

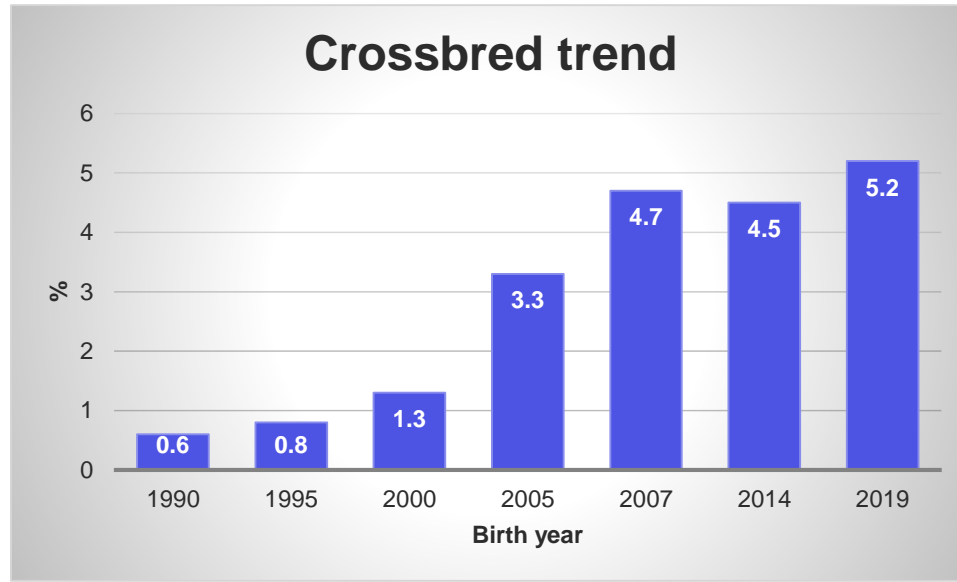
## Genomic predictions for wellness traits in crossbred dairy cattle

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# Trends



Crossbreed evolution in time using CDCB (Powell and Norman, 2011; Dechow, 2015; Guinan et al., 2019)

Pinedo and Velez (2019)

~ 9% of the herds in USA report having crossbred dairy cows

~27% of the organic herds have crossbred dairy cows

# WELLNESS TRAITS

## OBJECTIVE

- Evaluate predictivity of ssGBLUP for wellness traits in crossbreed dairy cattle



# DATA Traits

## Data and traits

- Producer-recorded data from herds who provided permission to Zoetis
- Pedigree and phenotype data
- Traits recorded as binary events, 1 if recorded, 0 if not.

Traits	Phenotypes count	
	Complete	Validation
Mastitis	6,077,691	6,076,638
Metritis	4,532,331	4,531,089
Lameness	4,619,008	4,618,330
Ketosis	3,040,725	3,039,883
Displaced abomasum	4,316,166	4,315,416
Retained placenta	5,235,789	5,234,517
Description	WT cross evaluation	960 IDs

(Vukasinovic et al., 2017; Gonzalez-Pena et al., 2020)

# DATA Pedigree and Genotypes

## Description of the pedigree

- 19 million animals
- depth of 20 generations

## Description of the scenarios for genotypes

Scenarios	Genotypes		
	Cross	HO	JE
1) Onlycross	44,232		
2) Connect 1	44,232	3,851	275
3) Connect 2	44,232	11,529	261
4) JE_ + Connect 2	44,232	11,529	60,335
5) HO	44,232	375,674	
6) HO_JE	44,232	375,674	60,335

## Model description

$$\lambda = X\beta + Z_h h + Z_a a + Z_p p + e$$

- $\lambda$ : liabilities to disease
- $\beta$ : fixed parity effects, heterosis (cov), and inbreeding (cov)
- $h$ : random herd-year-season effects
- $a$ : additive genetic effects
- $p$ : permanent environmental effects
- $e$ : random residuals
- $X, Z$ : incidence matrices

(Vukasinovic et al., 2017; Gonzalez-Pena et al., 2020)

## GENOMIC EVALUATION PLATFORM

BLUPF90 software family (Misztal et al., 2014)

- Program CBLUP90IOD2 v 3.37
  - Iteration on data
  - APY algorithm (random core of 25,000 animals)

Reliabilities:

- Program ACCF90GS v 2.43 (reliability approximation based on diagonal of GRM)

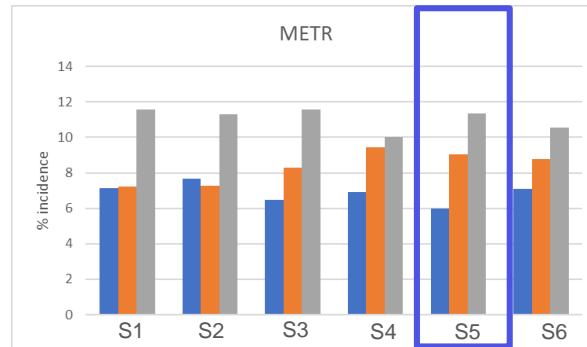
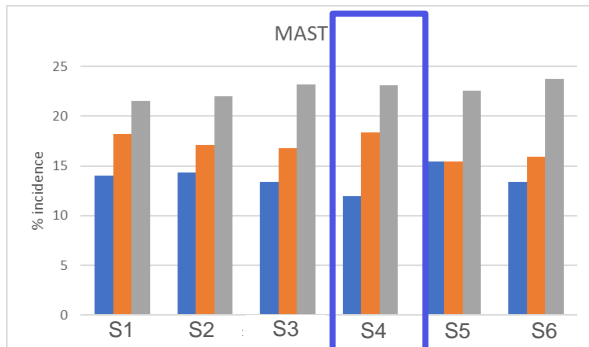
## gPTA and reliabilities for all the traits in each scenario (n= 44,232)

Scenarios Names	MAST		METR		RETP		DA		KETO		LAME	
	PTA	REL	PTA	REL	PTA	REL	PTA	REL	PTA	REL	PTA	REL
1) Onlycross	0.38	0.37	-1.03	0.36	-0.55	0.37	-0.51	0.32	-0.46	0.32	0.23	0.36
2) Connect 1	-0.33	0.42	-1.35	0.40	-0.72	0.41	-0.86	0.37	-0.67	0.36	-0.10	0.40
3) Connect 2	-0.25	0.46	-1.36	0.43	-0.76	0.45	-0.97	0.40	-0.60	0.39	0.12	0.44
4) JE_+ Connect 2	-0.67	0.39	-1.67	0.35	-0.82	0.37	-1.31	0.31	-1.25	0.32	-0.22	0.37
5) HO	-0.60	0.34	-2.13	0.33	-1.40	0.34	-1.37	0.27	-0.66	0.27	-0.07	0.31
6) HO_JE	-0.50	0.43	-1.93	0.41	-1.41	0.42	-1.23	0.35	-0.29	0.35	0.02	0.40

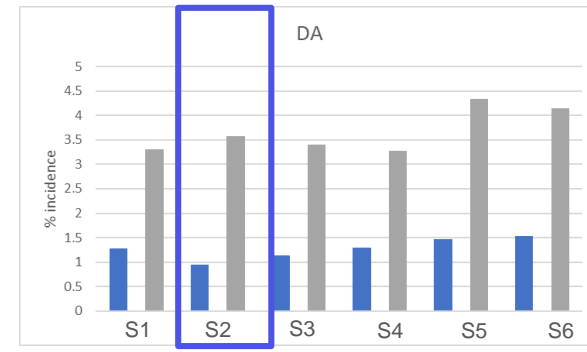
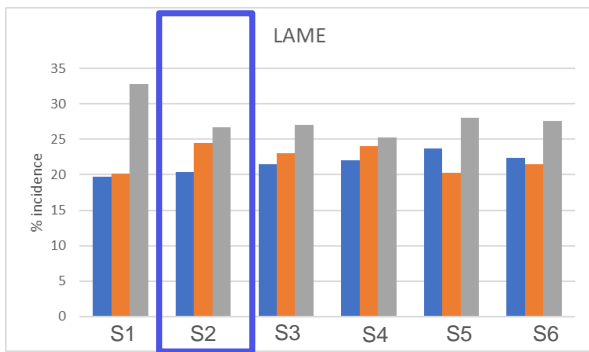
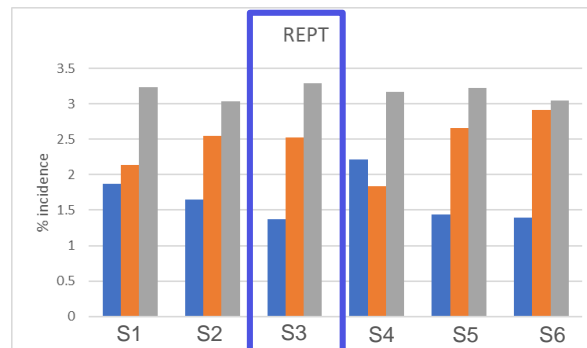
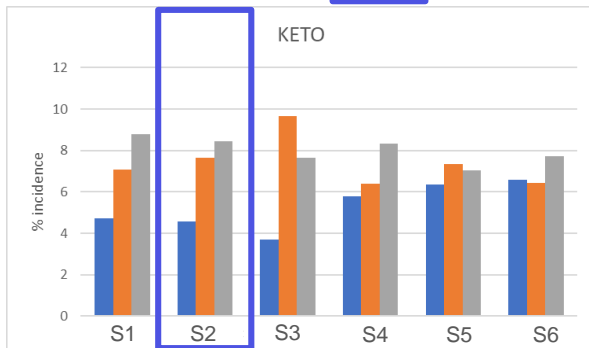
## gPTA high and low correlation between scenarios

Scenarios Names	MAST		METR		RETP		DA		KETO		LAME	
	Pair	Value	Pair	Value	Pair	Value	Pair	Value	Pair	Value	Pair	Value
High	2vs3	0.96	2vs3	0.94	3vs4	0.93	2vs3	0.93	2vs3	0.96	2vs3	0.92
Low	1vs6	0.69	1vs6	0.59	1vs6	0.58	1vs6	0.65	1vs6	0.75	1vs6	0.55

# Validation Test



Following McNeel et al. (2017)



## Best scenarios for cross based on the validation test

Scenarios	MAST	METR	RETP	KETO	DA	LAME
1) Onlycross						
2) Connect 1				X	X	X
3) Connect 2			X			
4) JE_+ Connect 2	X					
5) HO		X				
6) HO_JE						

# Conclusions

- The difference between the worst and best genetic groups in recorded disease incidence was 11.1%, 5.4%, 1.9%, 2.6%, 3.9%, and 6.4% for MAST, METR, RETP, DA, KETO, and LAME, respectively.
- The best scenarios separations and predictions were not precisely those with most of the purebreds, and probably enough connectivity between animals are required to create meaningful predictions.

*zoetis*