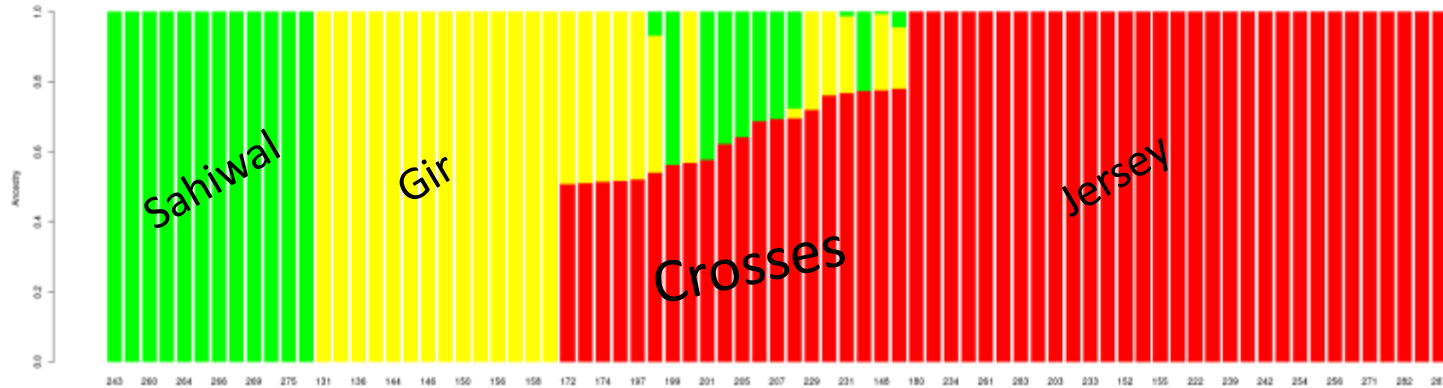
Breed composition: Admixture

Jersey
crosses

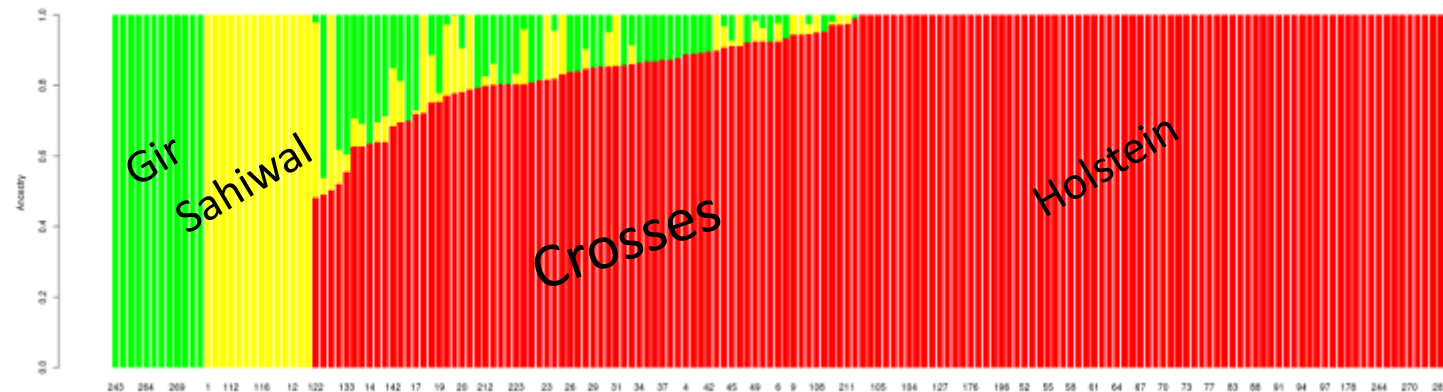


Breed composition: Admixture

Jersey
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Holstein
crosses

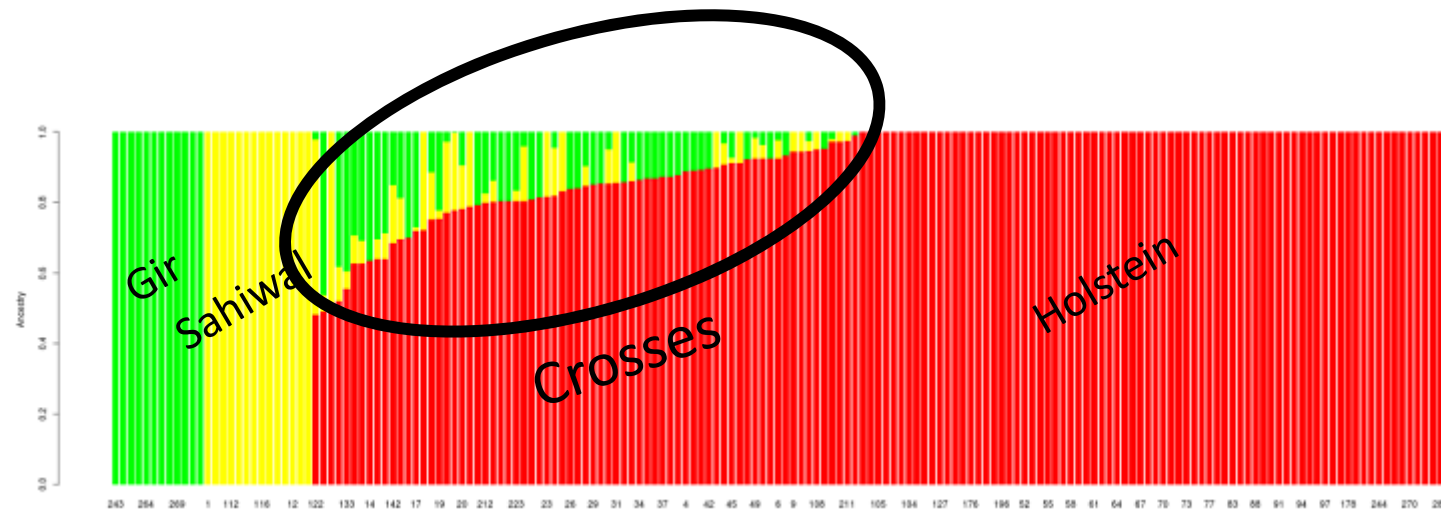


Breed composition: Admixture

Jersey
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Holstein
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Breed composition and breed assignation

- Purebreds: **Holstein vs Jersey vs Gir vs Sahiwal**: 100%
- Jersey crosses: % **Jersey** : good % **Sahiwal/Gir** : not always good

N°	From pedigree information	Jersey	Sahiwal	Gir
170	Jersey 50% Sahiwal 50%	0.51	0.49	-
203	Jersey 62.5% Gir 37.5%	0.69	-	0.31
155	Jersey 75% Sahiwal 25%	0.76	0.24	-
152	Jersey 75% Sahiwal 12.5% Gir 12.5%	0.77	0.22	0.01

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- Holstein crosses: % **Holstein**: often overestimated % **Sahiwal/Gir** : poor

N°	From pedigree information	Holstein	Sahiwal	Gir
106	Holstein 50% Sahiwal 50%	0.52	0.10	0.38
108	Holstein 50% Gir 50%	0.70	-	0.30
92	Holstein 75% Gir 25%	0.80	-	0.20
63	Holstein 75% Sahiwal 3.1% Gir 21.9%	0.80	0.16	0.04

Table 3: BovineSNP50 BeadChip Content Validation

Breed	Samples	Polymorphic Loci*	Mean MAF	Median MAF**
Angus	24	41,073	0.21	0.21
Beefmaster	23	43,114	0.22	0.22
Bos indicus Gir	21	23,567	0.11	0.02
Bos indicus Nelore	19	25,492	0.11	0.03
Brahman	22	29,444	0.13	0.07
Brown Swiss	21	35,971	0.19	0.17
Charolais	19	43,723	0.22	0.21
Guernsey	21	36,748	0.19	0.17
Hereford	24	42,132	0.22	0.23
Holstein	49	42,849	0.22	0.22
Jersey	23	35,346	0.18	0.15
Limousin	39	42,617	0.22	0.21
N'Dama	23	28,869	0.14	0.07
Norwegian Red	17	42,055	0.22	0.21
Piedmontese	21	41,912	0.22	0.21
Red Angus	10	42,388	0.21	0.20
Romagnola	21	38,524	0.20	0.19
Santa Gertrudis	21	41,783	0.22	0.21
Sheko	16	35,084	0.17	0.13
Overall	434	47,168	0.24	0.25

Why ? : the 50K Chip

- Only 40 animals of two *bos indicus* breeds used to construct and validate the chip ...

Source :

BovineSNP50 ® BeadChip Illumina Datasheet

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* MAF > 0.05

** Across all 54,609 loci

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Why ? : the 50K Chip

- Much less polymorphic (only ~50% SNP are polymorphic in Gir, in the BAIF project: **>18000 SNP are completely fixed**)
- Much less informative (**50%** of SNP have a **MAF ≤ 0.02** in Gir)

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- Much **less polymorphic**
(only ~50% SNP are polymorphic in Gir, in the BAIF project:
 - >18000 SNP are completely fixed)
- Much **less informative**
(50% of SNP have a $MAF \leq 0.02$ in Gir)

➔ An Indian (BAIF + NDDDB) initiative:

- create a new 50k chip adapted to Indian indigenous breeds and crossbreds : the « **IndusChip** »
(on going project)

Use of genomic tools in India is promising

- ❖ Bring original and useful information at **bull stud level**
- ❖ Can partly **compensate** the absence of large scale **pedigree (and performance) recording**
- ❖ Can contribute to a better characterization and understanding of the current **genetic diversity between and within breeds**
- ❖ Can improve the way **crossbreeding** is done
- ❖ Can be a first step for **genomic selection** of better bulls in crossbred and even indigenous populations



Thank you!

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Why ? Quality control at SNP level:

- Gen Train (cluster reliability) > 0.7
 - Call Freq >0.97
 - SNP from chromosome X, Y or unknown
 - **SNP monomorphic or with very rare alleles → 4749 SNP removed**
- overall **43,167 SNP used ... but ...**

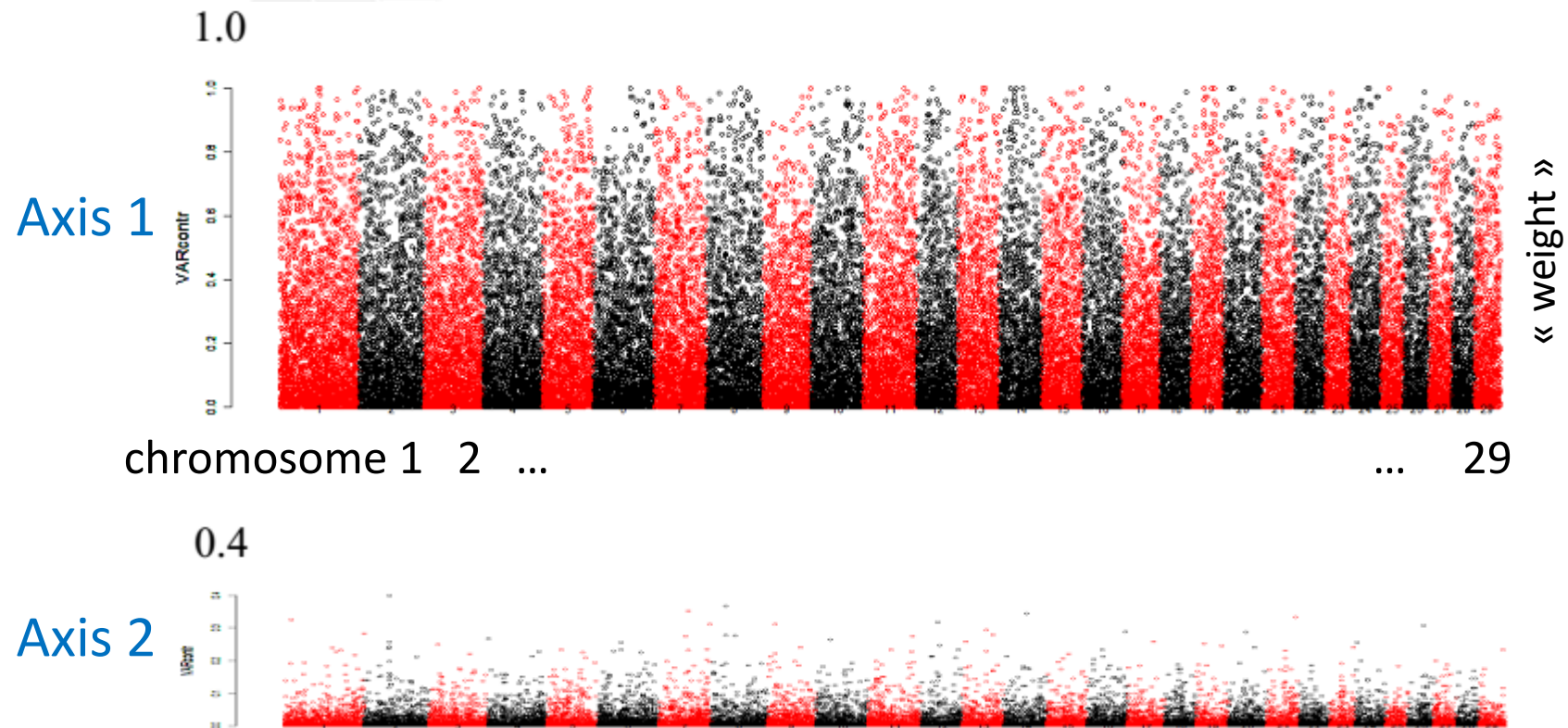
For **indigeous breeds** only: **11,957** monomorphic SNP

For Sahiwal + Gir only: **18,191** monomorphic SNP

(For Holstein + Jersey only: **6 134** monomorphic SNP)

- Call Rate > 0.95 → 7 animals removed

Why?: SNP “contributions” to axes 1 and 2



- Much more information to distinguish between exotic and indigenous breeds that between indigenous breeds

PCA for exotic purebreds

