The M3GE project: developing beef cattle multi-trait multi-breed multi-country genomic evaluations for sustainability traits and small populations

R. Bonifazi, S. Aivazidou, R.F. Veerkamp, F. Macedo, R. Evans, T. Pabiou, K. Quigley, K. Matthews, H. Bunning, G.M. Tarekegn, M. Cassandro, R. Finocchiaro, J. Layton, R.G.M.F. Damai, A. Quaglia, D. Vicario, L. Degano, M. Piazza, T. Roozen, M. Coffey, M. Burke, J. Vandenplas

Interbull Annual Meeting, Louisville, 22 June 2025

Aim

Present the M3GE project, its status,

and outlook on feed trait group

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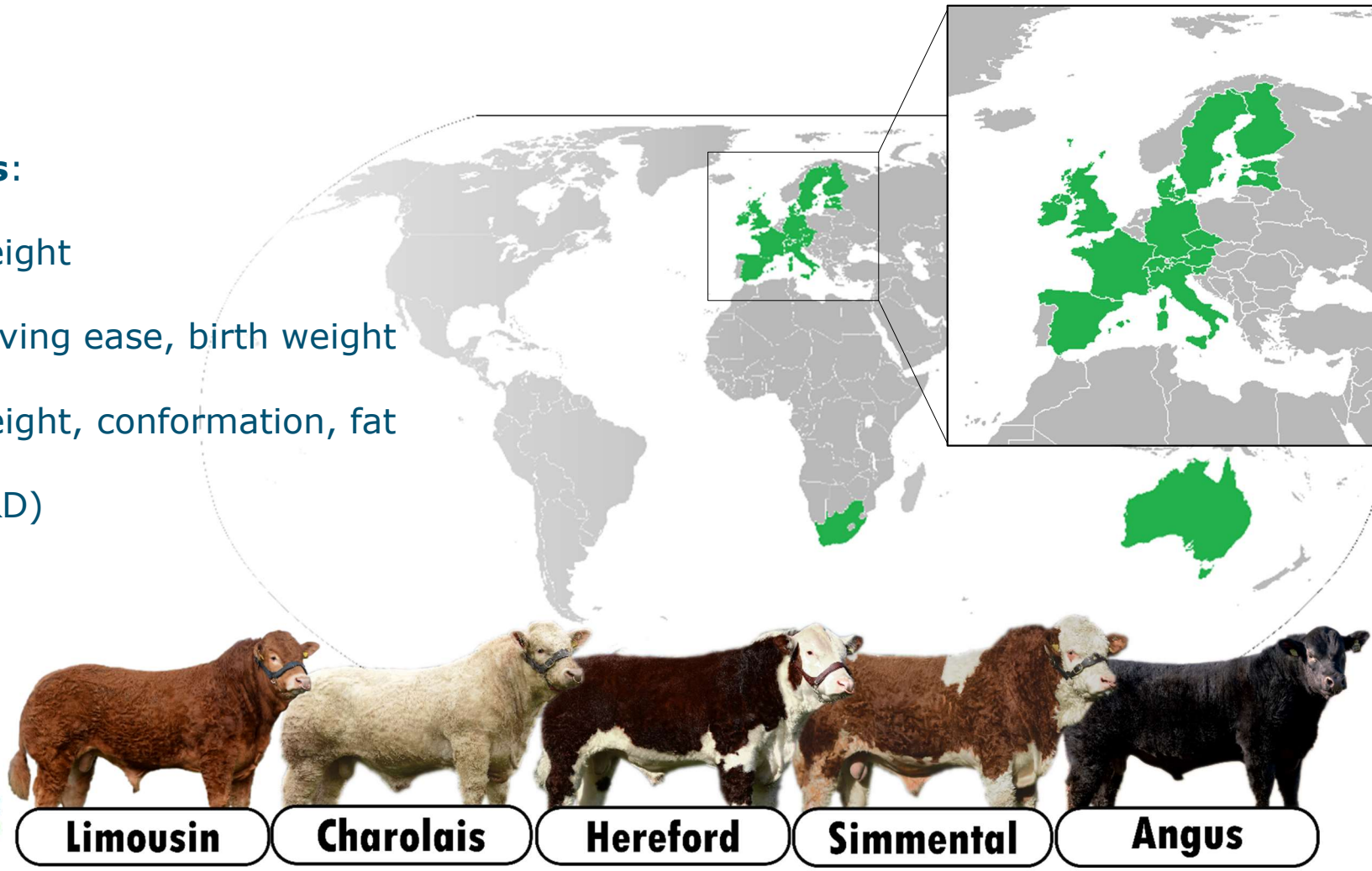
International evaluations for beef cattle

- **15 countries**
- Evaluated **traits**:
  - Weaning weight
  - Calving: calving ease, birth weight
  - Carcass: weight, conformation, fat
  - Fertility (R&D)
- **5 breeds**



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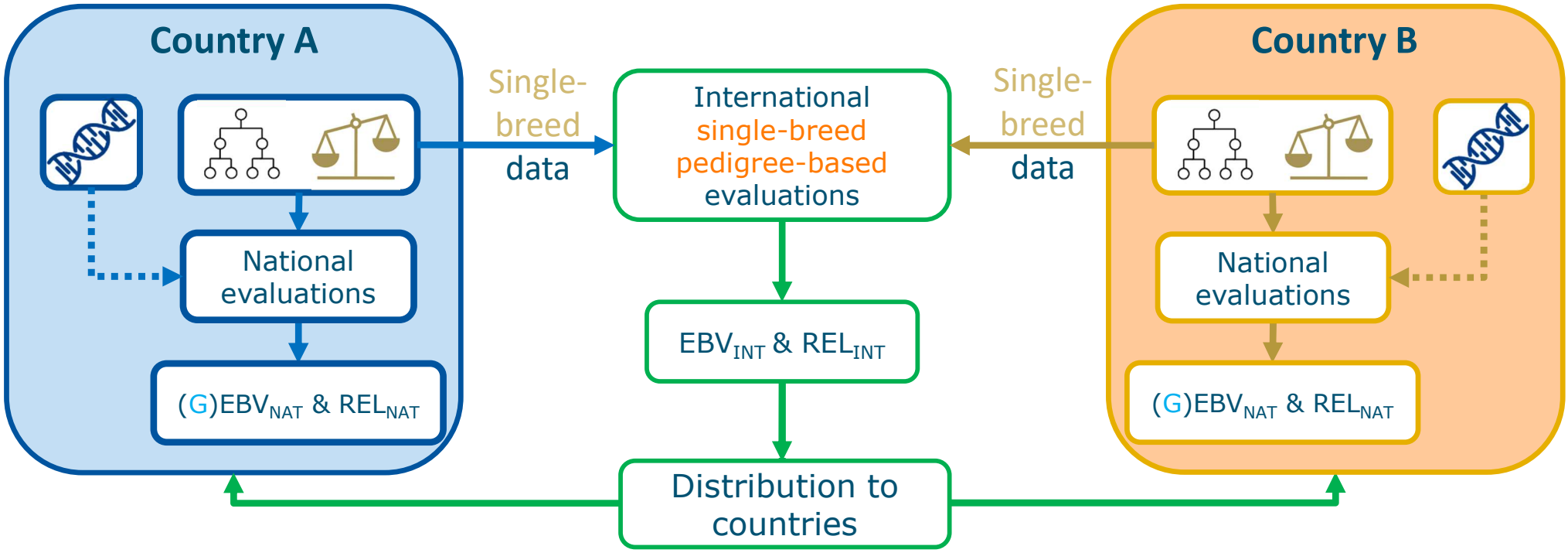
Current Interbeef evaluations



R&D: single-step single-breed international evaluations (Bonifazi et al., 2022)

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Roadmap to M3GE – context

- Countries requirements and current challenges:
  - New sustainability traits are difficult and expensive to measure
  - Small breeds risk to become non-competitive
  - Crossbreed data
- Develop genomic services for new (group of) novel traits of interest
- Expansion Interbeef portfolio (+ genomic, + breeds, + traits)
- New and improved services for countries

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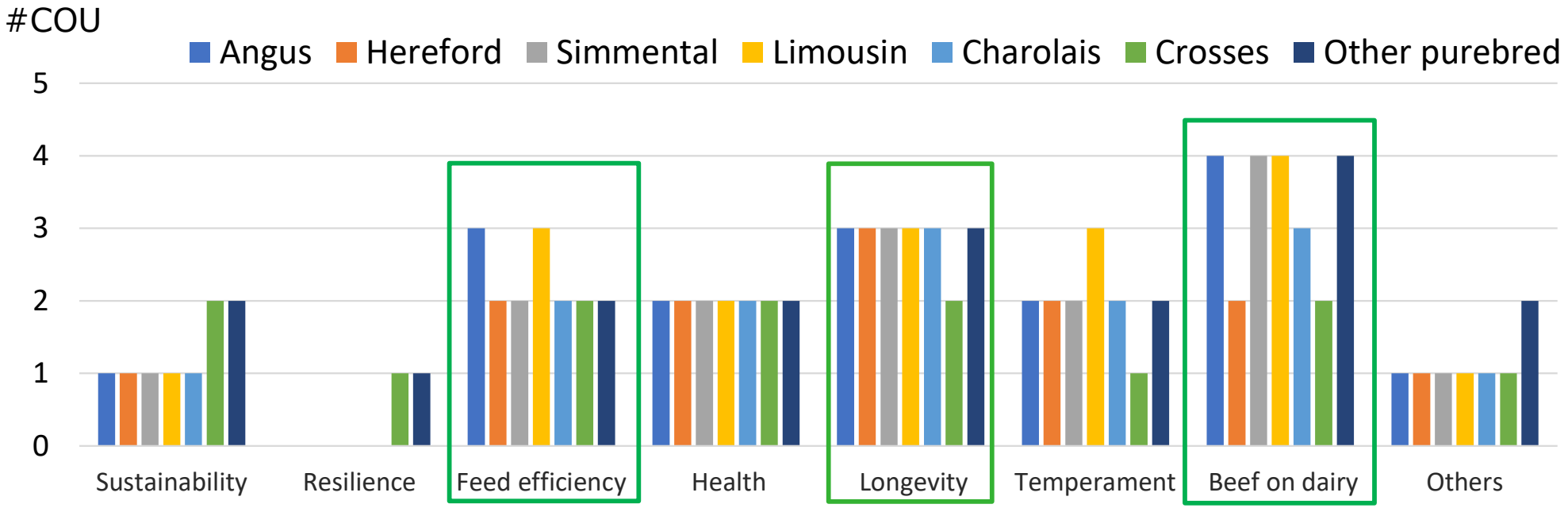
Preliminary survey

- Replies from 8 countries (67%)
- Most interesting traits: feed efficiency, longevity, beef on dairy
- Records on different breeds and crosses
- Both phenotypes and genotypes → single-step



M3GE project

- **Goal**: Develop multi-breed multi-trait international genomic beef cattle evaluations
- Potential advantages:
  - Improve accuracy of GEBVs by including data on (other) purebreed and crossbred
  - Leverage international collaboration for novel traits
  - Involve new (numerically-small and local) breeds (better usage of genetic resources, e.g., transboundary breeds)
  - Deliver GEBVs to breeders for traits not evaluated at national level

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Private-Public-Partnership

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4 years (2024-2027)

Data collected

- Following country's trait definition and national model
- **Two trait groups:**
  - **FEED**: Feed + indicator traits: Carcass (CAW, CAF, CCO), Liveweight (LWE), Growth (ADG, ACG)
  - **LONG**: Longevity + indicator traits: Calving (AFC, CAI)

- IDEA: pedigree and (repeated) records
- GenoEX-GDE: genotypes

GENOEX
INTERBULL
International Genotype Exchange Platform
International Genotype Exchange platform for Animal Breeding

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Data collected

		GBR	IRL	ITA				
Phenotypes Repeated records	**Trait**	AHDB+SRUC (PBD & XBD)	ICBF (PBD & XBD)	ANAFIBJ (HOL)	ANAPRI (SIM)	ANABIC (ITA breeds)	ANACLI (LIM & CHA)	Trait total
FEED		28.4K	8.4K	8.8K	900	27K	24K	98.5K
Indicator traits	CWE		12.9M				42K	13M
	CFA		12.9M					12.9M
	CCO		12.9M					12.9M
	LW1	581K	1.0M	26K	7.6K		6K	1.6M
	LW2		1.0M				192K	1.0M
	LW3		1.3M					1.3M
	ADG				7.6K	5.3K		12.9K
	CDG					355K		355K

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ITA breeds: Marchigiana, Chianina, Romagnola, Podolica, Maremmana

Data collected

		GBR	IRL	ITA				
Phenotypes Repeated records	**Trait**	AHDB+SRUC (PBD & XBD)	ICBF (PBD & XBD)	ANAFIBJ (HOL)	ANAPRI (SIM)	ANABIC (ITA breeds)	ANACLI (LIM & CHA)	Trait total
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	LW3		1.3M					1.3M
	ADG				7.6K	5.3K		12.9K
	CDG					355K		355K
LONG			10.2M			248K	239K	10.7M
Indicator traits	CAI		8.5M			912K		9.5M
	AFC		3.1M			255K		3.3M

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ITA breeds: Marchigiana, Chianina, Romagnola, Podolica, Maremmana

Data collected

		GBR	IRL	ITA				
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	LW1	581K	1.0M	26K	7.6K		6K	1.6M
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	LW3		1.3M					1.3M
	ADG				7.6K	5.3K		12.9K
	CDG					355K		355K
LONG			10.2M			248K	239K	10.7M
Indicator traits	CAI		8.5M			912K		9.5M
	AFC		3.1M			255K		3.3M
Genotypes		106K	3.0M	5.3K	3.3K	13.3K	12.9K	3.1M

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ITA breeds: Marchigiana, Chianina, Romagnola, Podolica, Maremmana

Feed – Italy

- Recoding in test centers (nucleus)
- HOL (ANAFIBJ)
  - Growing bulls (100-600 days)
  - Daily dry matter intake (Kg DMI/day)
  - Repeated records
- SIM (ANAPRI)
  - Young growing bulls (280-340 days)
  - Residual Feed Intake (Kg DMI/day)
  - Single record (repeated measurements summarized)
- ITA breeds, LIM, CHA (ANABIC & ANACLI)
  - Young growing bulls (200-400 days)
  - Residual Feed Intake (Kg DMI/day)
  - Repeated records

ITA breeds: Marchigiana, Chianina, Romagnola, Podolica, Maremmana

Feed – Ireland (ICBF)

- Test station (Tully)
- Mostly steers and heifers, few young bulls (~200-900 days)
- Commercial beef from targeted candidate sires
- Initially purebred, now mostly crossbred
- Daily dry matter intake (Kg DMI/day)
- Single record

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Feed – Great Britain (AHDB & SRUC)

- Research and mostly commercial farms
- Provided equipment and recording protocol
- Steers (~170-560 days)
- Crossbred
- Daily dry matter intake (kg DMI/day)
- Repeated weekly records (~7 weeks)

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Modelling feed at the national level

Country	GBR	IRL	ITA			
Org	AHDB&SRUC	ICBF	ANAFIBJ	ANAPRI	ANABIC	ANACLI
Breeds	PBD & XBD	PBD & XBD	HOL	SIM	ITA breeds	LIM & CHA
Trait	DMI	DMI	DMI	RFI	RFI	RFI
Model	ssGBLUP multi-breed single-trait	two-step genomic multi-breed multi-trait (3 LW, conformation, 3 carcass)	GBLUP single-trait	ssGBLUP single-trait	ssGBLUP multi-breed single-trait (breed as fixed effect)	ssGBLUP* multi-breed single-trait
h^2	0.14	0.30	0.32	0.29	0.05	*ongoing*
c^2	0.26		0.50		0.22	*ongoing*

ITA breeds: Marchigiana, Chianina, Romagnola, Podolica, Maremmana

** in development*

Feed – PCA

~4K SNPs in common

~18K genotyped animals

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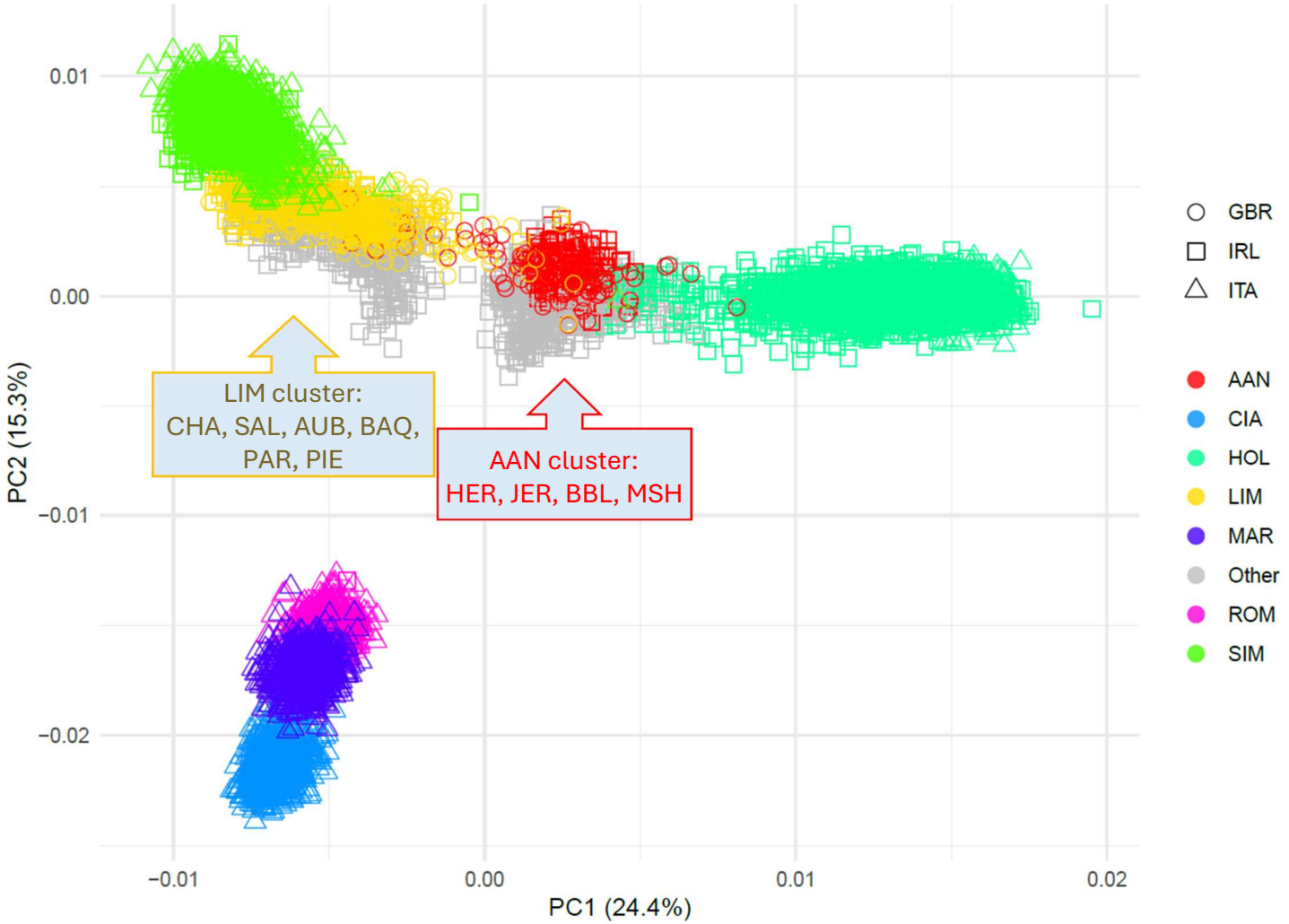

Feed – PCA including crossbreds

~4K SNPs in common

~18K genotyped animals

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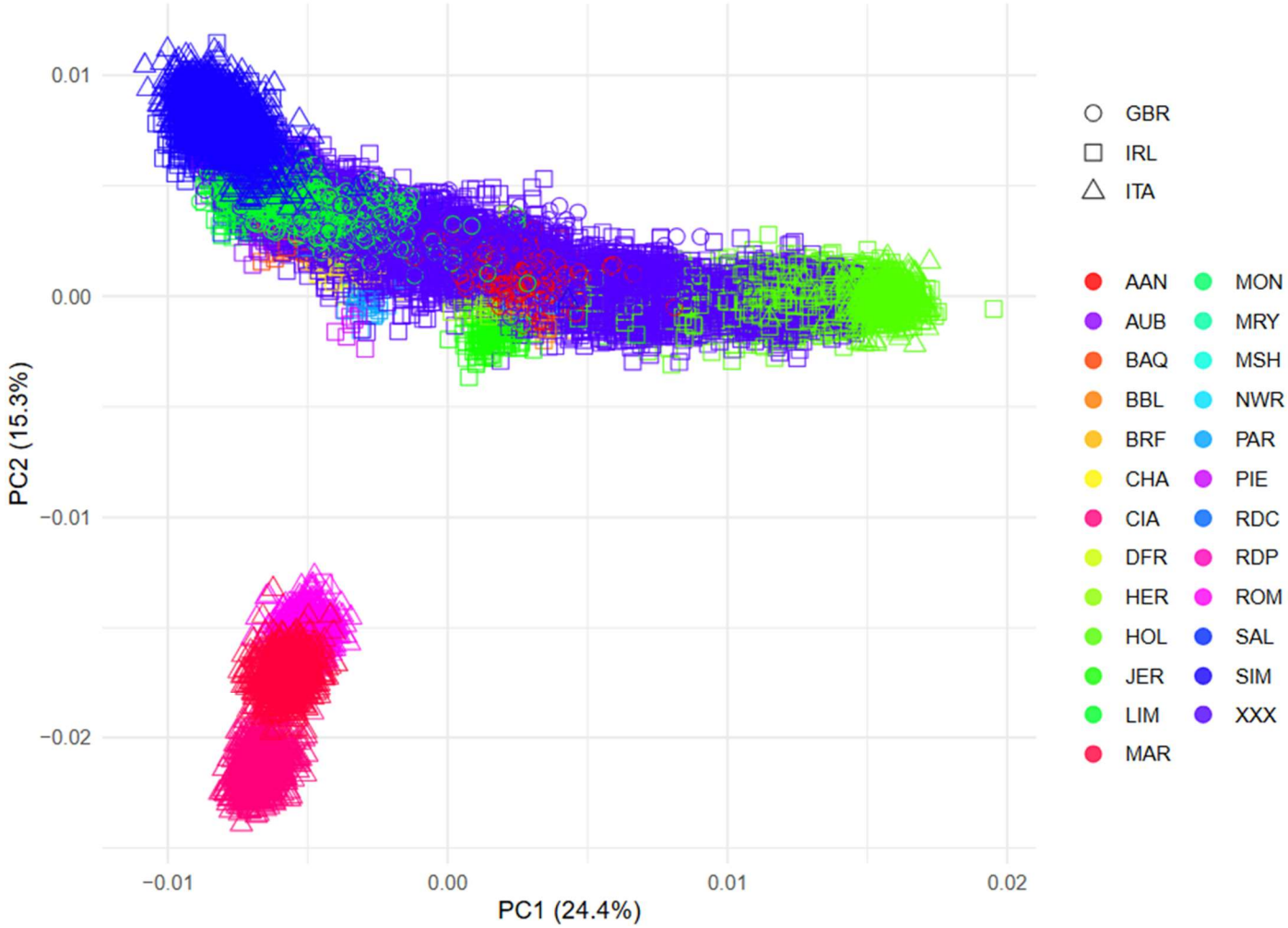

Next steps in M3GE project

- *Ongoing:* development of multi-breed international single-step model for FEED
- Share GEBVs, RELs, SNP effects with participating organizations
- Expansion to LONG
- Expansion to include indicator traits (multi-trait)

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Thank you for your attention

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renzo.bonifazi@wur.nl

Take-home messages

- M3GE: multi-trait multi-breed multi-country beef cattle genomic evaluations
- Data collected from 3 countries and 6 organizations: different purebred, crossbred, also small (local) populations
- *Ongoing* development of multi-breed multi-country genomic evaluation for FEED

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renzo.bonifazi@wur.nl