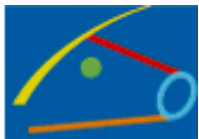


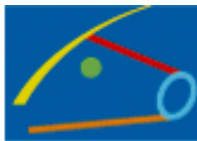
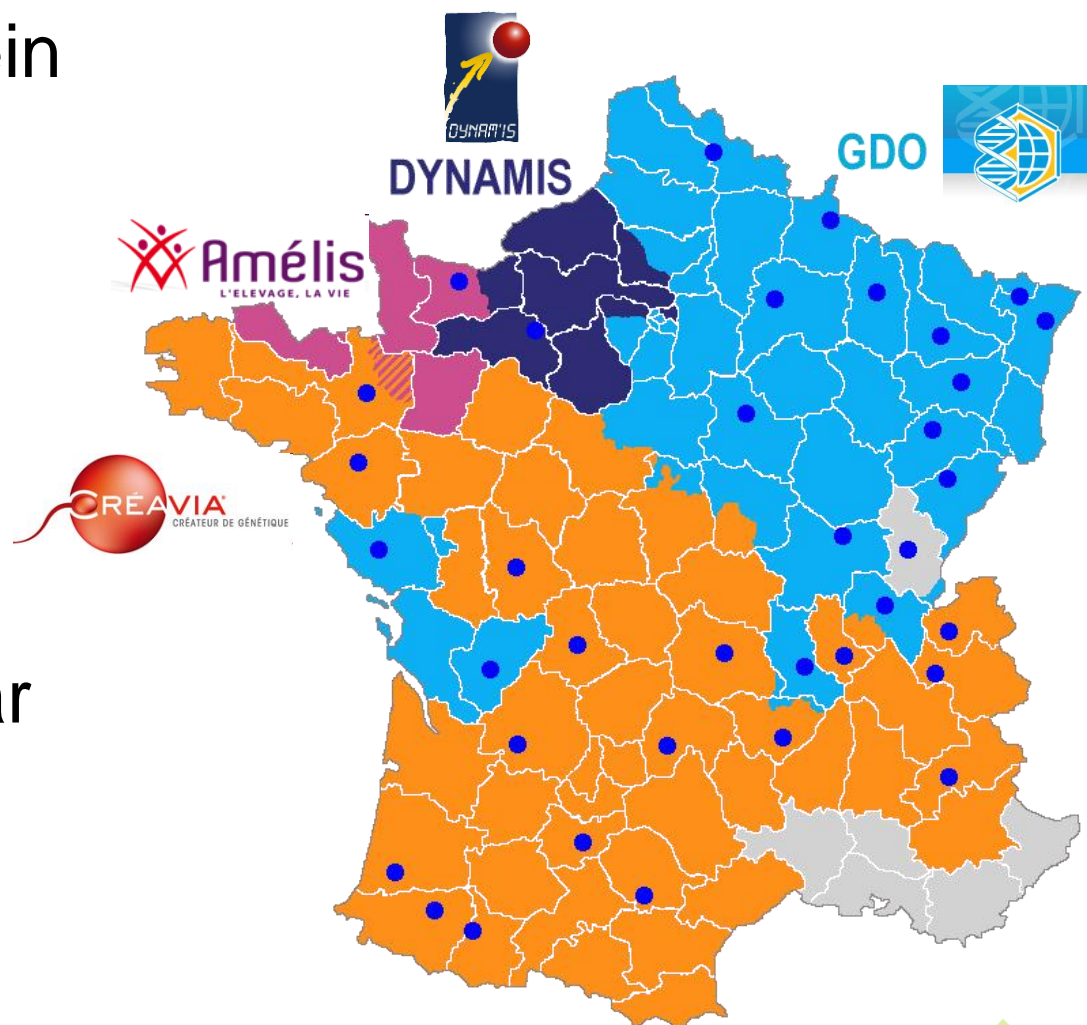
Genomic in Holstein breeding schemes: Example of the French Marker Assisted Selection L. Journaux

- **Short presentation of French Holstein breeding schemes**
- **Description of French MAS system**
- **Efficiency of the French MAS system**
- **Conclusion and perspectives**



Holstein and dairy production in France

- About 2.5 M Holstein (60% of dairy cows)
- 90% AI
- 2/3 to 3/4 milk recorded
- About 600 bulls progeny tested / year
- 4 efficient breeding schemes



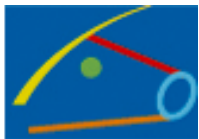
■ An old story

– Middle of 90's

- Investment in QTL detection

– Beginning of 2000

- First generation MAS
 - available for breeding companies
- 45 microsatellite markers , 8 traits, 30 000 genotypes
- +0.10 of reliability
- A tool for preselection before progeny test

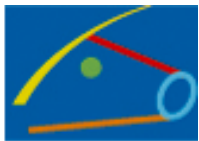


Illumina Bovine Chip : the tool of revolution

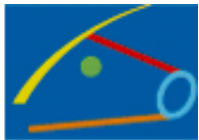
■ 2007

– A chip to “read”
54 000 markers

- 3 days
- Less than 300 €
- Open the doors
of genomic
selection



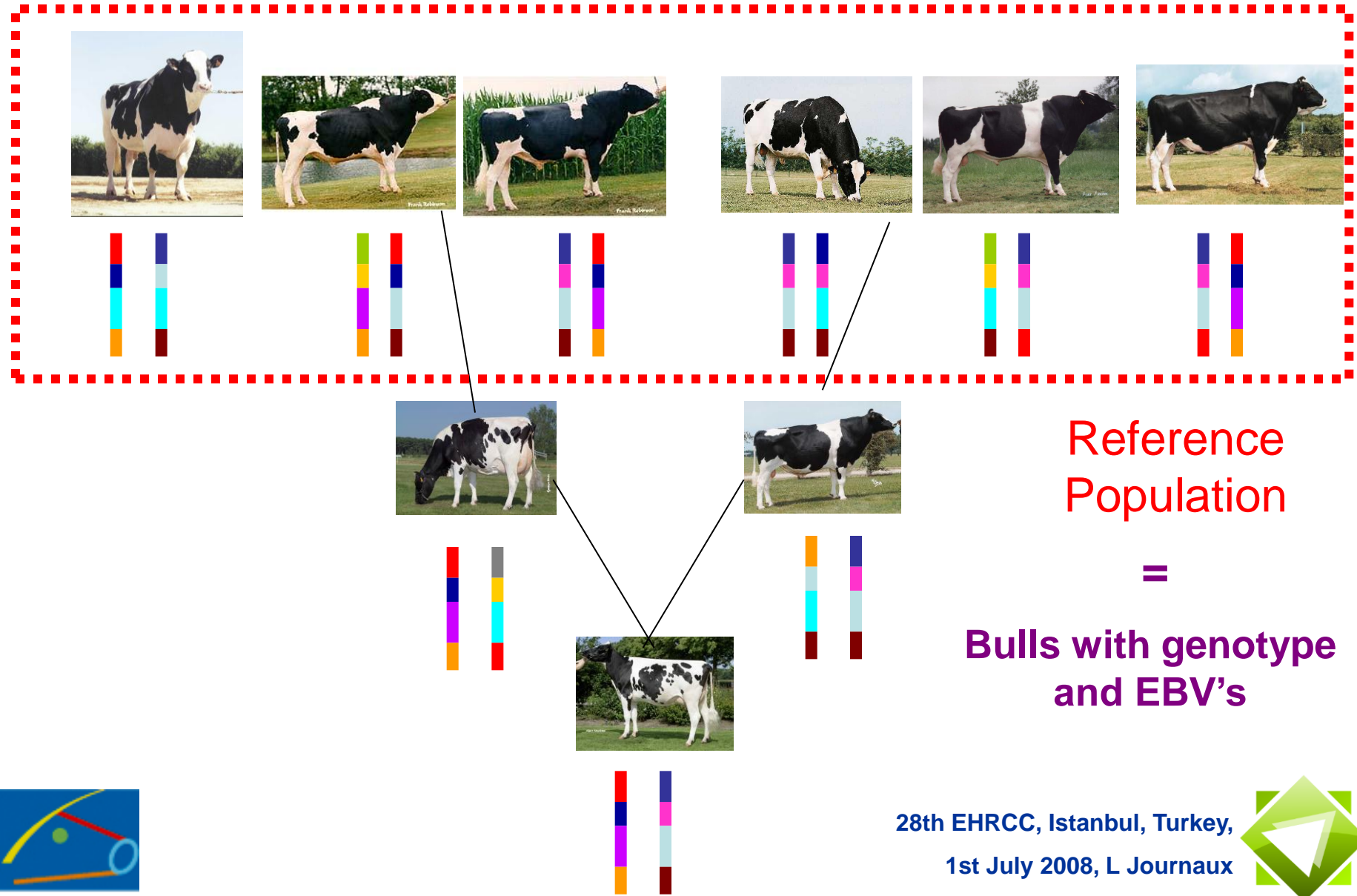
Genomic Selection: The principles



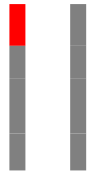
28th EHRCC, Istanbul, Turkey,
1st July 2008, L Journaux



Genomic Selection : the principles



Genomic evaluation



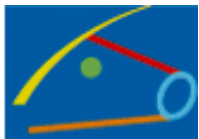
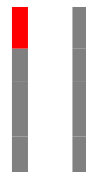
Reference
population

C????T



Hypothesis :
Regions of same color =
same DNA sequence

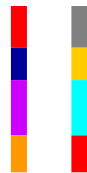
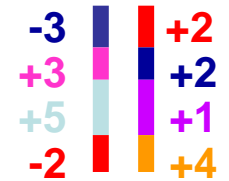
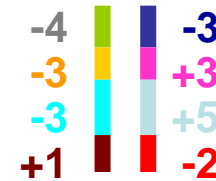
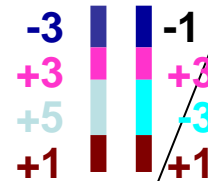
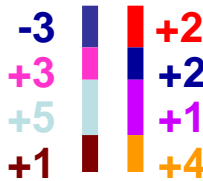
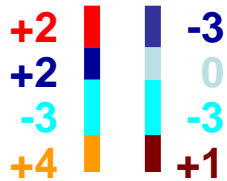
C????T



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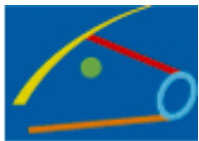


Genomic evaluation

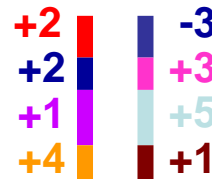
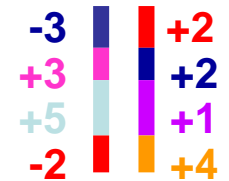
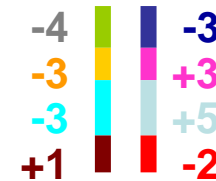
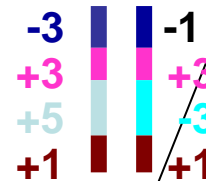
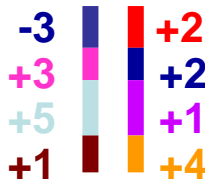
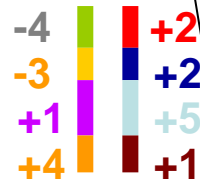
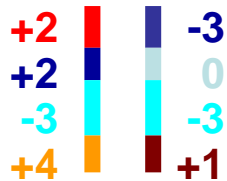


Reference population

We compute the effect of each region in reference population

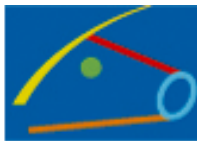


Genomic evaluation



Reference
population

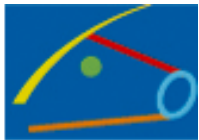
We obtain a DGV
of young animals



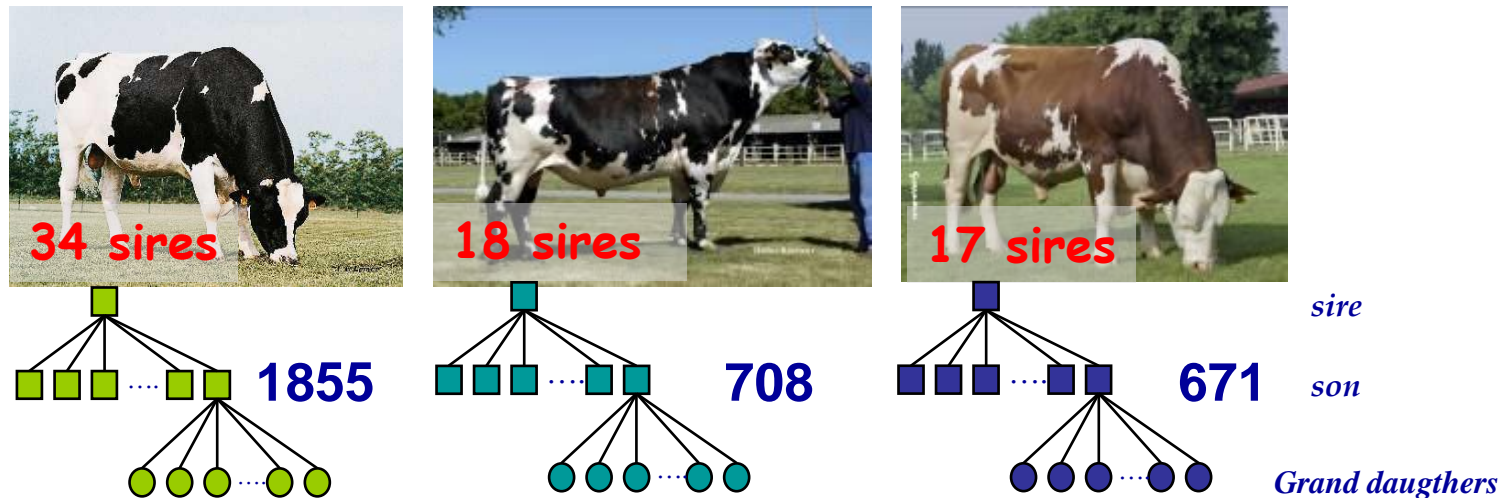
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The French tool: a MAS (marker assisted selection) approach



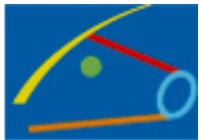
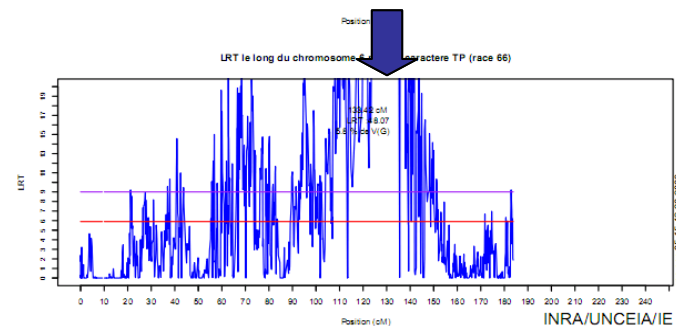
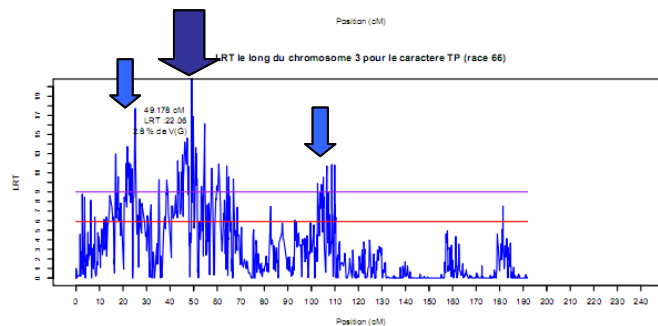
CARTOFINE Project (2006-2008)



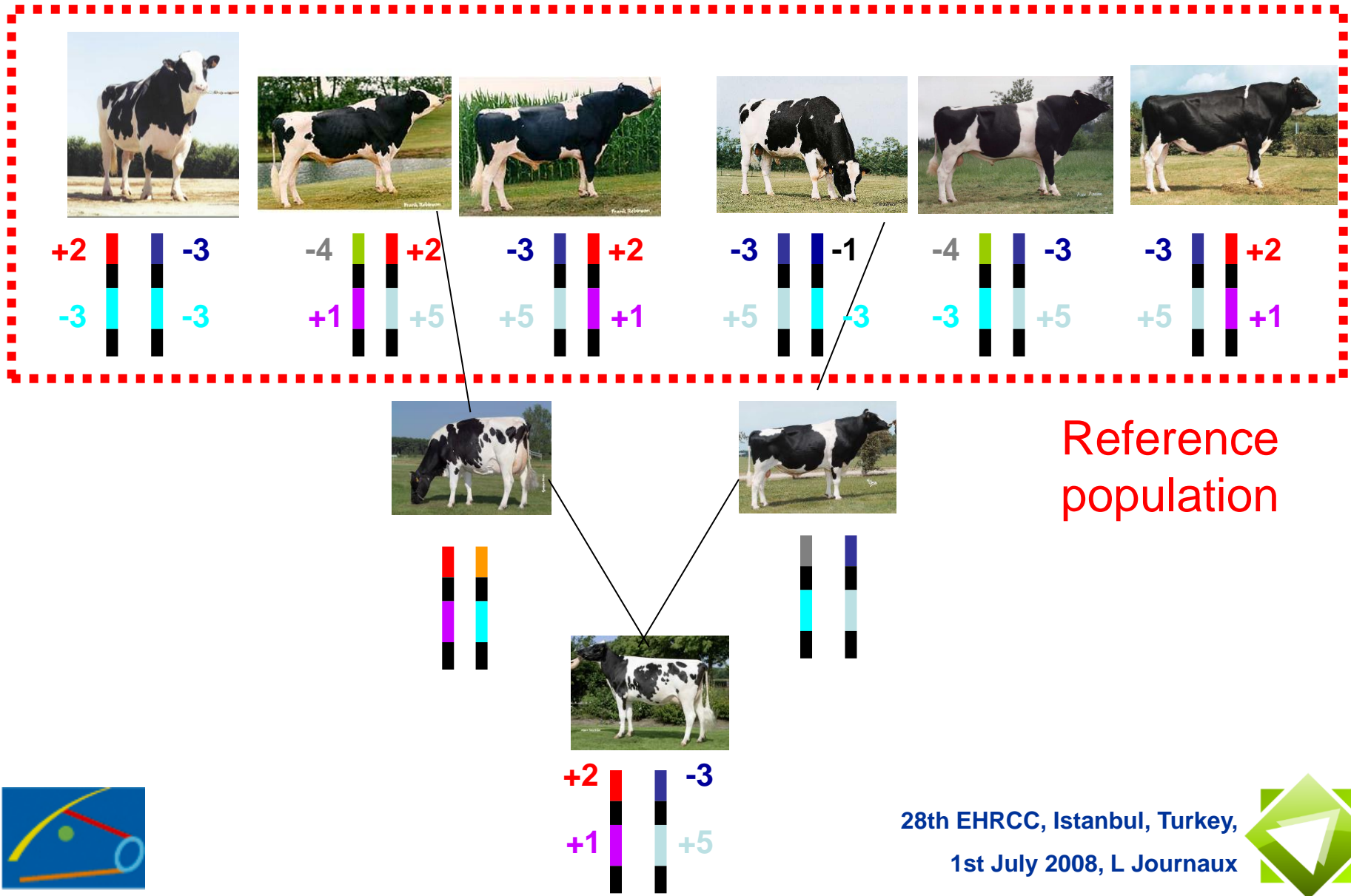
- Project founded by ANR and APIS-GENE
- INRA, UNCEIA, CNG, LABOGENA
- ~3200 sires genotyped on 54000 SNP Illumina chip
- 15 traits studied in a first step
 - Milk production (5), SCC (1), fertility (2), udder (3), body (2), locomotion (1), milking speed (1)



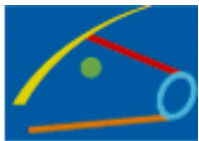
- **Statistic analysis**
 - **To identify QTL regions linked to the 15 traits (for 3 breeds)**
- **Large number of QTL identified**
 - **the 20 to 40 more significant regions for each trait were chosen for Marker Assisted Selection**



MAS2 : We estimate the effects of a predetermined list of QTL (~40 QTL)



- **MAS2 is computed each month**
 - For private use by breeding companies
- **Official publication are performed 3 times / year**
- **Publication is a GEBV**
 - Best linear unbiased estimation (BLUP) of
 - QTL effects
 - Parentage
 - Progeny

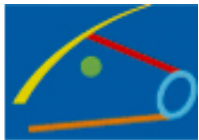


- **Since mid 2008**

- Second generation MAS is available for breeding companies

- +0.2 to 0.3 in reliability**

- Opportunity to use sires without progeny test



- **Increase size of reference population**
 - 2 063 Holstein (+24%)
- **Use of the latest genome map**
- **Update DYD (February 2009)**
- **Better construction of haplotypes**
- **Consequence**
 - 16 to 41 QTL per trait
 - 26 to 45% of genetic variance explained
 - More efficient estimation of
 - Sum of QTL effects
 - GEBV

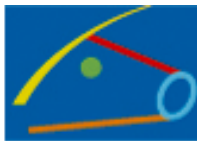
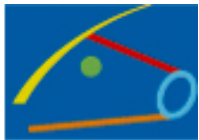


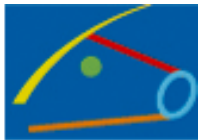
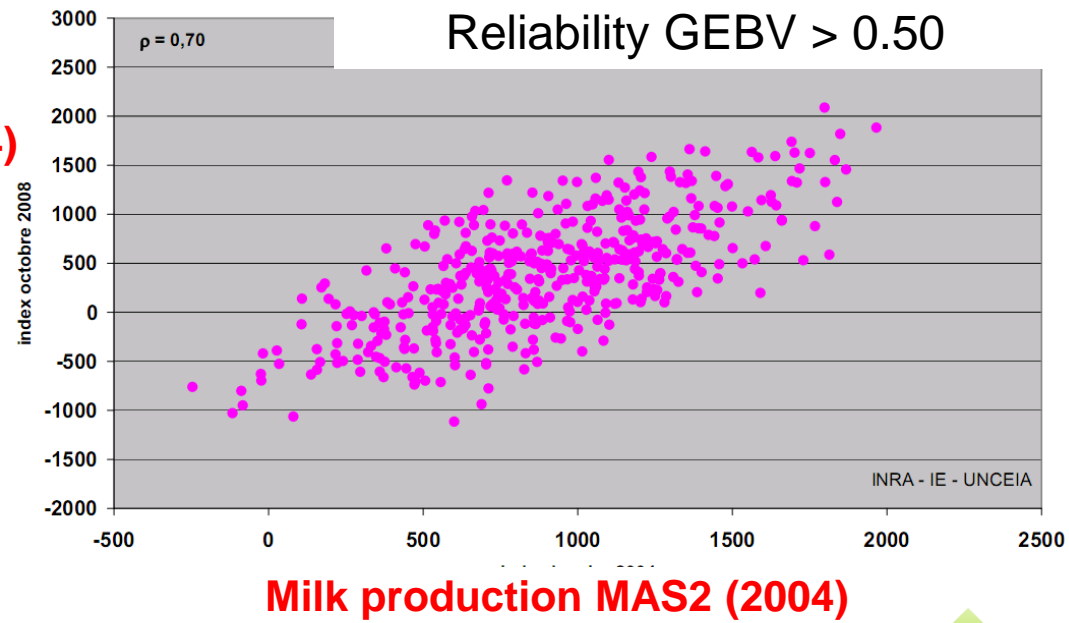
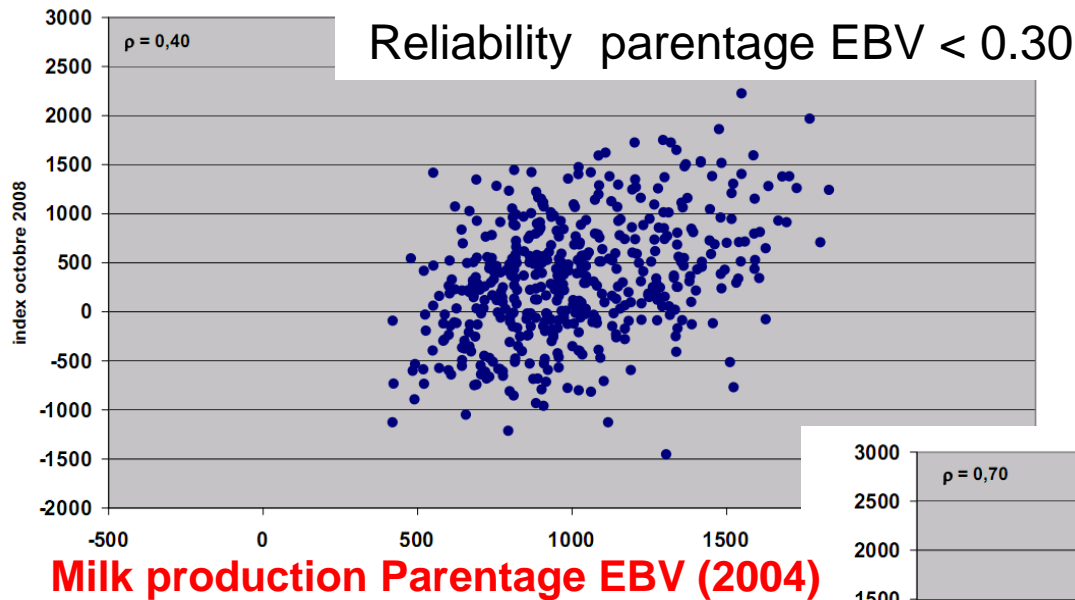
Illustration of efficiency of the French MAS2



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Gain in reliability with MAS2



Fritz, October 2008

28th EHRCC, Istanbul, Turkey,

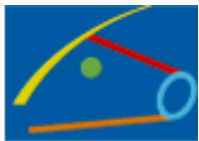
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Reliability of young bulls without progeny

Milk	0.62
Protein	0.56
Somatic cells count	0.58
Fertility	0.51
Rear udder height	0.55
Body depth	0.58
Milking speed	0.56

Note IBL 2009-5, June 2009



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1st July 2008, L Journaux

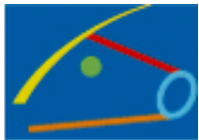
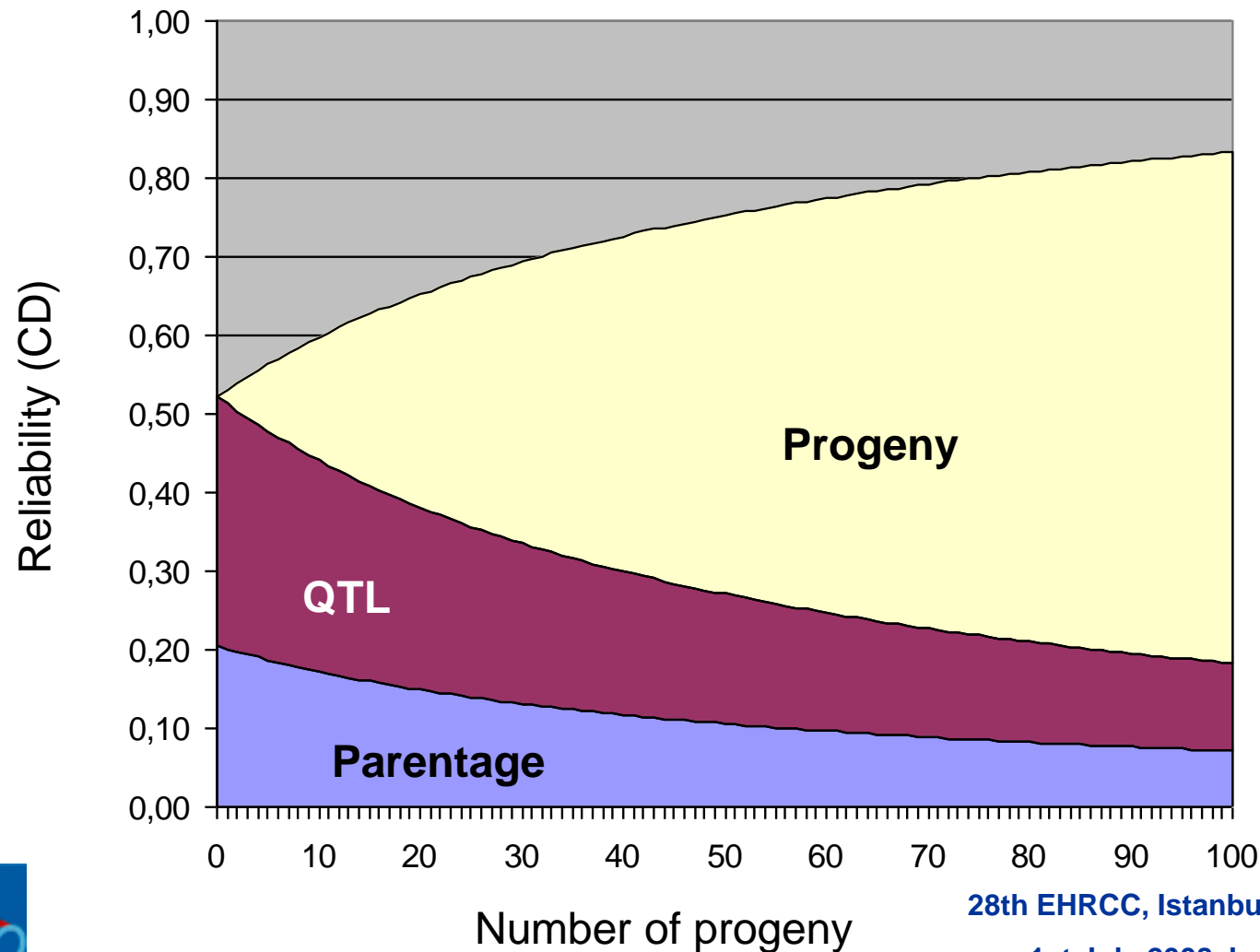


Contribution to reliability

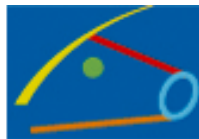
$h^2 = 0.15$

CD parentage = 0.30

CDqtl = 0.40



- **A reliable genomic evaluation in France**
 - For a better efficiency of the breeding schemes
- **June 2009**
 - Official publication of MAS2_{EBV}
 - 137 Holstein sires published
 - <http://www.inst-elevage.asso.fr>
 - Breeding companies can sell semen of MAS2 sires in France



Listing of MAS sires



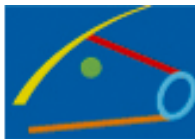
Edition du 18 juin 2009

Accueil

Nouvelle recherche : par **race** / **nom** / **numéro** - multicritère

137 taureaux évalués en race **Prim'Holstein** répondent à votre choix

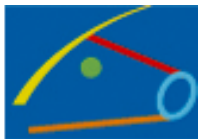
Rang	Nom	Père	ES	ISU	index génomiques					index polygéniques				
					IIEL	TP	TB	LAIT	MO	MA	CEL	LGF	FER	IIAI
1	BITAX	MASCOL ET	AMELIS 002	176	40	1.6	3.8	93	2	1.9	2.2	-	-	93
2	VILVORD	O-BEE MANFRED JUSTICE-ET	DYNAM'IS-L'AIGLE 003	175	52	2.6	3.0	803	1.1	0.7	1.3	-	1.8	94
3	BIOLET	GILLETTE BRILEA F B I	AMELIS 002	174	44	0.2	-0.2	1161	2.3	1.6	1.6	-	-	91
4	DEVONPORT	EMERALD-ACR-SA T-BAXTER	MIDATEST	173	42	-1.6	2.1	1132	3.3	2.3	1.3	-	1.1	-
5	CLIMB ISY	SANDY-VALLEY BOLTON-ET	AMELIS	170	41	-0.3	0.6	828	2.3	1.8	1.5	-	1.2	-
6	CAESAR	PICSTON SHOTTLE ET	GDO	170	36	0.9	0.5	1001	2.6	1.8	1.9	-	1.4	-
7	DONOVAN	RANDVIEW	CREAVIA	170	42	1.5	-0.8	1082	1.9	1.6	1.7	-	1.1	-
8	BURON	GILLETTE BRILEA F B I	AMELIS 002	170	47	0.5	0.3	884	1.6	1	1.4	-	-	92
9	BLACJAK	PICSTON SHOTTLE ET	DYNAM'IS-L'AIGLE 003	169	49	0.1	-1.0	1253	1.6	0.6	1.2	-	1.0	88
10	COOPER	J-K-R BW-MARSHLL BILLION-ET	CREAVIA	169	44	0.8	3.9	651	2.2	1.7	1.9	-	0.5	-
11	CASTER	JOSE	GDO	169	42	-1.1	0.2	1000	2.3	1.7	1.1	-	1.2	-



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- **Improvements of genetic evaluation are already planned before the end of 2009**
 - By increasing the size of the reference population
 - French resources (+2 000 sires)
 - EU resources
 - By increasing the number of traits
 - + 10 traits autumn 2009 (...All traits before the end of 2010)
- **Open the evaluation for all breeders**
 - Today the system is managed within a private research contract between UNCEIA and INRA
 - The system will be progressively opened to all breeders, in particular for females

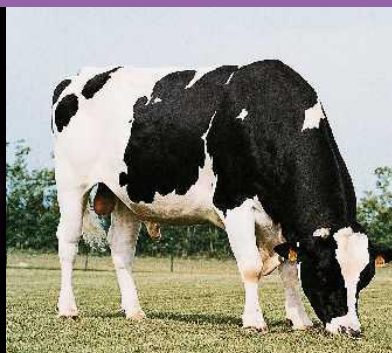




le réseau de la génétique animale



Organisme de Sélection
Prim'Holstein



Thank you for your attention