Instituto Nacional de Investigación Agropecuaria
URUGUAY

# Experiences in the use of genomics in ruminants in Uruguay

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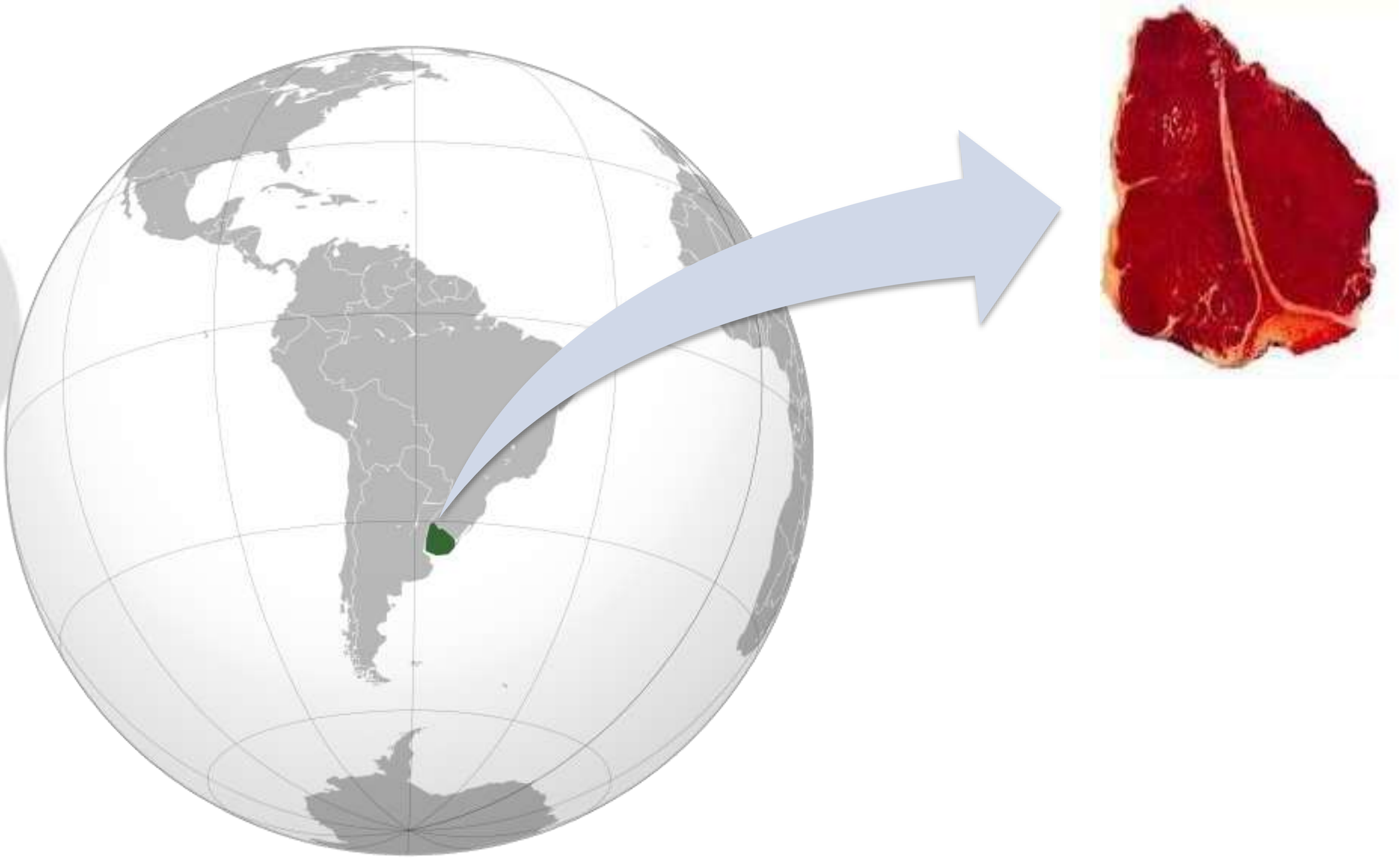
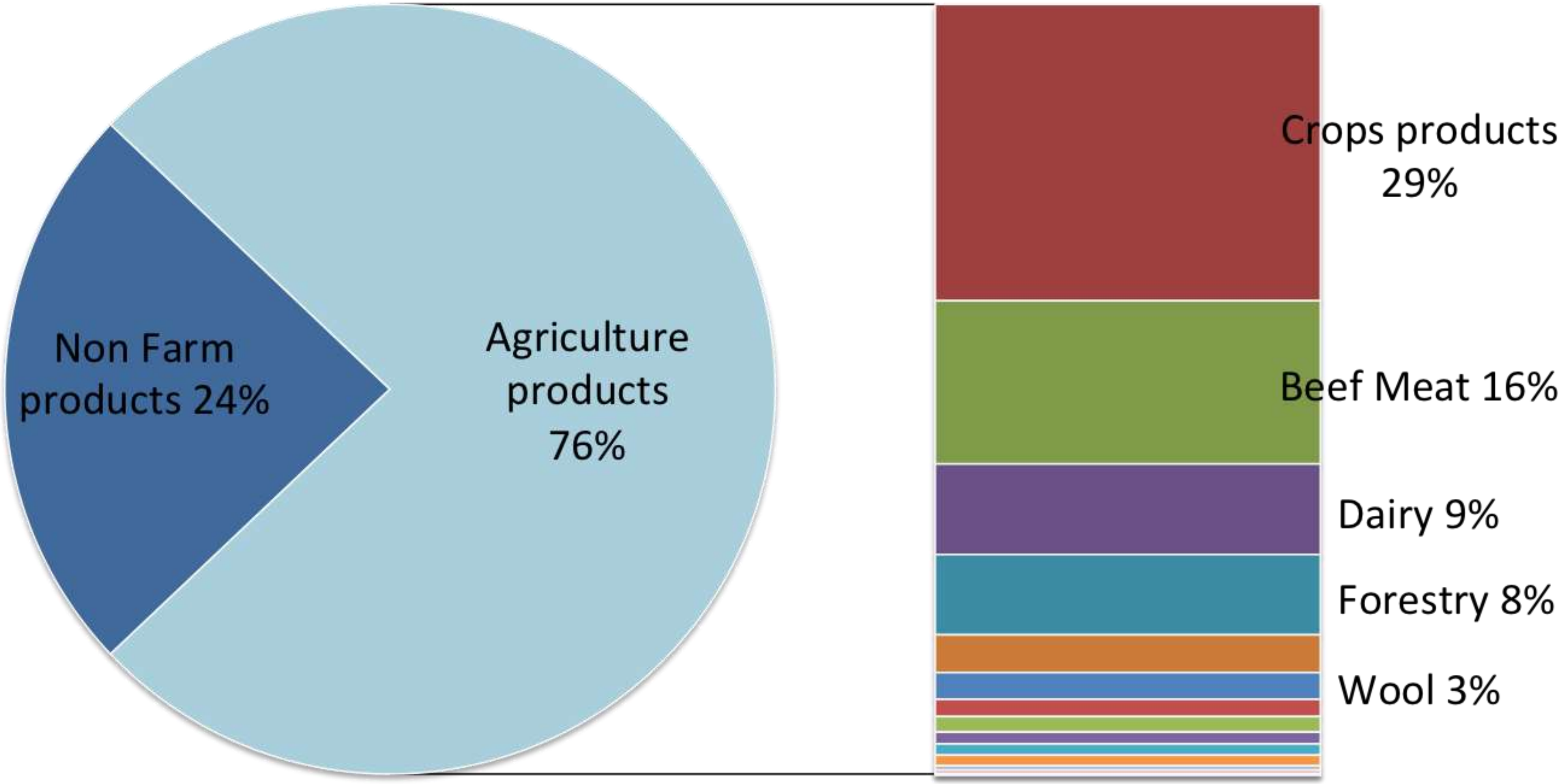
# Uruguay



# Agro-exporting country



DIEA – MGAP 2015

# Livestock production

**Beef cattle**

- 11.8 m
- 1070 k ton meat

**Dairy cattle**

- 770 k animals
- 440 k cows
- 2200 mil lt

**Sheep**

- 7.4 m
- 60 k ton meat
- 30 k ton whool

# Livestock genetic improvement

## National genetic evaluations

- Beef Cattle
  - Hereford
  - Angus
  - Braford
  - Limousine
- Dairy Cattle
  - Holstein
  - Jersey
- Sheep
  - Corriedale
  - Merino
  - Polwarth
  - Merlin
  - Romney Marsh
  - Texel
  - Hampshire Down
  - Ile de France
  - Poll Dorset
  - Highlander

# Animal Genomic DNA Bank
# INIA Las Brujas

# Animal Genomic DNA Bank

- Integrated technology platform to implement genomic and other "omics" research projects
- Base for the generation of training populations for genomic selection in sheep, beef and dairy cattle

# Animal Genomic DNA Bank

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| Breed | Number of samples | Population type |
|---|---|---|
| Merino | ~ 4700 | Stud/Research |
| Corriedale | ~ 3800 | Stud/Research |
| Texel | ~ 800 | Stud |
| Angus | ~ 2000 | Stud |
| Hereford | ~ 4900 | Stud |
| Holando | ~ 2000 | Stud/Commercial |
| Creole | ~ 400 | Research |
| Other Breeds | ~ 2000 | Research |

# “SNP Assisted Breeding” for Sheep extensive systems

# Very Low Density SNP panel: Development

# VLD SNP panel: development

| SNPs | Purpose | reference |
|---|---|---|
| **250** | INIA Parentage preselected (50k) | INIA Project ( + ANII) |
| **69** | ISGC Parentage | Kijas et al., 2012 |
| **2** | Horn/Poll | Dominik et al. 2011; Johnston et al. 2011 |
| **174** | FEC associated (16 from 50k) | INIA Project |
| **7** | Merino Breed specific | INIA Project (QC, population genetics, crossbreeding, prolific, etc.) |
| **5** | Corriedale Breed specific | |

Agreement between

EUREKAGENOMICS

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# Parentage SNPs: Uruguayan panel

| Panel | n | Criteria |
|---|---|---|
| **1** | 83 | Min Nº PE of 0.9999 for Corriedale, Merino and Texel |
| **2** | 96 | P1+7 rare SNP (>0-0.1) and 10 SNP MAF 0.1-0.4 |
| **3** | 141 | P2+ Kijas et al., 2012 (pass QC citeria) |
| **4** | 154 | P3+ FEC (pass QC criteria) |
| **0 Total** | **258** | P4 + others parentage SNP |

| Panel | Corriedale | Merino | Texel |
|---|---|---|---|
| **1** | 0.9999033 | 0.9999099 | 0.9999045 |
| **2** | 0.9999871 | 0.9999961 | 0.9999497 |
| **3** | 0.9999999... | 0.9999999... | 0.9999992 |
| **4** | 0.9999999... | 0.9999999... | 0.9999997 |
| **0 – Total** | **0.9999999...** | **0.9999999...** | **0.9999999...** |

$$P = 1 - 4\sum_{i=1}^{n} p_i^2 + 2\left(\sum_{i=1}^{n} p_i^2\right)^2 + 4\sum_{i=1}^{n} p_i^3 - 3\sum_{i=1}^{n} p_i^4$$

PE: combined exclusion probability according to Jamieson & Taylor, 1997

FMV_2_2011_1_6356

# Merino Breeding Nucleus

## Results Merino Breeding Nucleus (2015)

2 Dic 15: 200 samples sent to USA. (100 lambs, 9 sires, 91 dams)

7 Dic: samples arrived to USA

14 Dic: Affymetrix send genotype data.

16 Dic: Parentage verification and horn/poll

17 Dic: first distribution of ram with DNA parentage verification.

Call rate= 0.9937

13 samples fail (9 in the same plate)

affymetrix

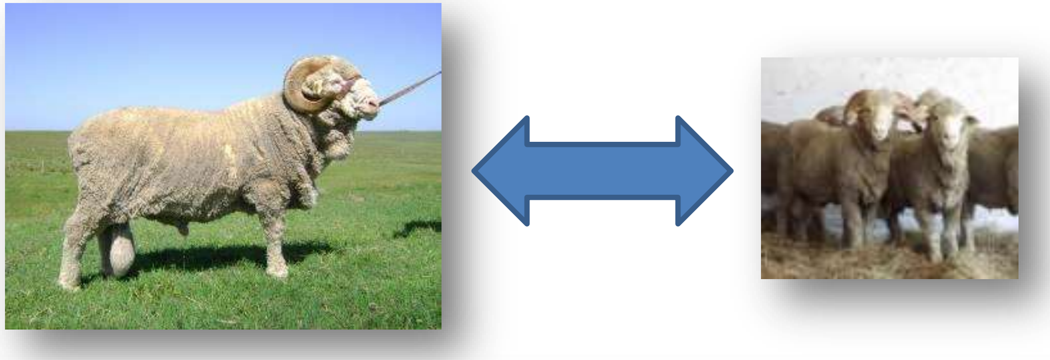
EUREKAGENOMICS.

INIA

# Parentage SNP: Errors of assignments

Parentage assignments (Sire-lamb): % error (Nº of pairs) by breed and stud

| Breed | | A | B | C | D | E | F | G | NUG |
|---|---|---|---|---|---|---|---|---|---|
| **Corriedale** | **% error** | **15.7** | **0.0** | **0.0** | **16.7** | **16.6** | **14.0** | **3.2** | |
| | **n** | 51 | 7 | 28 | 6 | 139 | 43 | 63 | |
| **Merino** | **% error** | **5.0** | **4.9** | **4.8** | **6.3** | **11.0** | **0.0** | **66.7** | **6.3** |
| | **n** | 40 | 41 | 21 | 112 | 73 | 22 | 6 | 223 |



# **Opportunities for the** VLD SNP panel

*cheap sheep chip*

1. Improve genetic gain: parentage verification
2. Increase Ram price by “parentage certified stamp”
3. Official use for pedigree animals (ARU)
4. Increase Ram price by “Poll allele stamp”
5. Reduce cost of labor (parentage assignment in field)

# Hereford Breeding Programme

- **Genetic evaluation system in place**
  - 280 thousands animals in the current database, 350 studs
  - Per year: 10000 new animals of 160 studs

- **Member of the Pan-American genetic evaluation**

- **Twice a year Expected Progeny Differences of breeding animals are published and available for several relevant traits**
  - Birth, weaning, 15-month and 18-month weights
  - Cow adult weight and milk
  - Eye muscle area and fat depth by ultrasound
  - Scrotal circumference
  - Selection index cow-calf operation

# International Hereford Project

- Sociedad Criadores de Hereford del Uruguay
- National Beef Cattle Evaluation Consortium (USA)
- Asociación Rural del Uruguay
- Instituto Nacional de Investigación Agropecuaria

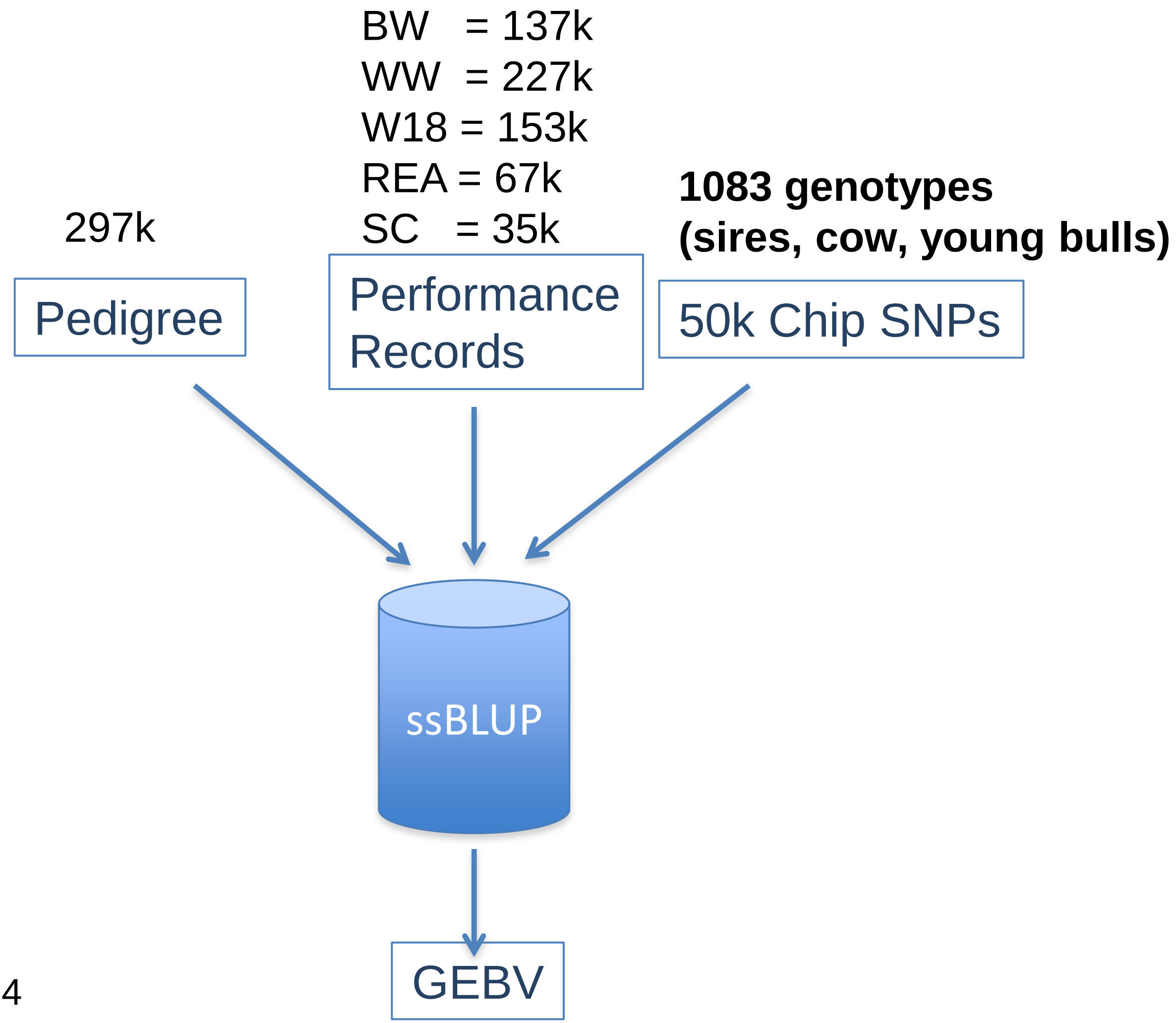
Build a training population for genomic selection in Uruguayan Hereford

Validation of prediction equations from PanAmerican training population

# Uruguayan Hereford Genomic Population

- ~ 1100 Hereford animals (males & females)
- Colaboration:
  - **Hereford breeders**
    - Hair, blood and semen samples from high accuracy sires
  - **16 Hereford Studs**
    - Young bulls from generation 2010 + sires
  - **AI companies**
  - **National Herd-Book (ARU)**
    - Hair samples. Agreement ARU – INIA

# Genomic predictions - Hereford Uruguay
# Single Step GBLUP



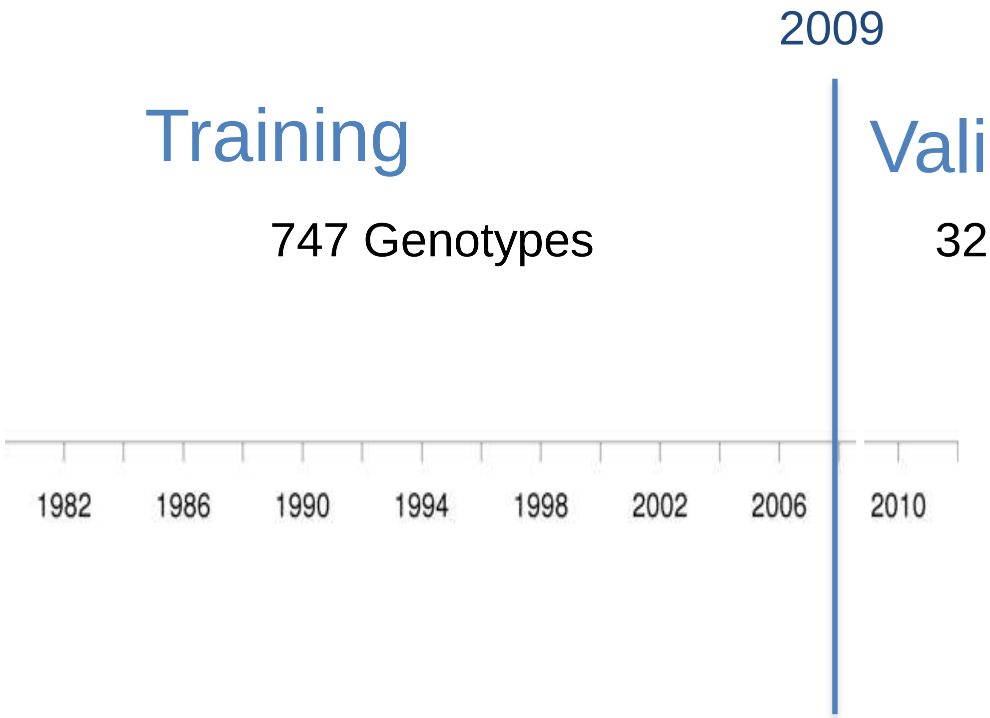
BW = 137k
WW = 227k
W18 = 153k
REA = 67k
SC = 35k

297k

**1083 genotypes**
**(sires, cow, young bulls)**

Aguilar y Ravagnolo 2014

# ssGBLUP Hereford Uruguay
# Cross Validation



## Training

747 Genotypes

## Validation

329 Genotypes

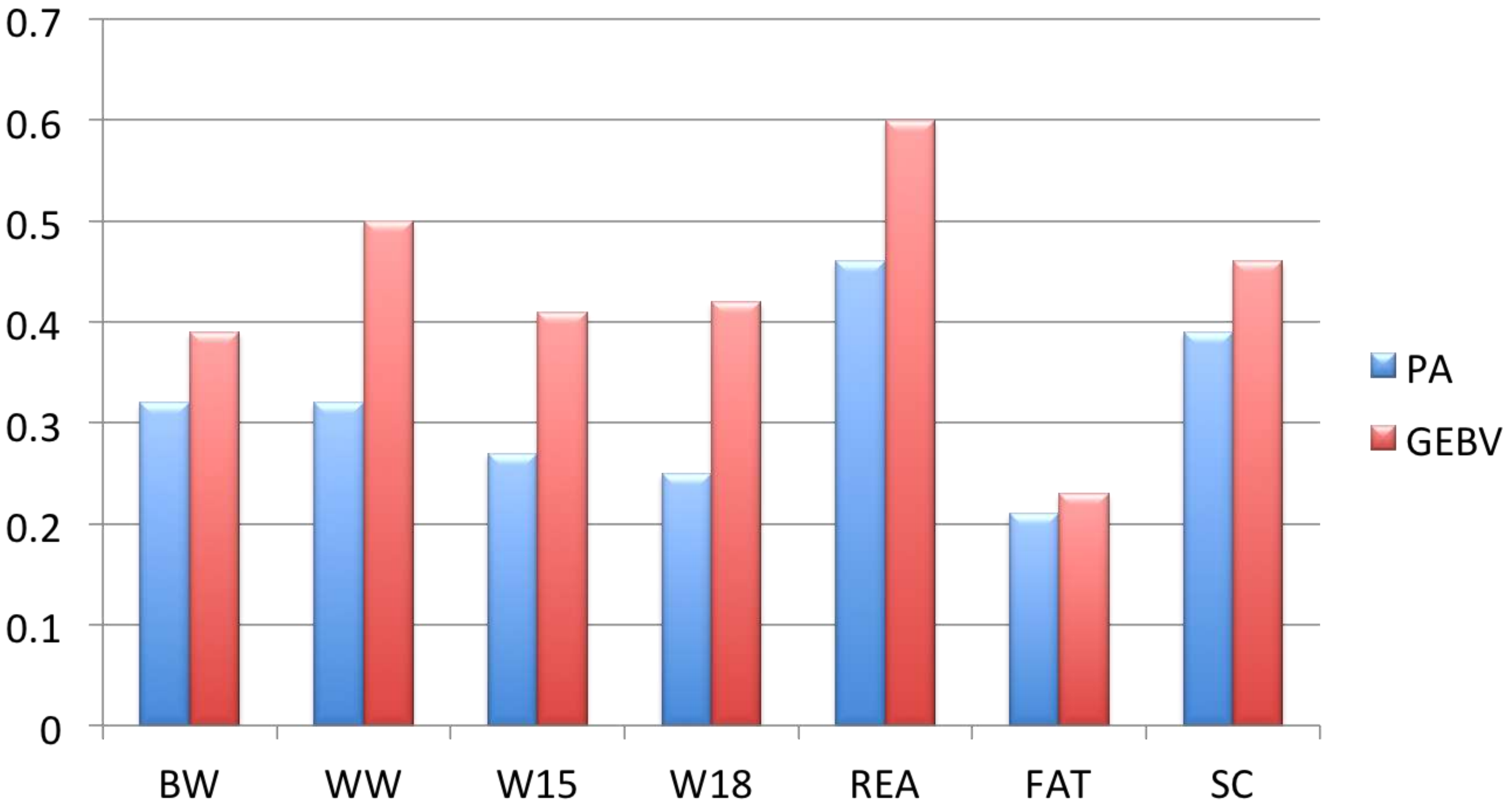
1) Remove Phenotypes
2) Genetic Evaluation
   - Traditional
   - Genomic

3) Correlation with Y

4) ACC = Cor (GEBV,Y) / h

Aguilar y Ravagnolo 2014

# ssGBLUP Hereford Uruguay
# Cross Validation



Aguilar y Ravagnolo 2014

# PanAmerican Genetic Evaluation

- **Official GE-EPDs for Uruguayan Hereford since August 2016**
- **Genomic predictions available for breeders for next evaluation December 2016**
- **Industry adopting the technology**

# Genetic improvement:
# feed efficiency & carcass quality

- **Genetic improvement by “traditional” selection limited because of:**
  - Difficulties and high cost of data recording
  - Longer generation interval (i.e. progeny testing for carcass and meat quality)
  - Low selection intensity due to low number of animals with data for any of these traits

- **Genomics in animal selection**

- **Integration of genomic information into genetic evaluation :**
  - Increase genetic gain by higher accuracy at early ages
  - Animals with EPD estimated using genomic information

- **Building training (reference) populations**

# Enhancing competitiveness of the Uruguayan beef industry by implementing genomic tools to genetically improve feed efficiency and carcass quality of Hereford breed

- Three years project:
  - Jan 2014 – Jan 2017

- Consortium of public and private organizations

- Funding: US$ 2 million
  - 25% Hereford Breeders
  - 35% Other institutions
  - 45% National funding

HEREFORD URUGUAY

Hereford Breeders Association

Rural Association

ASOCIACION RURAL DEL URUGUAY 1871

INIA URUGUAY

National Agriculture Research Institute

Ministry of Agriculture

MINISTERIO DE GANADERÍA AGRICULTURA Y PESCA
REPÚBLICA ORIENTAL DEL URUGUAY

Uruguay inac

National Meat Institute

Biological Research Institute

IIBCE

ANII
AGENCIA NACIONAL
DE INVESTIGACIÓN
E INNOVACIÓN

INIA

# Feed efficiency

| TRAINING POPULATION FEED EFFICIENCY | | YEARS | | |
|---|---|---|---|---|
| ANIMALS | INTAKE TEST PHASES | 2014 | 2015 | 2016 |
| **BULLS** | Adaptation | **Test 1** | **Test 4** | **Test 7** |
| autumn | Warm-up | 50 animals | 49 animals | 45 animals |
| calving | TEST | 11 herds | 11 h | |
| **BULLS** | Adaptation | **Test 2** | **Test 5** | |
| spring | Warm-up | 120 animals | | |
| calving | TEST | 39 herds | | |
| | Adaptation | **Test 3** | T | |
| **STEERS** | Warm-up | 113 animals | | |
| | TEST | 5 herds | | |

626 Hereford animals
Sired by 200 bulls
From 60 breeding herds

- Animal age
- By origin: from at least two sired
- Bulls:
  - ✓ in genetic evaluation
  - ✓ with birth and weaning weights
- Steers:
  - ✓ pedigree sires in genetic evaluation (confirmed by DNA)

**Close to the target of 1000 animals**

**Good representation of herds in genetic evaluation**

**Linked to Hereford population**

# Canada – Uruguay
# Collaborative Project on Feed Efficiency

March 2016

**OBJECTIVES**

International genetic evaluation

Integration training populations

Genomic associations studies

**PRODUCTS**

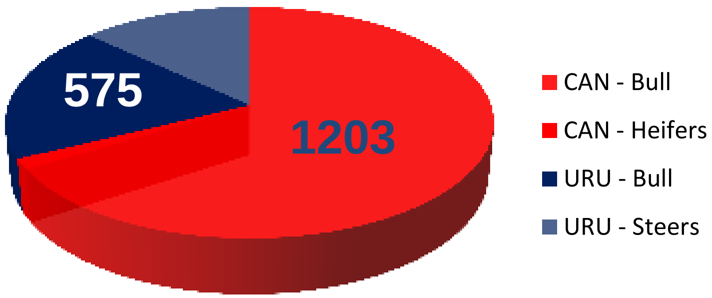
Estimated Progeny Differences

Genomic EPD

Significant genome regions

- **Joint databases**
  - Phenotypic records of purebred animals
    - Similar test trials protocols
  - Pedigree data
    - Unification of databases using international animals ID
    - 4 generations of animal with feed efficiency records
    - ~ 7000 animals (CAN+UY)
    - Need to improve genetic connexion

**Feed efficiency phenotypes**



# Canada – Uruguay
# Collaborative Project on Feed Efficiency

**OBJECTIVES**

International genetic evaluation

Integration training populations

Genomic associations studies

**PRODUCTS**

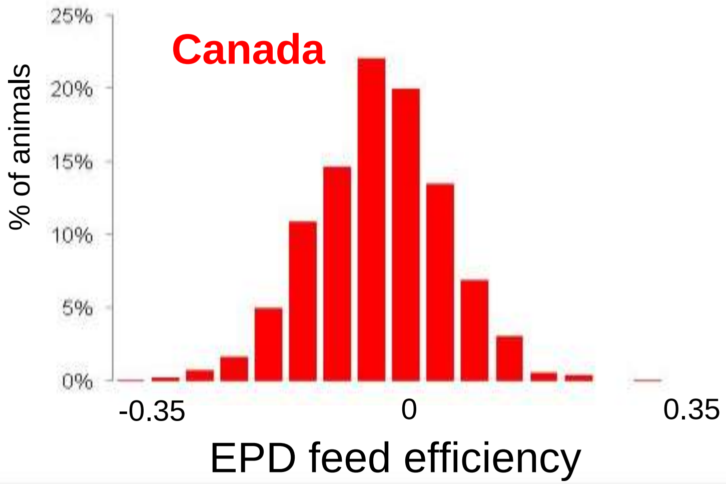
Estimated Progeny Differences

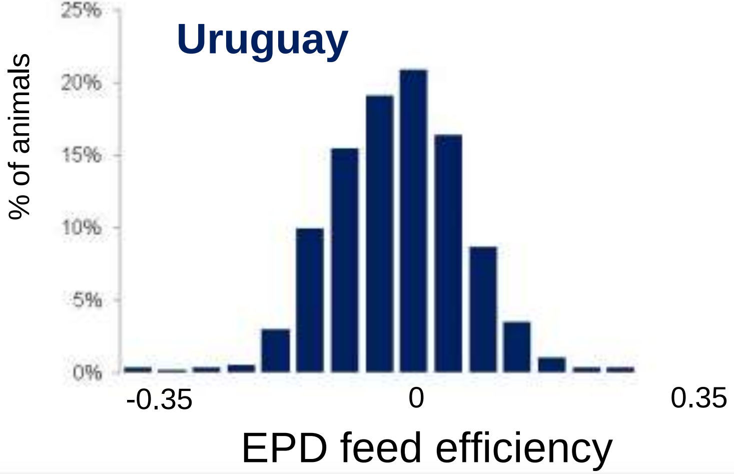
Genomic EPD

Significant genome regions

- **Data analysis**
  - Calculation of residual feed intake (RFI)
  - Estimation of Expected Progeny Differences (EPD)
    - First step: feed efficiency as RFI
    - Larger database: selection index

**Published in August 2016**





# Canada – Uruguay
# Collaborative Project on Feed Efficiency

**OBJECTIVES**

International genetic evaluation

Integration training populations

Genomic associations studies

**PRODUCTS**

Estimated Progeny Differences

*Genomic EPD*

Significant genome regions

- **Integration of training populations (genomic data)**
  - URUGUAY: 1000 bulls and steers with phenot
    + 1100 genotypes with genetic ev
  - CANADA: 400 bulls (700k SNPs) + 1900 bulls an

2017

**Publishing genomic EPDs**
**4000 CAN & UY**
**genotyped animals**

## GENOMIC EPD

- Estimated with larger training populations
  - ✓ **Higher accuracies**
  - ✓ **Stronger connectivity** between populations
- Larger number of animals with EPDs and comparable
  - ✓ **High selection intensity**

# Training population

# carcass and meat quality

| TRAINING POPULATION FEED EFFICIENCY | |
|---|---|
| ANIMALS | INTAKE TEST PHASES |
| BULLS autumn calving | Adaptation |
| | Warm-up |
| | TEST |
| BULLS spring calving | Adaptation |
| | Warm-up |
| | TEST |
| STEERS | Adaptation |
| | Warm-up |
| | TEST |

- – **Steers after feed efficiency evaluation are finished on grass (+concentrate).**
- **Carcass traits:**
  - – hot and cold carcass weight,
  - – conformation and fatness grades,
  - – quarters, primal and cuts weights.
- **Meat quality:**
  - – meat and fat colour,
  - – intramuscular fat percentage,
  - – pH, tenderness (Warner Braztler), and fatty acid profile

# Training population

# carcass and meat quality

| TRAINING POPULATION FEED EFFICIENCY | |
|---|---|
| ANIMALS | INTAKE TEST PHASES |
| **BULLS** | Adaptation |
| autumn | Warm-up |
| calving | TEST |
| **BULLS** | Adaptation |
| spring | Warm-up |
| calving | TEST |
| **STEERS** | Adaptation |
| | Warm-up |
| | TEST |

+

**Research project**

- Steers with know paternity
- Progeny from Sires with EPD in National Genetic Evaluation
- Similar slaughter protocols and measures

**TRAINING POPULATION**
so far:
- 755 steers
- Genotypes
- 80k / 700k SNP

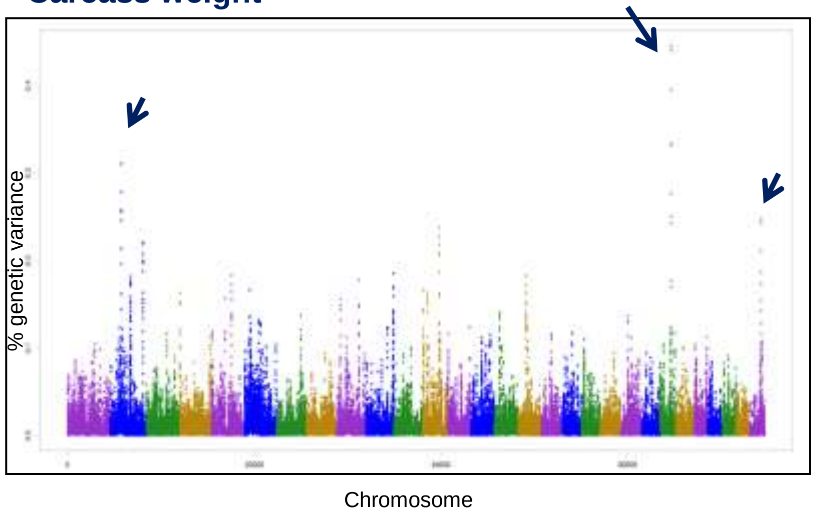
# Training population carcass and meat quality

- **Target number for 2017:**
  - 350 + 650 steers (other research projects)
- **Aims:**
  - Impact on accuracies of genomic EPDs
  - Identification of more relevant genomic regions
    - Better understanding of genetics of traits
    - Identification of markers that explain more of genetic variance
      - Smaller SNP panels (lower genotyping cost)

GBLUP 4-fold cross-validation

| TRAIT | n | Accuracy |
|---|---|---|
| Carcass weight | 510 | 0.39 |
| Pistola cut | 510 | 0.36 |
| Rump and loin | 509 | 0.34 |
| IMF | 486 | 0.30 |
| Tenderness | 506 | 0.32 |

**Carcass weight**



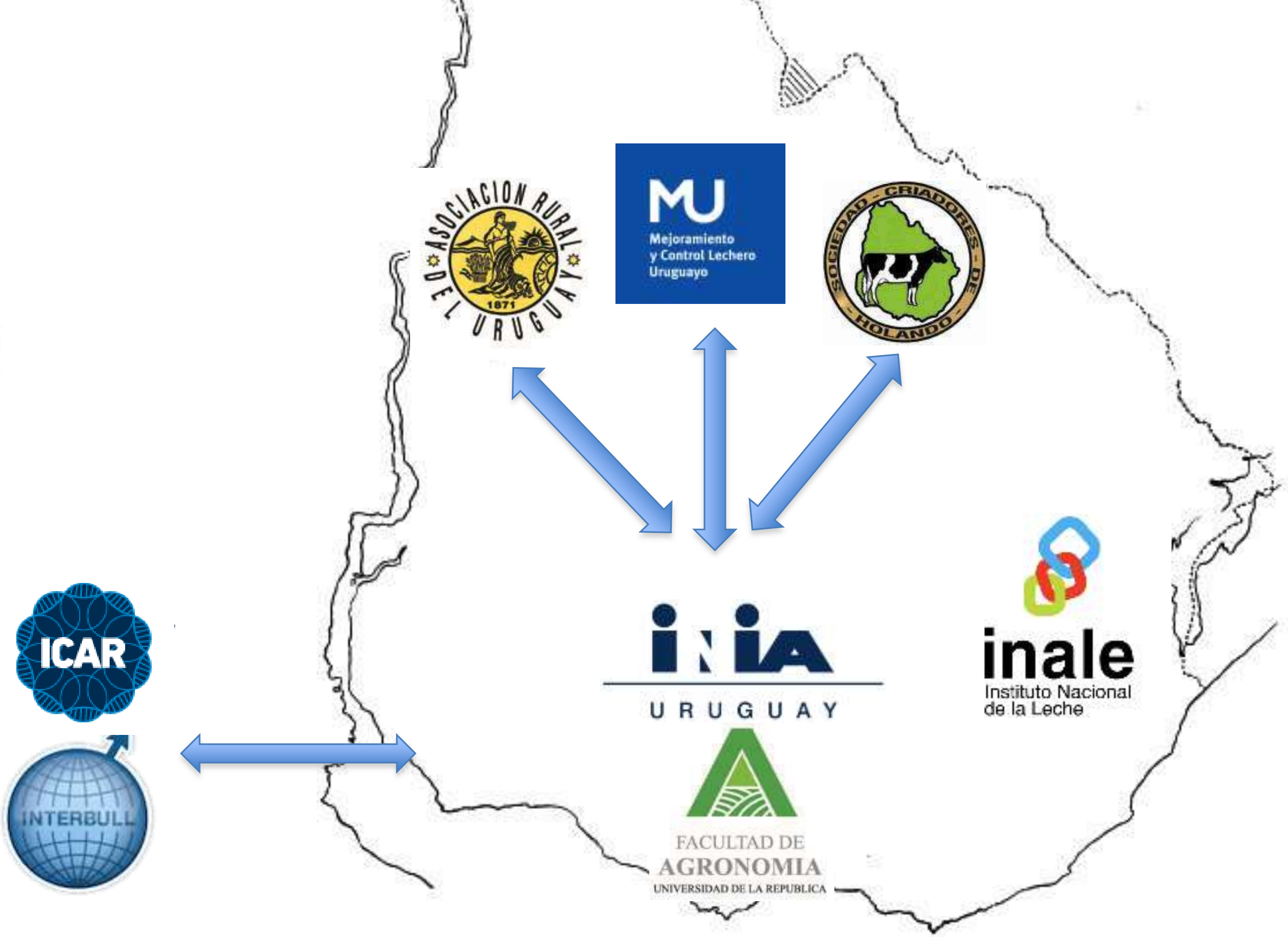
# Angus breeding programme

- **Genetic evaluation system in place**
  - 120000 animals in database
  - 140 herds
  - 8000 new animals by year

- **Expected Progeny Differences of breeding animals are published and available for several relevant traits**
  - Birth, weaning and 18-month weights
  - Cow adult weight and milk
  - Eye muscle area, fat depth and intramuscular fat by ultrasound
  - Scrotal circumference

**uilding training populations to implement genomic election**

# National Dairy Genetic Evaluation



# History National Genetic Evalution

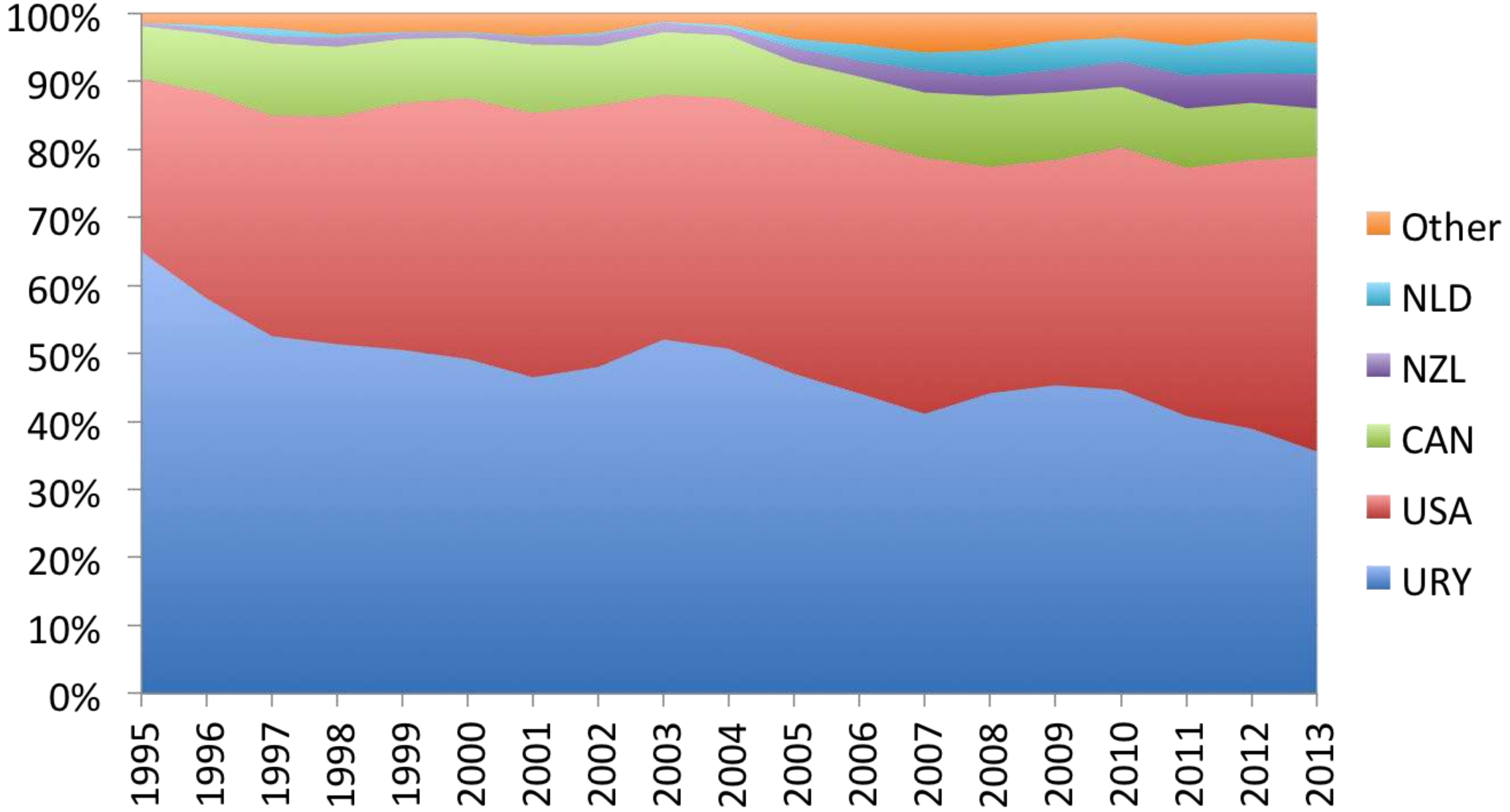
- 1994 – Productivity: Milk production (Fat)
- 1995 – Type traits
- 2003 – Productivity: fat and protein
- 2004 – Linear type traits.
- 2012
  - Selection index: IEP
  - Interbull - MACE evaluations
- 2015
  - Female fertility trait
  - Test Day Model
- 2016
  - Update IEP index (fertility)

# Genetic evaluation in numbers

- **> 6.3 M** test day records
- **~ 340000** cows with records
- **~ 7400** sires with daughter (63 % domestic)

- **925** sires used by Interbull with daughter information in URY
- **85** sires with daughter information only from URY

# Cow's sire origin



# Incorporation of genomic information in the Holstein national genetic evaluation

- Uruguay current situation
  - Need several years to obtain accurate genetic merit of sires (7-8 years)
  - Domestic sires (~ 30%) generally selected from parental index
  - Imported bulls: Interbull (MACE,GMACE)
  - but domestic bulls potential use genomic

# Uruguayan Holstein Dairy Genetic Evaluation

- Prediction of genetic merit in Uruguayan system of production
- More than 20 years of national genetic evaluation
  - Domestic and imported parents with daughters in Uruguayans herds
  - Production and linear traits

- Base for:
  - Integration into international genetic evaluation
  - Training population for genomic selection

# Training population

- Proven sires (domestic & imported)
  - limited availability of semen from historical parents
- Most recent sires
  - AI companies and breeders studs
- National Herd-Book (ARU) hair samples from parentage test
- Cows from stud and commercial herds

# Training population so far

DNA / Hair samples

- **1277** animals from genetic evaluation
  - **1125** females
  - **152** sires with daughter
    - **76** domestic

- Exploring international exchange (ARG, IRL, BRA, BEL, ... )

# In summary

- National genetic evaluation systems in place
- Integration of genomic information into genetic evaluations and delivering genomic proofs in some breeds
- Building training populations for genomic selection
- Undergoing development of genomic EPD for feed efficiency in beef cattle
- Expanding training population for carcass and meat quality traits

Sociedad Criadores Merino Australiano del Uruguay

Sociedad de Criadores Angus Uruguay

Secretariado Uruguayo de la Lana
SUL

SAC

inale
Instituto Nacional de la Leche

CORRIEDALE
La Raza más Completa

CORRIEDALE
La Raza más Completa

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Thank you

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