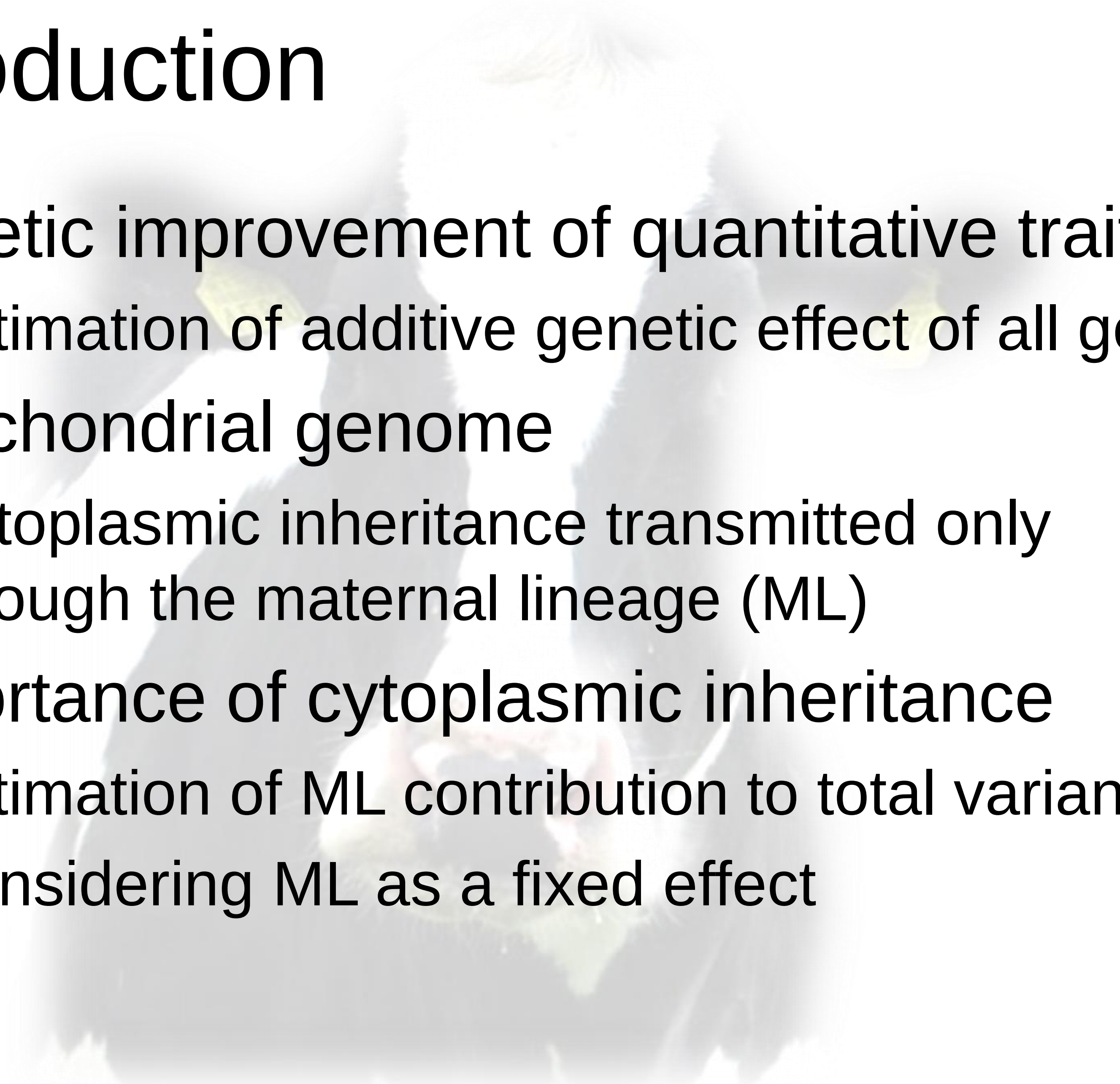
Variance estimation of maternal lineage effect on milk traits in Croatian Holstein cattle

Spehar M.[1], Ferenčaković M.[2], Brajkovic V.[2], Curik I.[2]

[1]Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia,

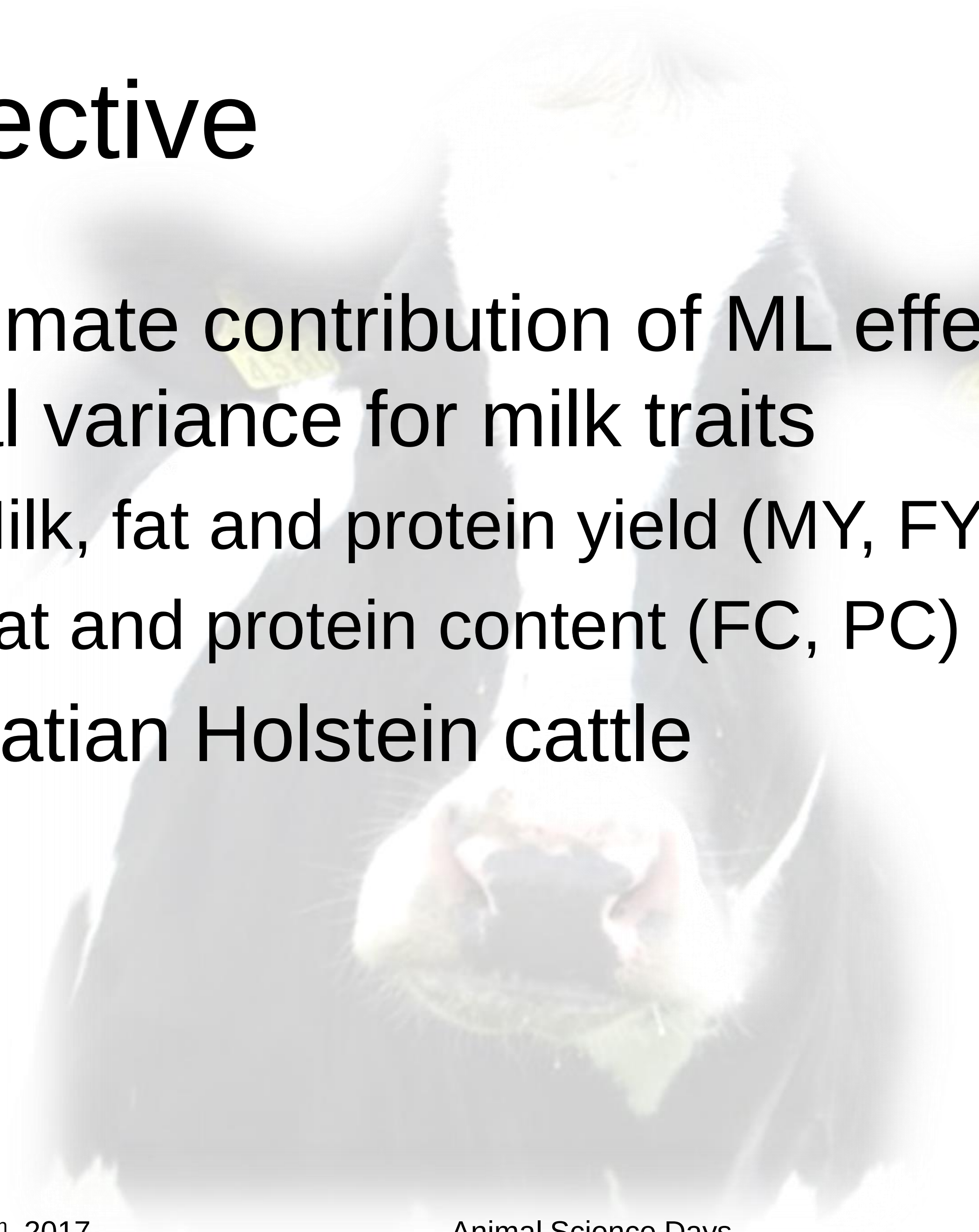
[2]University of Zagreb, Faculty of Agriculture, Department of Animal Science,
Svetošimunska 25, 10000 Zagreb, Croatia

Introduction



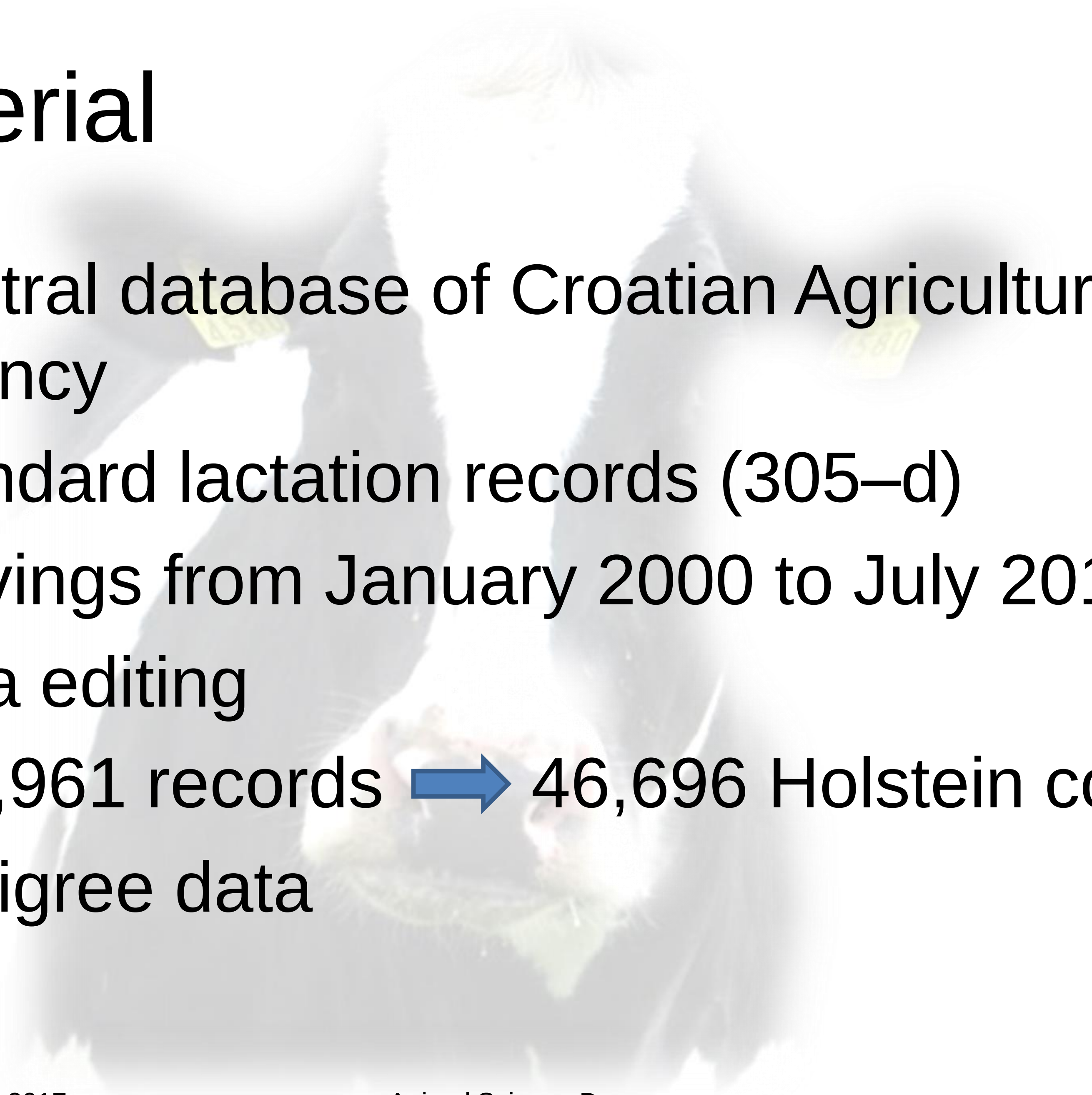
- Genetic improvement of quantitative traits
  - Estimation of additive genetic effect of all genes
- Mitochondrial genome
  - Cytoplasmic inheritance transmitted only through the maternal lineage (ML)
- Importance of cytoplasmic inheritance
  - Estimation of ML contribution to total variance
  - Considering ML as a fixed effect

Objective



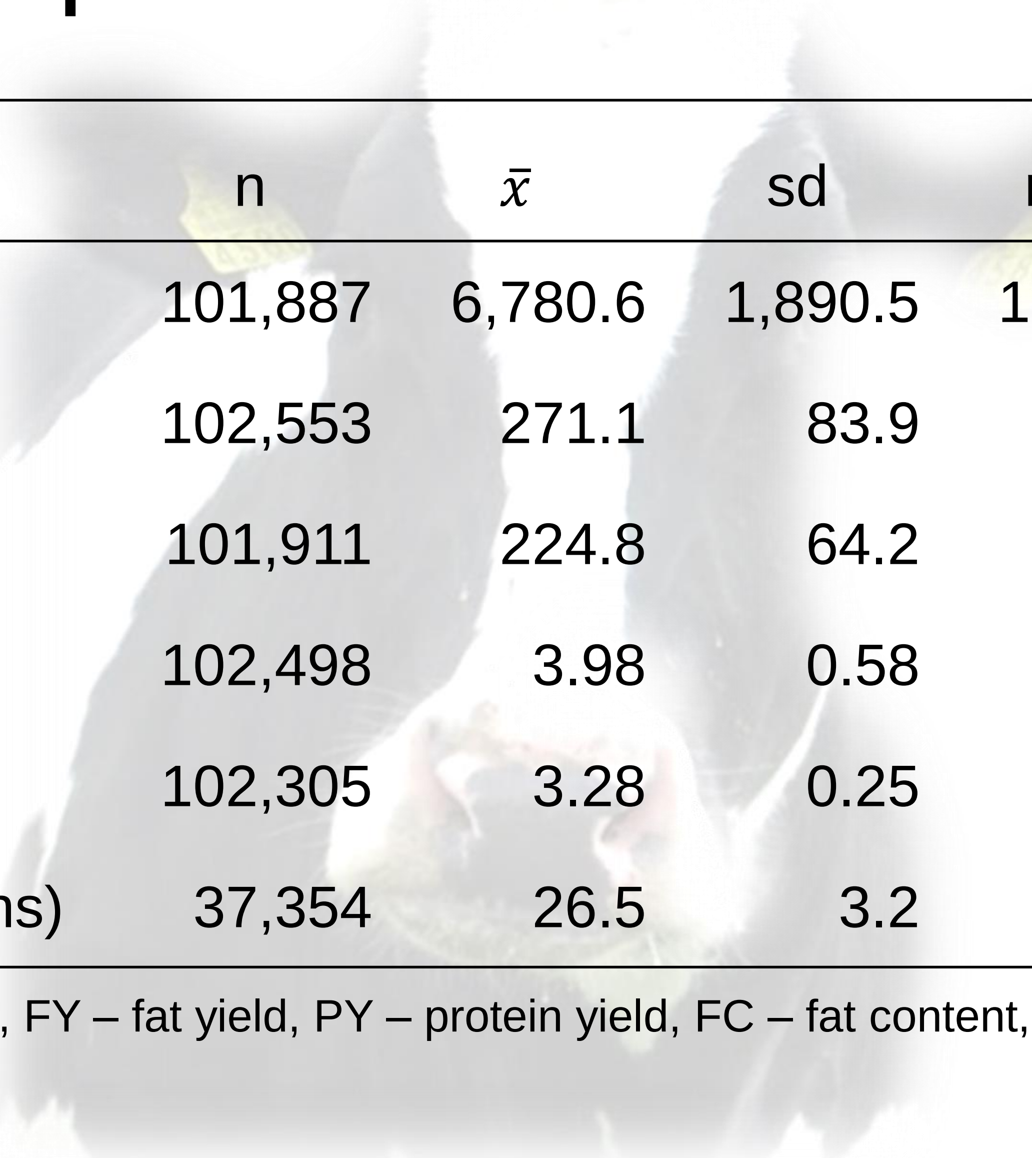
- Estimate contribution of ML effect to the total variance for milk traits
  - Milk, fat and protein yield (MY, FY, PY)
  - Fat and protein content (FC, PC)
- Croatian Holstein cattle

Material



- Central database of Croatian Agricultural Agency
- Standard lactation records (305–d)
- Calvings from January 2000 to July 2015
- Data editing
- 102,961 records → 46,696 Holstein cows
- Pedigree data

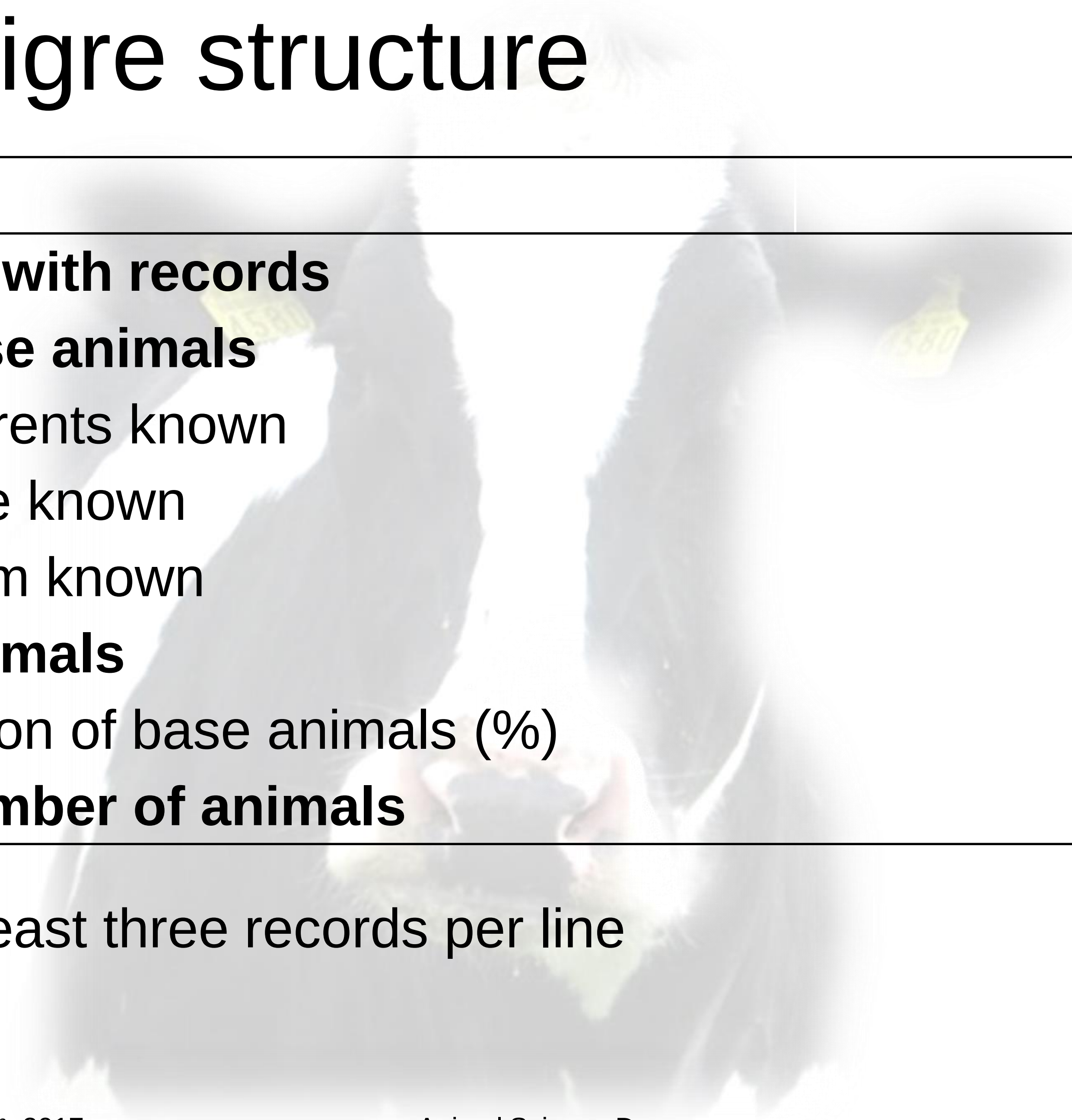
Descriptive statistics



Trait	n	$\bar{x}$	sd	min	max
MY (kg)	101,887	6,780.6	1,890.5	1,053.3	11,999.9
FY (kg)	102,553	271.1	83.9	80.1	600.0
PY (kg)	101,911	224.8	64.2	80.0	582.8
FC (%)	102,498	3.98	0.58	2.00	6.00
PC (%)	102,305	3.28	0.25	2.00	5.26
Age (months)	37,354	26.5	3.2	18.0	37.0

MY – milk yield, FY – fat yield, PY – protein yield, FC – fat content, PC – protein content

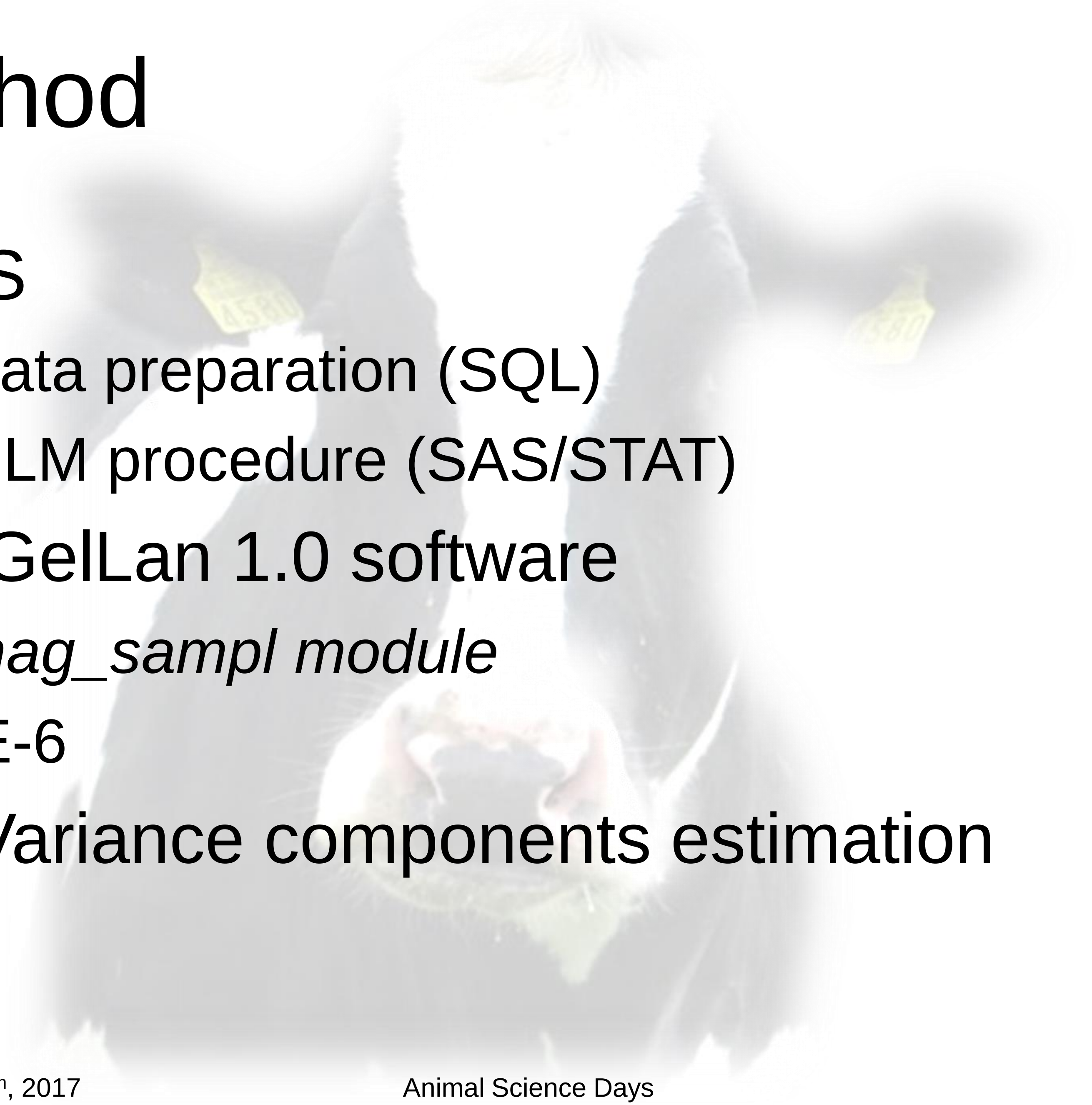
Pedigre structure



Item	Number
Animals with records	46,696
Non–base animals	73,201
- both parents known	60,193
- only sire known	8,997
- only dam known	4,011
Base animals	4,197
- proportion of base animals (%)	5.4
Total number of animals	77,398

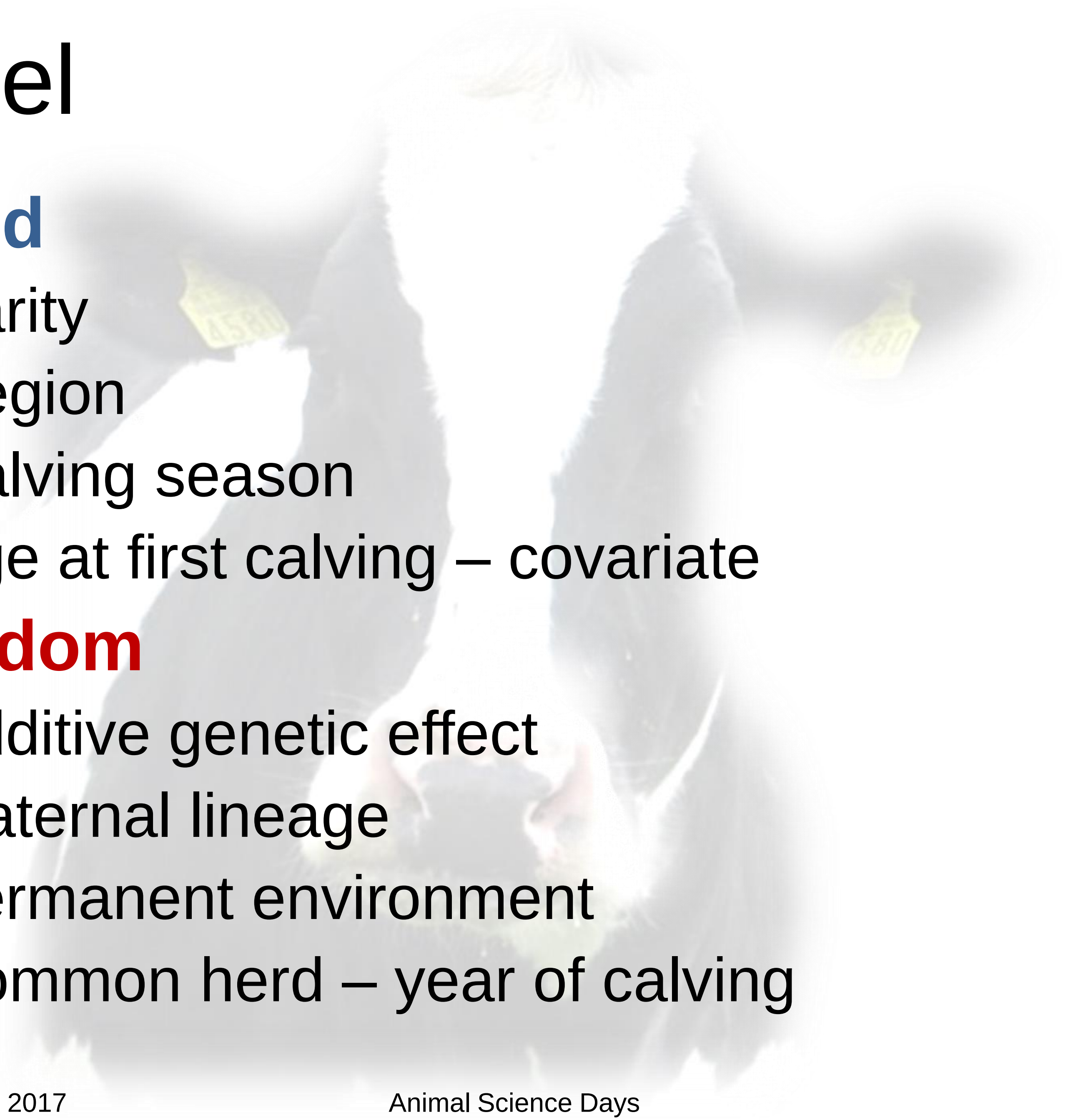
ML - at least three records per line

Method



- SAS
  - Data preparation (SQL)
  - GLM procedure (SAS/STAT)
- MaGelLan 1.0 software
  - *mag_sampl module*
- VCE-6
  - Variance components estimation

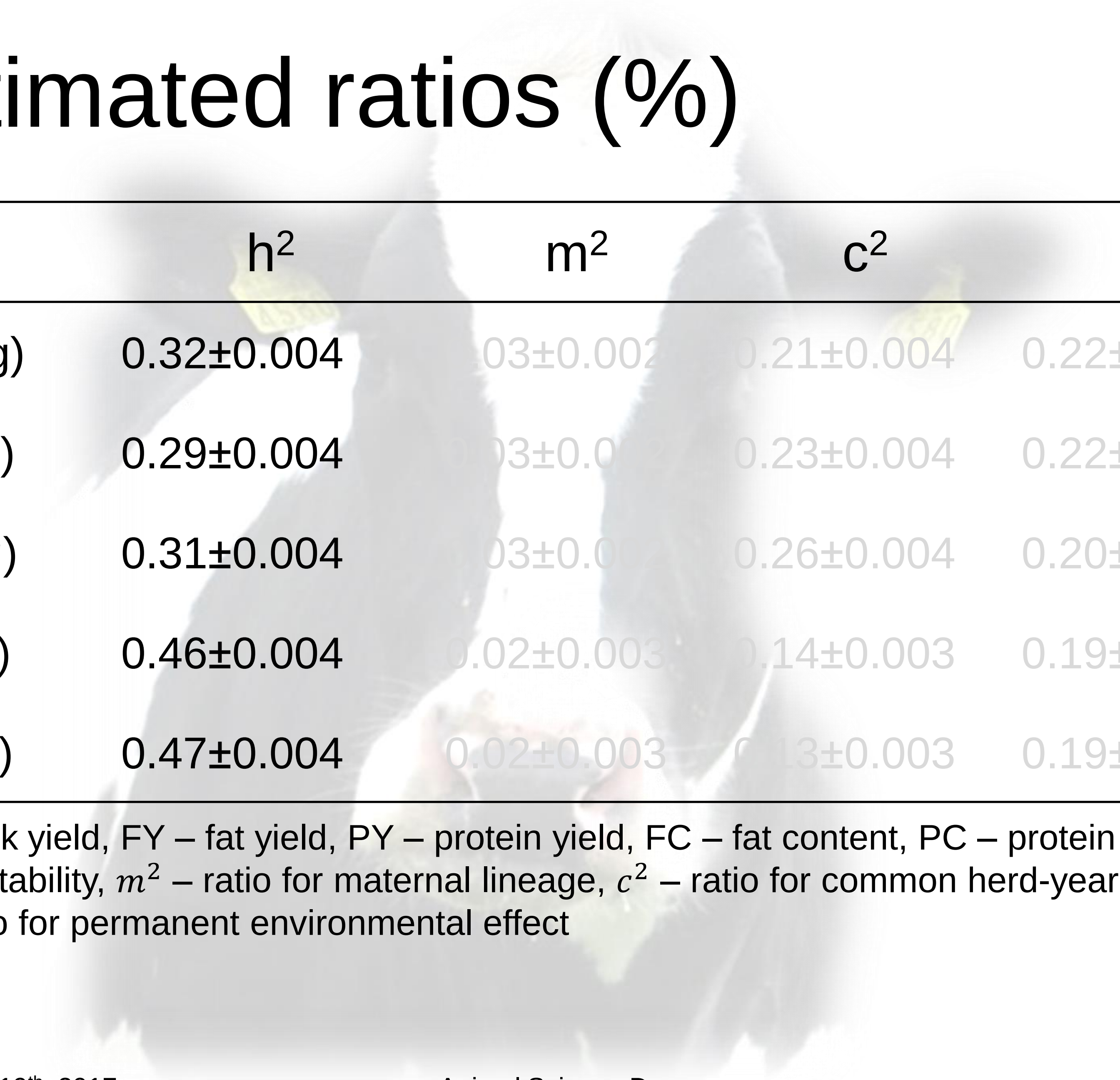
Model



- **Fixed**
  - – Parity
  - – Region
  - – Calving season
  - – Age at first calving – covariate
- **Random**
  - – Additive genetic effect
  - – Maternal lineage
  - – Permanent environment
  - – Common herd – year of calving

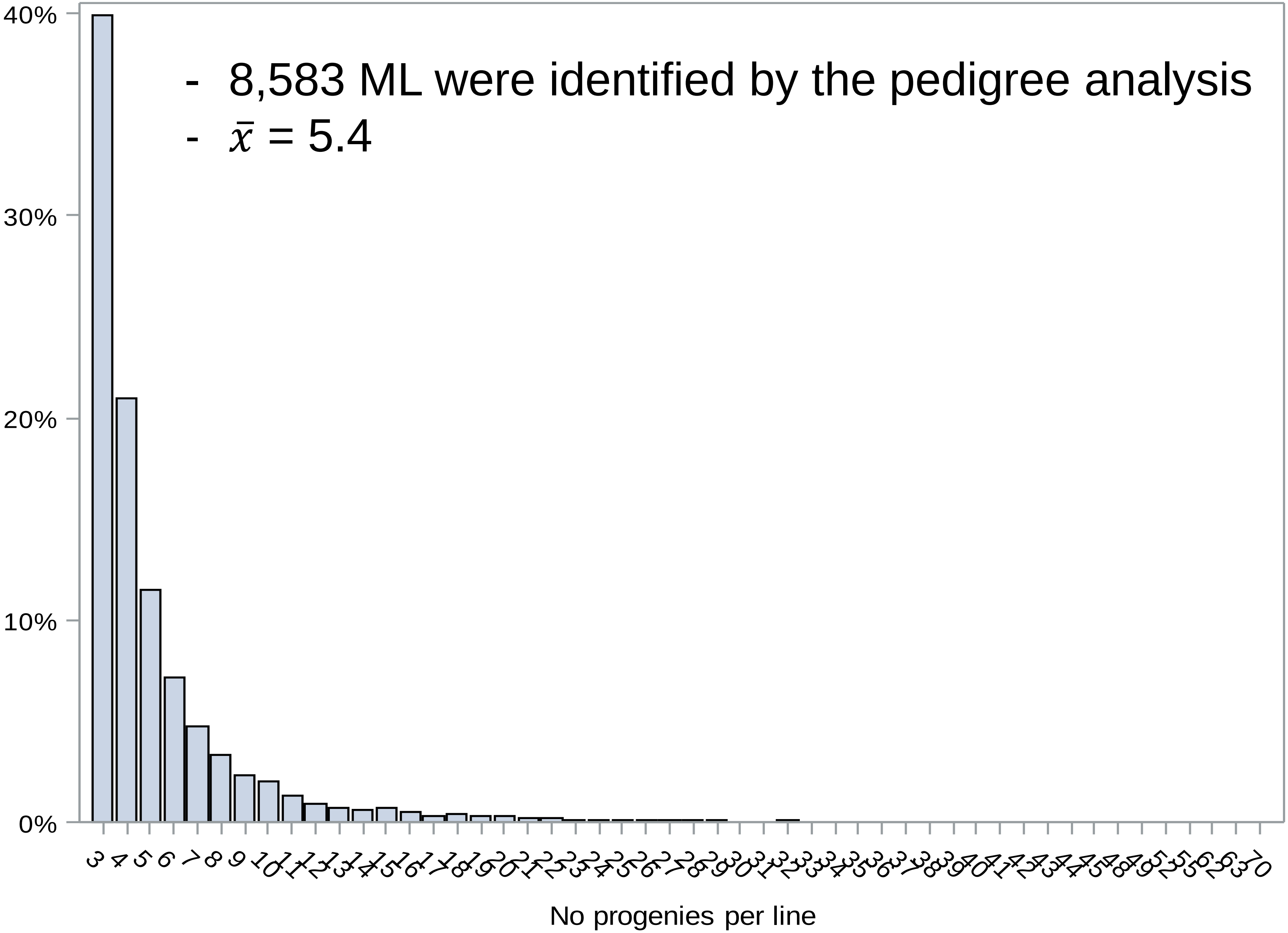
Results

Estimated ratios (%)



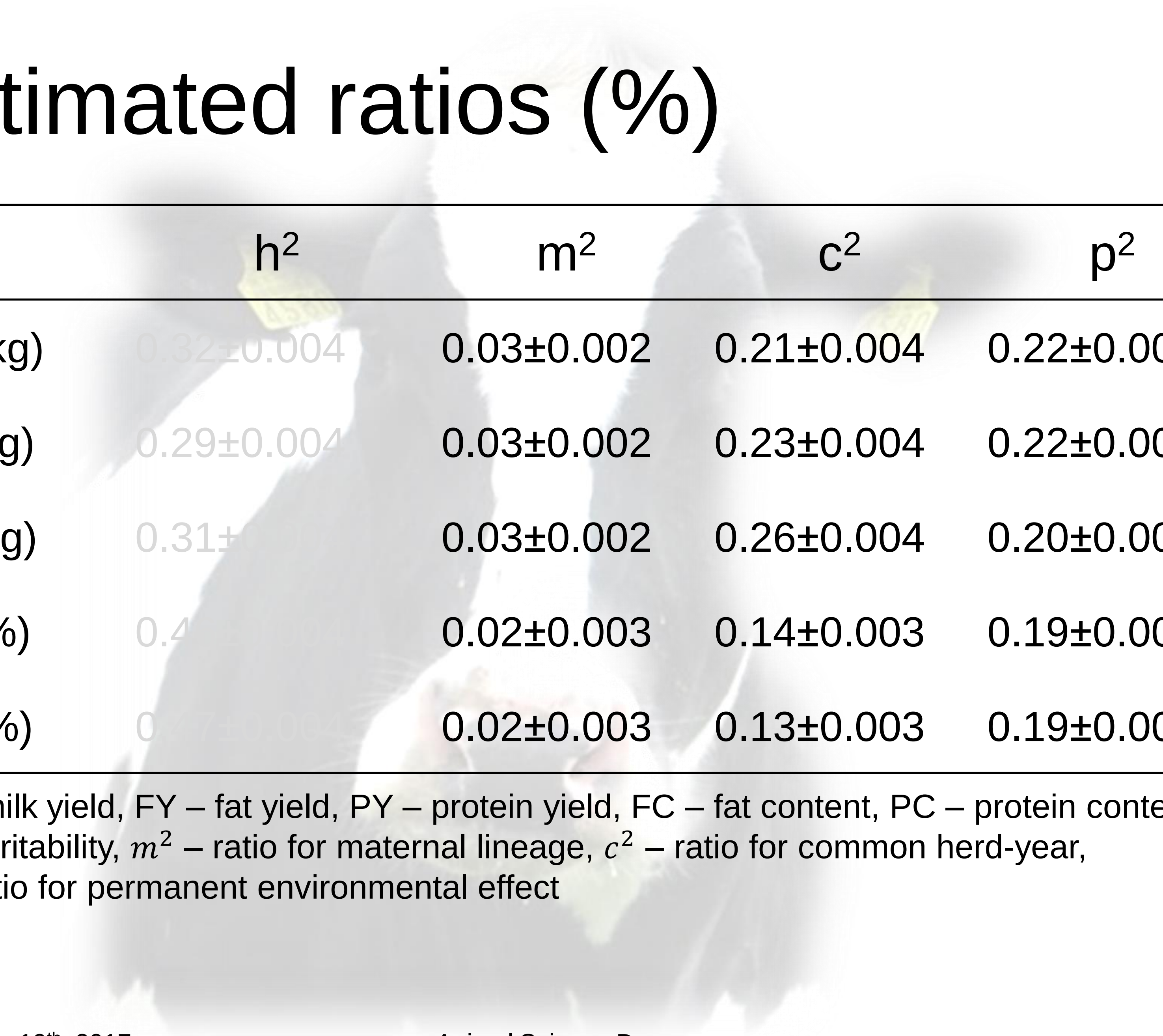
Trait	h^2	m^2	c^2	p^2
MY (kg)	0.32±0.004	0.03±0.002	0.21±0.004	0.22±0.002
FY (kg)	0.29±0.004	0.03±0.002	0.23±0.004	0.22±0.002
PY (kg)	0.31±0.004	0.03±0.002	0.26±0.004	0.20±0.002
FC (%)	0.46±0.004	0.02±0.003	0.14±0.003	0.19±0.002
PC (%)	0.47±0.004	0.02±0.003	0.13±0.003	0.19±0.002

MY – milk yield, FY – fat yield, PY – protein yield, FC – fat content, PC – protein content, h^2 – heritability, m^2 – ratio for maternal lineage, c^2 – ratio for common herd-year, p^2 – ratio for permanent environmental effect



- 8,583 ML were identified by the pedigree analysis
- $\bar{x}$ = 5.4

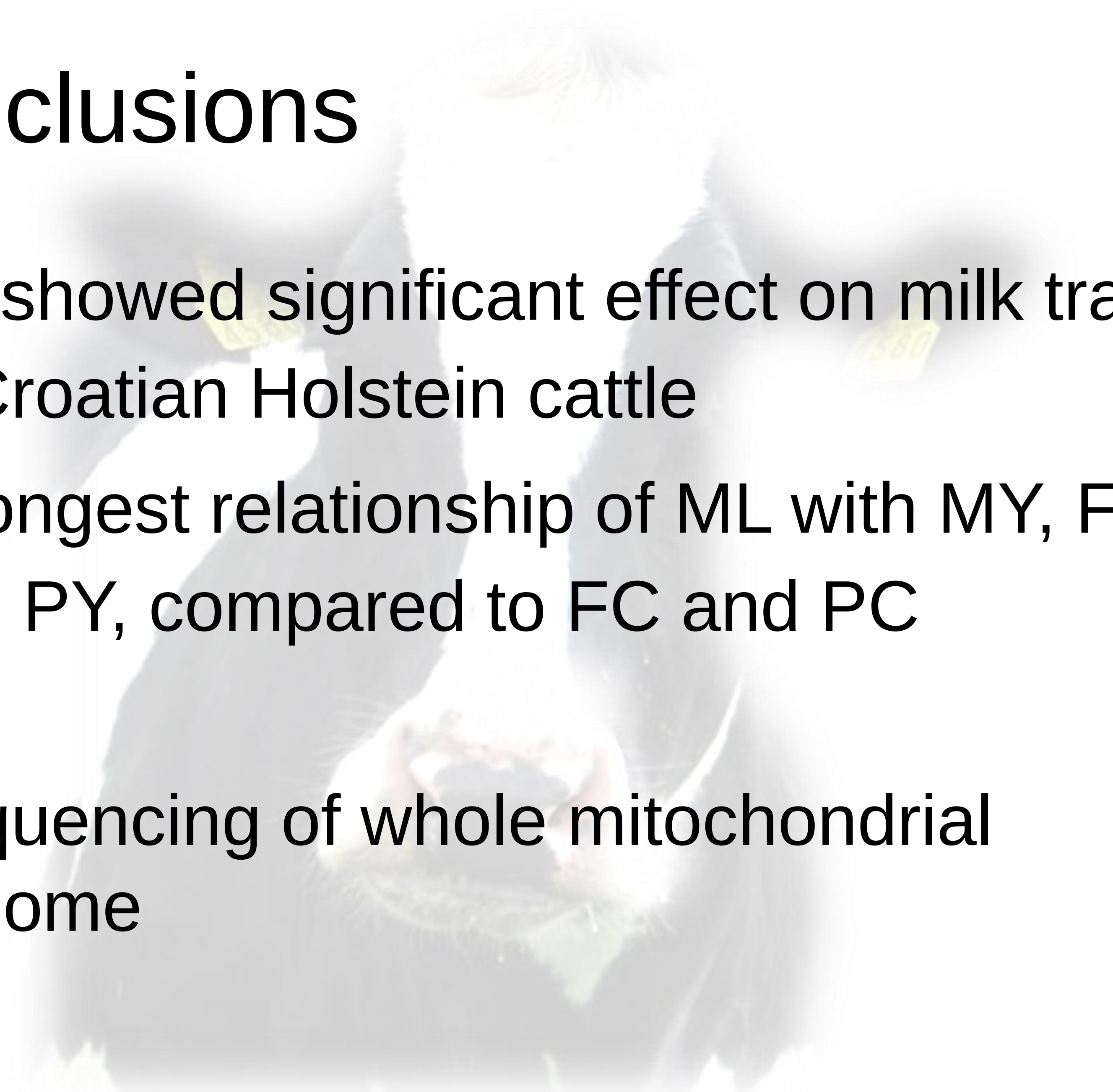
Estimated ratios (%)



Trait	h^2	m^2	c^2	p^2
MY (kg)	0.32±0.004	0.03±0.002	0.21±0.004	0.22±0.002
FY (kg)	0.29±0.004	0.03±0.002	0.23±0.004	0.22±0.002
PY (kg)	0.31±0.004	0.03±0.002	0.26±0.004	0.20±0.002
FC (%)	0.4[illegible]±0.004	0.02±0.003	0.14±0.003	0.19±0.002
PC (%)	0.47±0.004	0.02±0.003	0.13±0.003	0.19±0.002

MY – milk yield, FY – fat yield, PY – protein yield, FC – fat content, PC – protein content, h^2 – heritability, m^2 – ratio for maternal lineage, c^2 – ratio for common herd-year, p^2 – ratio for permanent environmental effect

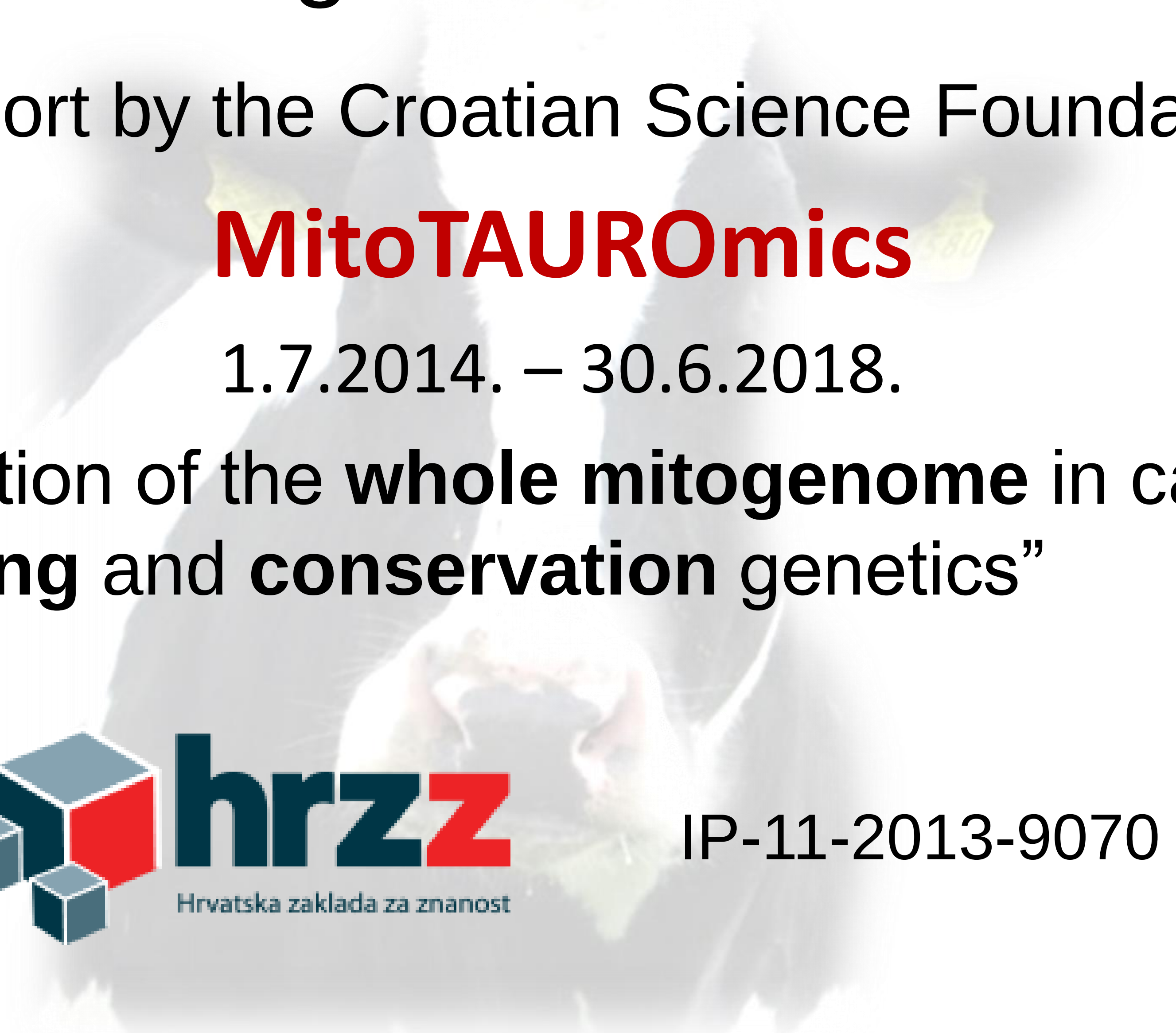
Conclusions



- ML showed significant effect on milk traits in Croatian Holstein cattle
- Strongest relationship of ML with MY, FY, and PY, compared to FC and PC

- Sequencing of whole mitochondrial genome

Acknowledgement



- Support by the Croatian Science Foundation

MitoTAUROmics

1.7.2014. – 30.6.2018.

“Utilisation of the **whole mitogenome** in cattle **breeding** and **conservation** genetics”

hrzz
Hrvatska zaklada za znanost

IP-11-2013-9070

EAAP
European Federation of Animal Science

69th EAAP Annual Meeting
Dubrovnik, Croatia,
27 – 31 August 2018