



**Parco
Tecnologico
Padano**

Entrepreneurial research in ag-biotech

Next generation European system for cattle improvement and management

Gene 2 Farm

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- **Theme 2: Food, Agriculture, Fisheries and Biotechnology**
- Work Programme Topic: **KBBE.2011.1.3-06: Development of next generation European system for cattle evaluation (especially **DOUBLE PURPOSE** cattle -> **Non Holstein breeds**)**
- Funding Scheme: **Research for the benefit of SMEs**



Gene2Farm Overview

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- Addressing the needs of the cattle industry, in particular of the SMEs and end users, for an accessible, adaptable and reliable system to apply the new genomic knowledge to underpin SUSTAINABILITY AND PROFITABILITY OF EUROPEAN CATTLE FARMING.
- Carrying out a comprehensive programme of work from STATISTICAL THEORY DEVELOPMENT, through genome sequencing, to address new phenotyping approaches and the construction of tools, that will be validated in conjunction with SMEs and industry partners.
- OPTIMIZATION AND CUSTOMIZATION GENOMIC SELECTION, BREEDING AND POPULATION MANAGEMENT AND BETWEEN BREED PREDICTIONS.
- GENOME SEQUENCING
 - key animals and exchange data with other international projects to create the most comprehensive bovine genome sequence database.
- EXTENDED PHENOTIPIC DATA COLLECTION
 - Exploring opportunities for extended phenotypic collection, including the **use of automated on farm systems** and will develop standardisation protocols that, in consultation with ICAR, could be used by the industry for data collection and management.
- EDUCATION & TRAINING
 - Finally a dissemination programme will ensure that training needs of the industry are served from an entry level training programme for farmers to **advanced summer schools** for the SMEs and expert user community.



Gene2Farm Objectives

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- to derive complete genome information to understand genome structure and to design high and low density genotyping panels.
- to develop the tools to impute higher density genome information from lower density genotype data and to make exchange information easier.
- to address the needs for measuring a wider range of biological variables underlying important commercial traits, in order to provide data on additional important traits for use in selection.
- to develop appropriate statistical models and applications for using the genomic and phenotypic information in order to optimise and customise genetic selection strategies.
- to disseminate the information to the SMEs, the wider cattle breeding industry and to end users.



Research for the benefit of SMEs

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9 SME

2.	ZuchtData	ZD	Austria
3.	GENO Breeding and A.I. Association	Geno	Norway
4.	Swissherdbook cooperative Zollikofen	SHB	Switzerland
5.	Associazione Nazionale Allevatori Bovini della Razza Bruna	ANARB	Italy
6.	Swiss Brown Cattle Breeders Federation	SBZV	Switzerland
7.	Czech Simmental Breeders Association	CESTR	Czech Republic
8.	Associazione Nazionale Allevatori Bovini di Razza Pezzata Rossa Italiana	ANAPRI	Italy
9.	English Guernsey Cattle Society	EGCS	UK
10.	Federación de asociaciones de Ganado Selecton	FEAGAS	Spain

3 Other

11.	European Brown Swiss Cattle Federation	EBSF	Italy
12	European Simmental Cattle Federation	EVF	Germany

13.	Biosciences Network Limited	BKTN	UK
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6 RTD

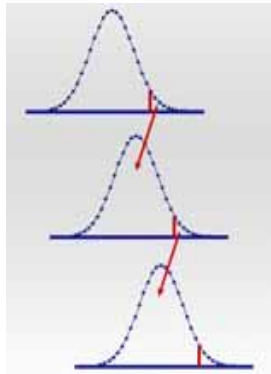
1.	Parco Tecnologico Padano	FPTP	Italy
14.	Norwegian University of Life Sciences	UMB	Norway
15.	Roslin Institute, University of Edinburgh	UEDIN	UK
16.	Wroclaw University of Environmental and Life Sciences	UPWROC	Poland
17.	Universidad of Zaragoza	UNIZAR	Spain
18.	Aristotelio Panepistimio Thessalonikis	AUTH	Greece



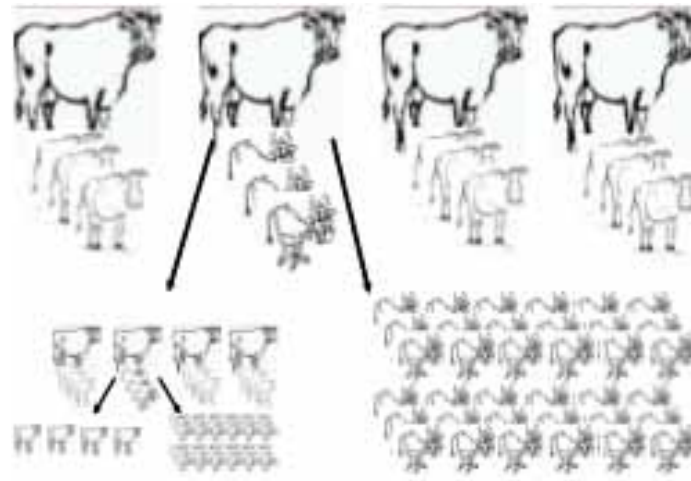
Phenotypic to Genomic Selection

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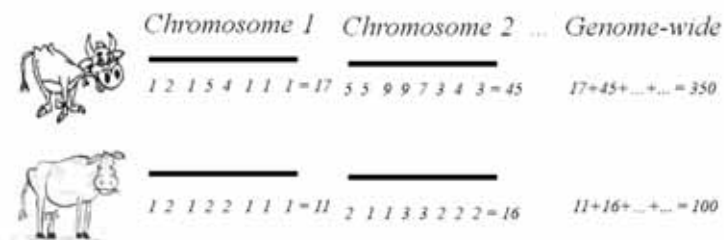
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➤ Phenotypic selection (until '80s)



➤ Progeny testing ('80s → 2010)



➤ gEBVs (since 2010 -> new era)



Project Targets

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↗ Use of genomic information (non only EBV):

- ↗ Mate selection
- ↗ Inbreeding control
- ↗ Applications in small populations

↗ Novel phenotypes

- ↗ Better prediction of the biology
- ↗ Additional commercially important traits

↗ Genomic information

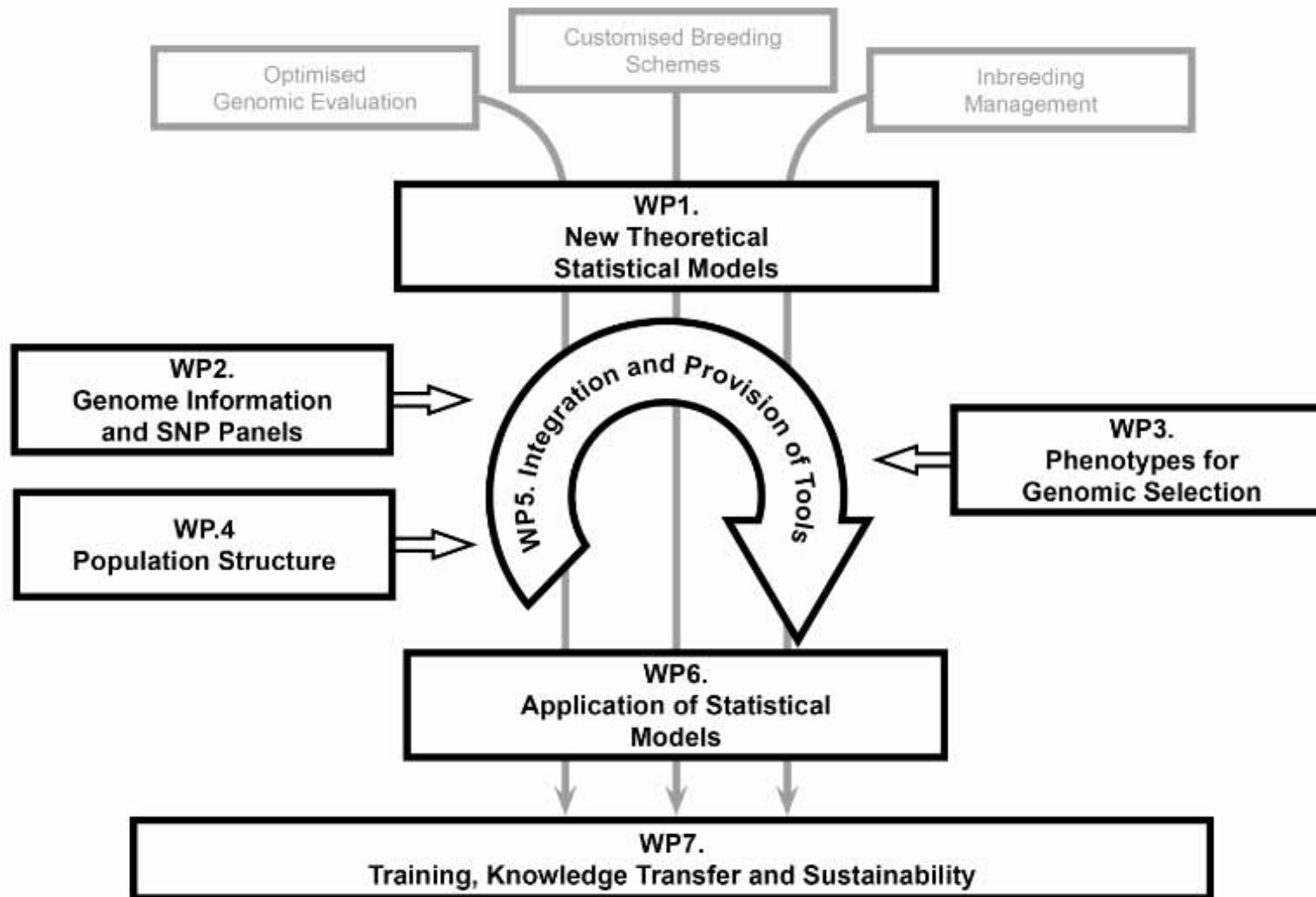
- ↗ Optimised SNP panels
- ↗ Genotyping by sequencing
- ↗ Epigenetics



Project Overview

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Project Interactions

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↗ Advisory board

↗ Curt van Tassell

USDA

↗ Filippo Miglior

Canadian Dairy Network

↗ Ben Hayes
Industries

Department of Primary

↗ Daniel Gianola

Uni Wisconsin

↗ Organisations eg:

↗ Fabre /Effab

↗ EAAP

↗ ICAR / INTERBULL

↗ Projects eg:

↗ 1000 bull genomes

↗ Other national and International projects



WPs and Leaders

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➤ WP1 Novel statistical models, for genome selection, software development and testing

WP Leader Theo Meuwissen

➤ WP2 Genome information and SNP Panels

WP Leader Giulietta Minozzi

➤ WP3 Phenotypes for cattle improvement and management

WP Leader Giorgios Banos

➤ WP4 Population structure

WP Leader Miguel Toro

➤ WP 5 Integration and provision of tools

WP Leader Alessandra Stella

➤ WP 6 Application of statistical models to different situations in specific breeds

WP Leader Trygve Roger Solberg

➤ WP7 Training, Knowledge Transfer and Sustainability

WP Leader Huw Jones



WP3: Phenotypes for cattle improvement and management (Giorgios Banos)

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↗ Task 3.1. Assessment of current practices and classification of needs

↗ Task Leader: Hermann Schwarzenbacher (ZD) Month 0-12

↗ Task 3.2. On-farm recording.

↗ Task Leader: Trygve Roger Solberg (GENO) Month 3-13

↗ Task 3.3. Novel Phenotype collection approaches.

↗ Task Leader: Alessandra Stella (FPTP) Month 8-33

↗ Task 3.4. Beef cattle data recording at the abattoir.

↗ Task Leader: Daniele Vicario (ANAPRI) Month 11-33

↗ Task 3.5. Standardisation procedures of traits measured across different breeds

↗ Task Leader: Enrico Santus (ANARB) Month 18-33

↗ Task 3.6. Recommendations for large-scale application.

↗ Task Leader: Georgios Banos (AUTH) Month 32-48



Meetings

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➤ KO Meeting : Lodi (ITALY) February 2012

➤ Cork, IRELAND - May 2012

➤ Jointly to annual ICAR/INTERBULL meeting

➤ Ski, NORWAY - GENO headquarter - October 2012



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Gene **2** Farm

<http://155.253.6.233/gene2farm/>

(Web site under construction)

Projected start date

1st January 2012

End

31st December 2016

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