Changes in the French Brown Swiss Al program related to the use of Intergenomics breeding values

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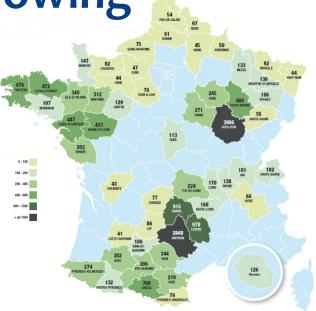


Brown Swiss in France

A small population, that is growing

* 18,000 purebred milk recorded cows

- * 54 % growth in the last 20 years
- * 1 % of dairy cows in the country
- * 4 % of Brown Swiss cows in Europe

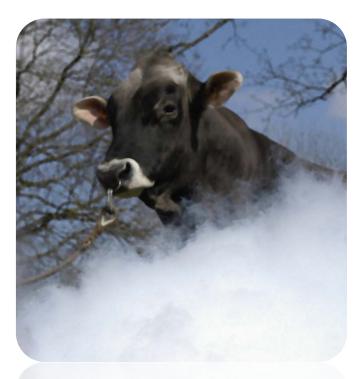




Brune Génétique Services

A merged breed organisation for:

- * Herd Book tasks
- * Al breeding program:
 - * 45,000 inseminations / year
 - * 10 young sires sampled / year
 - * 30 % of AI with foreign bulls





BGS, partner of Intergenomics



An international Brown Swiss genomic evaluation

- * 2009 : seven countries sign Intergenomics agreement
 - * Put together a common reference population (~5000 sires)
 - * Build an international genomic evaluation (Interbull)
- * 2011 : first routine run in december
- * BGS started to use ITG_GEBV right from the start



How was impacted our program?

New technology, new methods:

- * End of sampling program

 10 young sires sampled -> 10-12 young sires marketed
- * Reduction of semen production per bull : 20,000 units stored -> 10,000 units
- * Investment in genotyping a lot of animals 130 candidates genotyped per year
- Development of sexed semen3-4 young sires available



How was impacted our program?

More bull dams matings planned

- * to secure enough interesting male birth
- * 300 matings to get 130 interesting calves
- * use of genomics sires as sire of sons

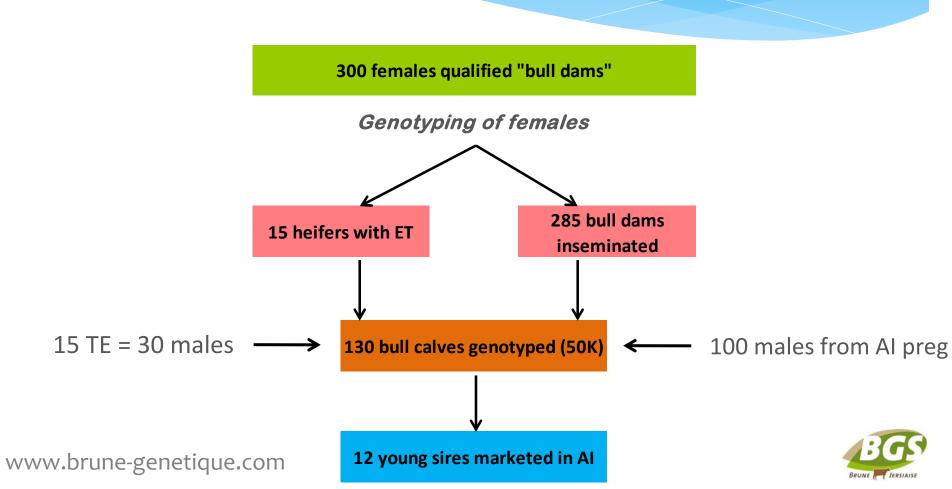
Genotyping of females

* for the selection of ET donors





New breeding scheme



First results of GEBV pre-selection

From 40 % to 60% gain of genetic level

| | genotyped | Selected |
|-------------------|-----------|----------|
| Number | 175 | 30 |
| Number of sires | 26 | 11 |
| Total Merit (ISU) | 140 | 160 |
| Milk | 472 | 780 |
| Kg P | 21 | 33 |
| SCS | 0,5 | 0,7 |
| Fertility | 0,4 | 0,6 |
| Udder | 0,8 | 1,2 |



Position of young versus old sires

Sires with ISU > 150 – Intergenomics FR scale

| | France | All countries | % FR sires |
|-------------|--------|---------------|------------|
| All | 61 | 700 | 8,7 % |
| Old sires | 4 | 95 | 4,2 % |
| Young sires | 57 | 605 | 9,4 % |
| % of young | 93,4 % | 86,4% | |

- * 9 sires out of 10 are young in the Total Merit TOP LIST
- * Twice more French sires in the young sires TOP LIST



International ranking per country

Sires with ISU > 150

| Sire country code | Cow population | Young sires | Old sires |
|-------------------|----------------|-------------|-----------|
| DEU | 169,379 | 301 | 44 |
| CHE | 169,353 | 99 | 16 |
| ITA | 98,204 | 65 | 12 |
| FRA | 17,355 | 57 | 4 |
| USA | 14,000 | 42 | 14 |
| AUT | 54,965 | 38 | 5 |
| CAN | 2,375 | 3 | 0 |
| Total | 525,631 | 605 | 95 |



International ranking of BGS sires

Sons of Huxoy

* # 3, 4 and 5 international

Sons of Prohuvo

* # 1 international

Sons of Dally

* # 1, 8 and 14 international

Sons of Payssli

* # 7 and 18 international

Sons of Alibaba

* # 3, 9 and 12 international

Sons of Brookings

* # 6 international

Genomics are boosting
the competitiveness
of French BS program,
independantly of
sampling capacity



Use of genomics in IA

BS breeders show a lot of confidence in genomics

Inseminations done with young sires:

* Before: 3,824 8,6 %

* After: 11,531 25,3 %

* 2013 forecast: 40,0 %

Increasing use of sexed semen:

* up to 10% of purebred females get 1 sexed IA



Perspectives

Intergenomics agreement 2.0

- * Future share of all genotypes, young and old
- Transparency of G-evaluations, publication of ALL bulls GEBV
- * General interest of the breed :

access to the best genetics available world-wide

Development of national MAS-G evaluation:

- * Males and females get official evaluation in France
- * Future use of LD chip, to reduce costs
- * New services coming from common breeds "pipelines"



Conclusion

- * France is small within BS world, but **fully benefits from** international BS cooperation **"Intergenomics"**
- * Genomics are **re-designing** AI breeding programs
- * Size still matters:
 - * the more you genotype, the more you identify extreme sires!
 - * the more data you compile, the more **reliability** you will get



