Pitfalls and opportunities of genetic and genomic evaluation in the Buffalo species: experiences from Italy

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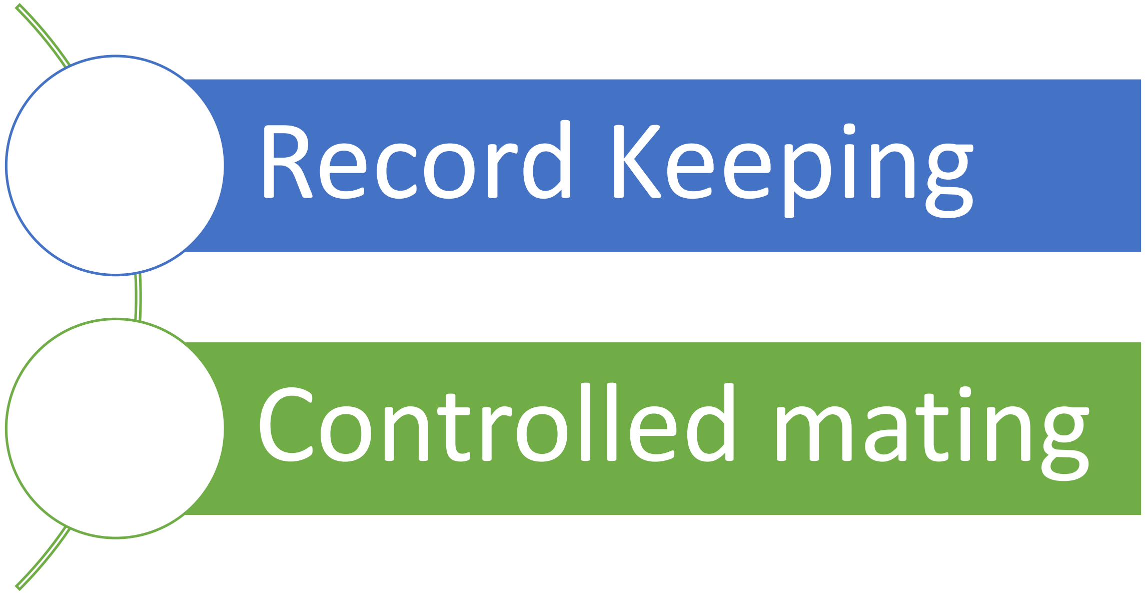
Background

Sir Robert Bakewell



Record Keeping

Controlled mating

modern breeding strategies

Experiences in the domestic river buffalo

Background

- World Buffalo population :
  - > 234 million individuals
  - ~ 15 % of total milk production
- **Italy**:
  - > 90 % of the European population
  - Large census increase over the last 10 years (Mozzarella di Bufala Campana cheese)
  - ANASB data base (2020):
    - > 35k lactating buffaloes officially registered
    - > 650k lactation records
    - > 10000 type traits evaluations

Background

- Late 1990's:
  - first selection scheme based on a BLUP animal model
  - main breeding objectives = kg of milk and kg of Mozzarella (PKM)
  - Aprox 18 male calves/year

- 2017:
  - New breeding objectives (milk contents, udder morphology and feet and legs
  - New selection Index (IBMI)

- Artificial Insemination:
  - still moderate (around 30-40%)
  - additional problems in developing an accurate BLUP evaluation

Objective

- The aim of this study was to present:

1. methodological approaches which have been already implemented in the BLUP evaluation of the Italian Mediterranean Buffalo (BMI)

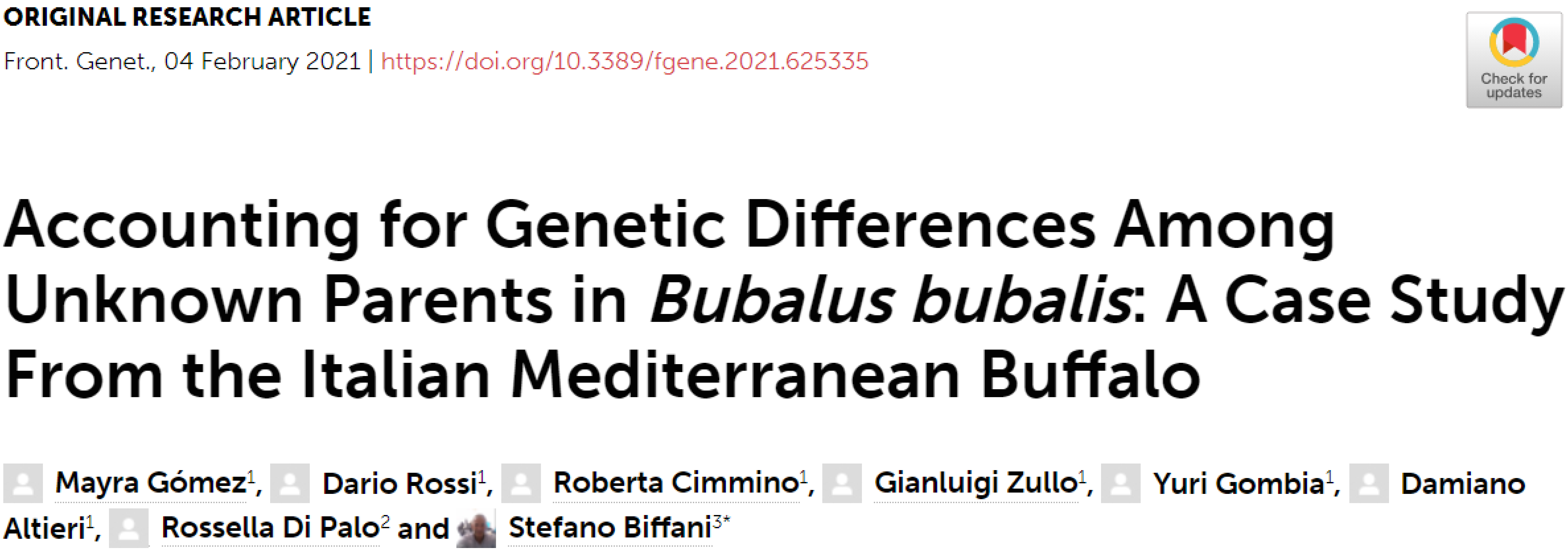
2. results of the application of ssGBLUP in the BMI

1: On the use of genetic groups

- natural mating still common in buffalo
  - Incomplete pedigree information
    - bias in the prediction of both variance component (VC) and EBV

- Westell et al (1988): use genetic groups!

1: On the use of genetic groups



ORIGINAL RESEARCH ARTICLE

Front. Genet., 04 February 2021 | https://doi.org/10.3389/fgene.2021.625335

Check for updates

Accounting for Genetic Differences Among Unknown Parents in *Bubalus bubalis*: A Case Study From the Italian Mediterranean Buffalo

Mayra Gómez[1], Dario Rossi[1], Roberta Cimmino[1], Gianluigi Zullo[1], Yuri Gombia[1], Damiano Altieri[1], Rossella Di Palo[2] and Stefano Biffani[3]*

1: On the use of genetic groups

- Data:
  - 7,714 buffalo cows (DNA tested) plus a pedigree file including 18,831 individuals
  - 5 composite traits + 10 linear traits

- Methods:
  - Step 1: VC & BV using the official corrected pedigree
  - Step 2: VC & BV using 4 “modified” pedigrees
    - 2 different proportion of missing genealogies (30 or 60% of buffalo with records)
    - 2 different grouping strategies, year of birth (Y30/Y60) or genetic clustering (GC30, GC60)

1: On the use of genetic groups

- Results:
  - VC & h2: largest effect for Udder Teat and Body Depth when 60% pedigree is missing and a genetic clustering based on pedigree is used to set up genetic groups

  - Buffalo cows with record:

average correlation across traits from different scenarios	Y30	GC30	Y60	CG60
	0.91	0.88	0.84	0.79

  - AI bulls:

average correlation across traits from different scenarios	Y30	GC30	Y60	CG60
	0.89	0.92	0.76	0.81

2: on the use of ssGBLUP

Availability of a medium density (90k) SNP chip + Single Step G Blup approach

Taylor & Francis
Taylor & Francis Group

Italian Journal of Animal Science

ISSN: (Print) (Online) Journal homepage: https://www.tandfonline.com/loi/tjas20

Genomic investigation of milk production in Italian buffalo

Alberto Cesarani, Stefano Biffani, Andre Garcia, Daniela Lourenco, Giacomo Bertolini, Gianluca Neglia, Ignacy Misztal & Nicolo Pietro Paolo Macciotta

To cite this article: Alberto Cesarani, Stefano Biffani, Andre Garcia, Daniela Lourenco, Giacomo Bertolini, Gianluca Neglia, Ignacy Misztal & Nicolo Pietro Paolo Macciotta (2021) Genomic investigation of milk production in Italian buffalo, Italian Journal of Animal Science, 20:1, 539-547, DOI: 10.1080/1828051X.2021.1902404

2: on the use of ssGBLUP

- Data:
  - 80.147 test-day (Milk, fat & protein yields)
  - 4127 buffalo cows
  - 498 genotypes (463 + 35 bulls)
  - 7730 individuals in the pedigree

2: on the use of ssGBLUP

- Model:
  - 3-trait repeatability animal model
  - pedigree-based (BLUP) vs single step genomic BLUP (ssGBLUP)
  - 5 scenarios
    - A = genotypes available only for 35 bulls;
    - B = genotypes available only for the 50 candidates;
    - C = genotypes available for 50 candidates + 35 bulls;
    - D = genotypes available for 463 cows
    - E = genotypes available for 463 cows + 35 bulls.
  - Validation by LR method

2: on the use of ssGBLUP

- Results:
  - Genetic parameters:

	MY	FY	PY
BLUP	0.25 ± 0.02	0.16 ± 0.01	0.25 ± 0.01
ssGBLUP	0.23 ± 0.01	0.15 ± 0.01	0.23 ± 0.01

  - Candidate cows: correlations between breeding values

MY	FY	PY
0.96	0.95	0.95

2: on the use of ssGBLUP

- Results:

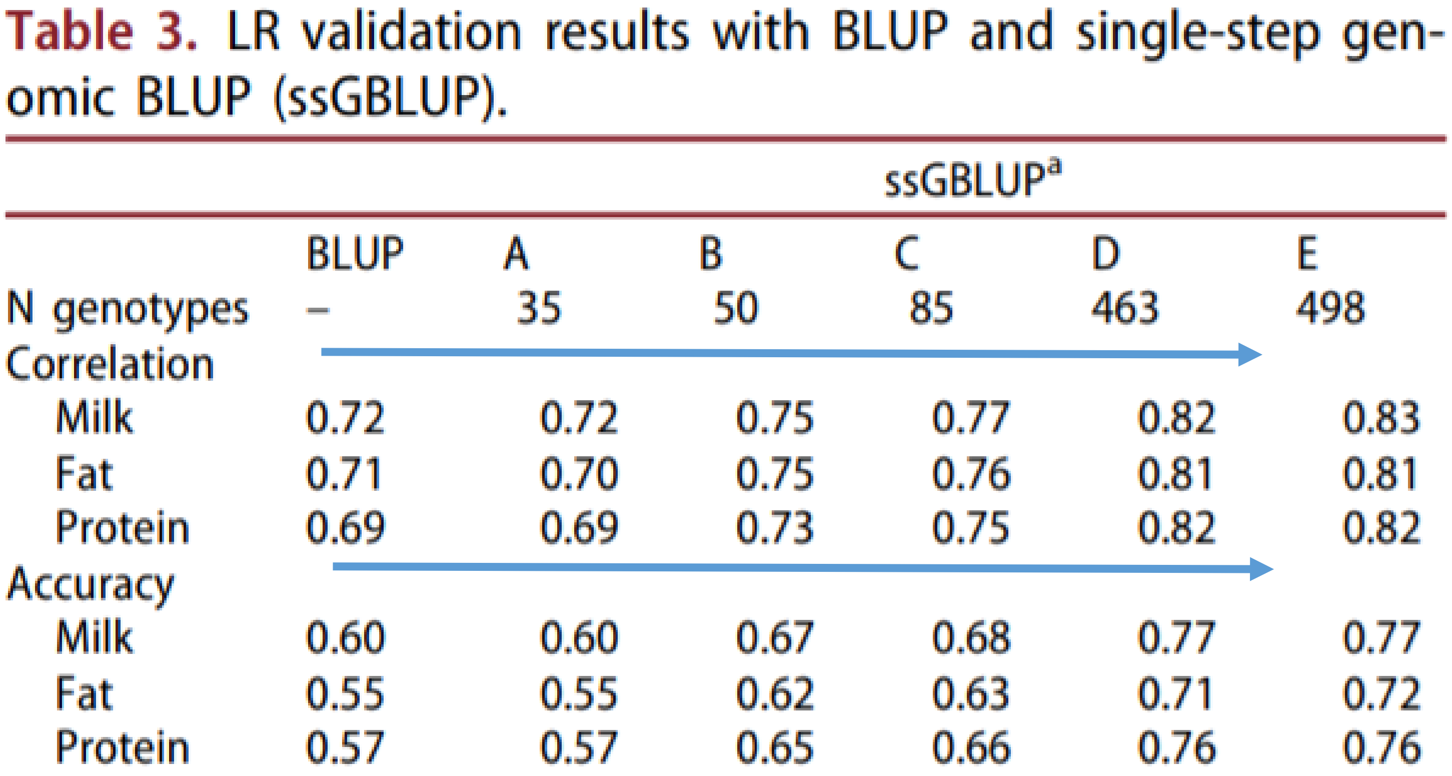


Table 3. LR validation results with BLUP and single-step genomic BLUP (ssGBLUP).

		ssGBLUP[a]				
	BLUP	A	B	C	D	E
N genotypes	–	35	50	85	463	498
Correlation						
Milk	0.72	0.72	0.75	0.77	0.82	0.83
Fat	0.71	0.70	0.75	0.76	0.81	0.81
Protein	0.69	0.69	0.73	0.75	0.82	0.82
Accuracy						
Milk	0.60	0.60	0.67	0.68	0.77	0.77
Fat	0.55	0.55	0.62	0.63	0.71	0.72
Protein	0.57	0.57	0.65	0.66	0.76	0.76

Final remarks

- **well-known** methodologies can be inplemented to cope with missing pedigree even in the Buffalo species
- Interesting results from **ssGBLUP** application, especially as regards the inclusion of genotypes for females.

Thank you for the attention