

The application of several genomic models for the analysis of small holder dairy cattle data

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Background of Data Analyzed

Data for the study generated by the African Dairy Genetic Gains (**ADGG**) Project

Platform for **ADGG** is a multi-country, multi-institution ILRI-led pioneering proof of concept which is:

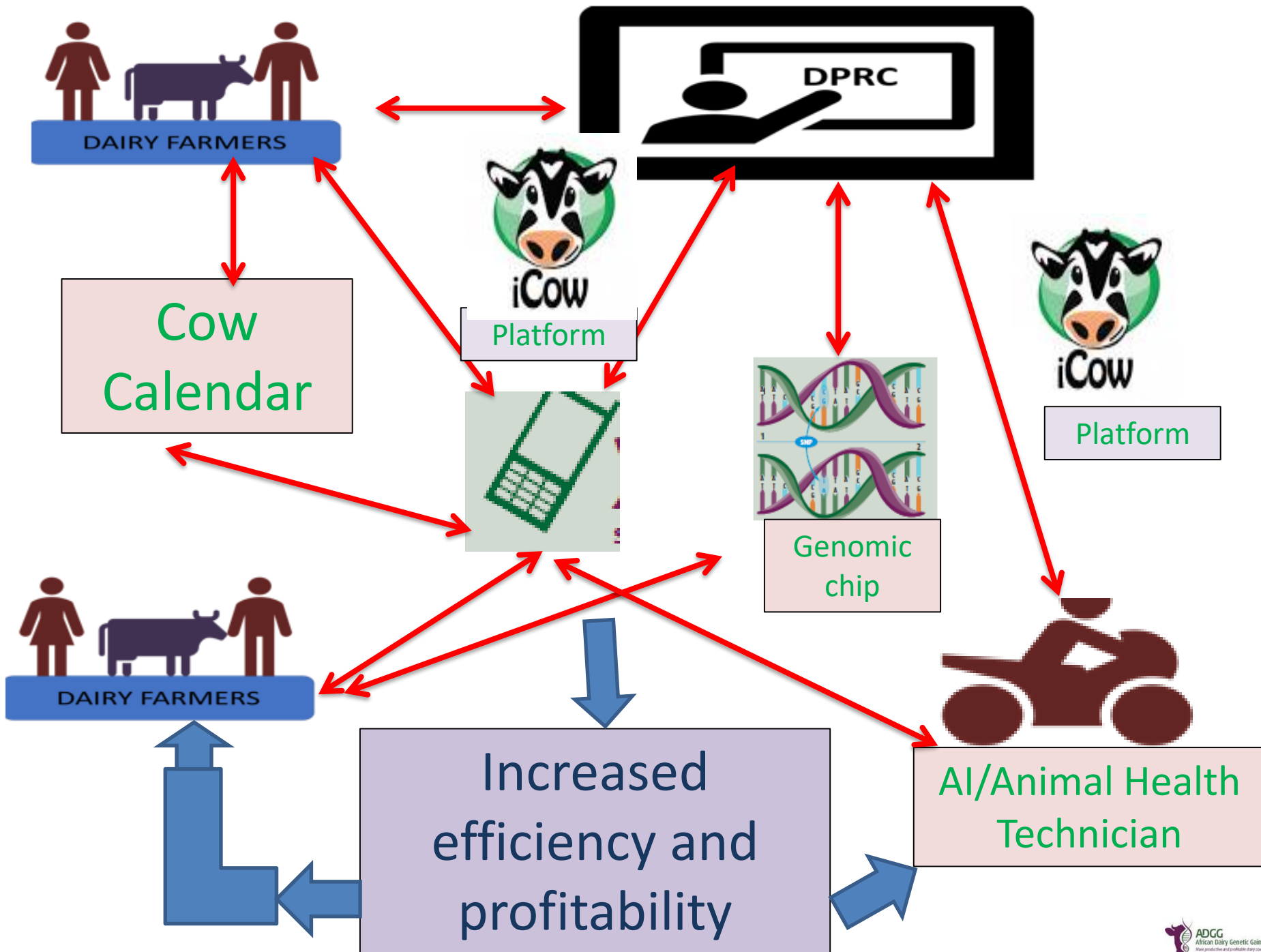
developing and testing a multi-country genetic gains platform that uses on-farm performance information and basic genomic data for identifying and proving superior crossbred bulls for AI delivery and planned natural mating for the benefit of smallholder farmers in Africa



ADGG: Approach and Objectives

Innovative application of existing & emerging technologies

1. To establish National Dairy Performance Recording Centers (**DPRCs**) for herd and cow data collection, synthesis, genetic evaluation and timely farmer-feedbacks
2. To develop & pilot an ICT platform (**FFIP**) to capture herd, cow level & other related data & link it to **DPRCs** (*feeds back key related herd/cow summaries, dairy extension & market info. etc.*).
3. To develop low density genomic chip for breed composition determination & related bull certification systems for crossbred bulls



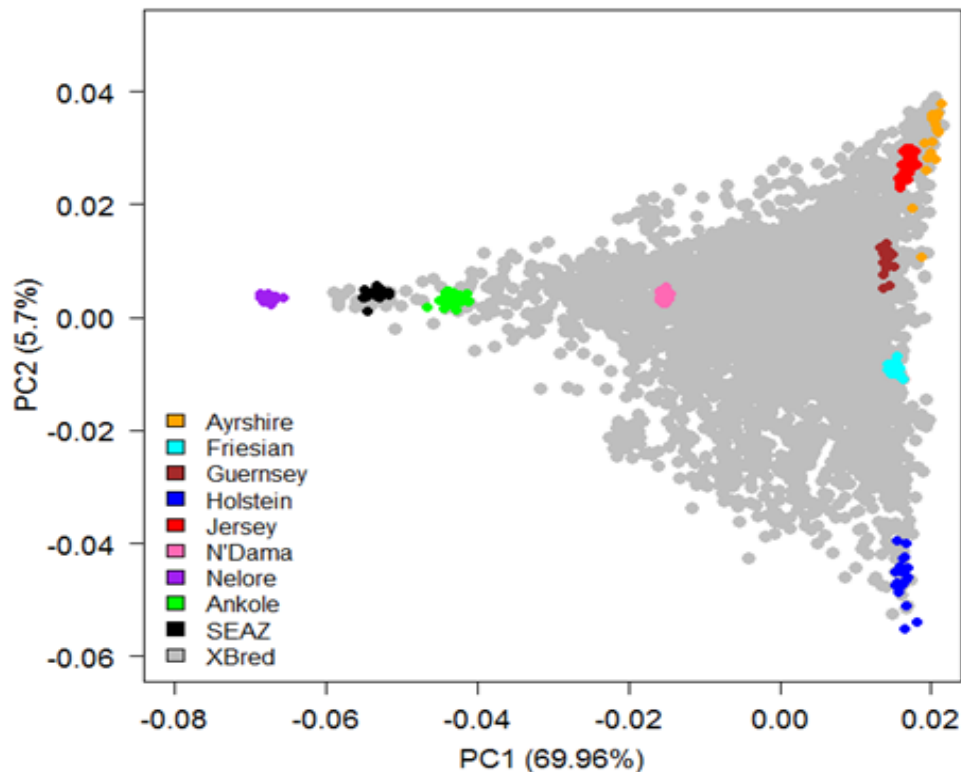
Genotyping strategy

- GeneSeek Genomic Profiler (GGP) Bovine 50K used for genotyping:
 - 47843 SNPs returned
 - About 1500 considered to have private content and not distributed
- About 5600 animals genotyped from Tanzania using hair samples
- About 6500 Hair samples collected in Ethiopia
- After QA, 40581 SNPs remained and these were imputed to HD

PCA

First 3 PCs explain 69.96, 5.7 and 2.71 % of the genetic variance

First PC separates exotic dairy from Nelore, with N'Dama about half way between the two major Taurus groups



Average breed proportions of 4614 Tanzanian crossbred samples

	Dairy	Ayrshire	Friesian	Guernsey	Holstein	Jersey	N'Dama	Nelore
Average	0.785	0.176	0.296	0.089	0.133	0.091	0.04	0.176
SD	0.171	0.173	0.196	0.111	0.177	0.117	0.032	0.143
MAX	0.99998 1	0.99994	0.99994	0.985	0.991	0.99994	0.295	0.902
MIN	0.00005	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001

Performance data

- Test day records extracted for Tanzania: 47,807 records from 11,438 cows
- Pedigree file : 56,960 animals

Genetic Parameter estimation

- Subset of 1930 cows with 9193 test days records with genotypes were used
- Cows classified to 4 breed classes based on proportion of exotic genes : >0.875 , $0.61-0.875$, $60-36$, and < 0.36
- G matrix used for all analysis
- Models Examined
- **Fixed Regression model** : Fixed ward, age nested parity, test-year-season, fixed curves with Legendre polynomials nested within breed classes by parity interaction plus random herd animal and pe

Genetic Parameter estimation

- Fixed Regression model + plus dominance as random effect and D matrix computed from genotypes
- Fixed Regression model but fitting proportion of exotic versus non-exotic as separate random effects
- Random regression model with Legendre polynomials of order 2 for animal and Pe effects
- Bayesian models (Bayes A, B, and C) using YD deviations from fixed regression model with weights - function on the number of records each cow has and the variance of YD

Genetic parameters

Parameters	FRM	FRM + Dominance	RRM
Heritability	0.14 ± 0.04	0.14 ± 0.04	0.26
Variance due to Pe	0.10 ± 0.04	0.08 ± 0.08	0.16
Variance due to herd	0.26 ± 0.02	0.26 ± 0.02	0.24
Variance due to dominance		0.03 ± 0.08	

Validation

- Cross-classified validation excluding records of a particular breed class (FRM)
- Forward validation: 254 cows born after 2014

Cross –Validation results

Class of cows	N	GBLUP		GBLUP + Dominance	
		Corr	Reg	Corr	Reg
>0.875	705	0.28	1.7	0.27	1.7
0.61-0.875	942	0.28	1.6	0.27	1.6
0.36 – 0.60	239	0.38	1.7	0.37	1.8
<0.36	43	0.44	2.6	0.42	2.6

Forward validation results

Model	Corr	Reg
FRM	0.31	1.2
FRM + Dominance	0.30	1.2
RRM	0.43	1.1
BayesA	0.11	0.08
BayesB	0.21	0.21
BayesC	0.10	1.4

Genomic prediction

Two approaches : **GBLUP**

- About 2000 cows with genotypes and data
- 530 Males with only genotypes
- 1537 cows with only genotypes
- FRM used for parameter estimation
- Single step
 - Data as in GBLUP
 - Plus cow with sire or dam or both identified
 - 638 cows with 2787 test day records were included

Example of some Cow GEBVs

AnimalTag	HairsampleID	noTDs	MeanMilk	MeanYD	GEBV	StdGEBV
TZN0000000000001	00001	10	20.400	1.319	3.560	129
TZN0000000000002	00002	4	18.375	2.490	2.983	124
TZN0000000000003	00003	3	20.833	3.029	2.799	123
TZN0000000000004	00004	10	16.400	0.927	2.697	122
TZN0000000000005	00005	1	30.000	9.100	2.651	121
TZN0000000000006	00006	4	17.500	1.796	2.639	121
TZN0000000000007	00007	6	18.333	1.189	2.556	121
TZN0000000000008	00008	6	17.667	0.926	2.524	120

Conclusions

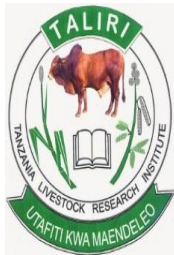
- Large body of data ever collected in small holder systems in Sub Saharan Africa
- Given data set, validation results are encouraging and use for selection team of cross bred bulls for national AI centers
- Presents a noble opportunity for proper modeling and prediction of breeding values for the initiation of a meaningful breeding programs

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Animal scientist, Nobel Prize Laureate for Physiology or Medicine–1996

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