



EAAP

69th ANNUAL MEETING

Dubrovnik, Croatia
27th to 31st August 2018



Conventional and traditional livestock production systems – new challenges

Impact of the mitogenome inheritance on the milk production traits in Holstein cows

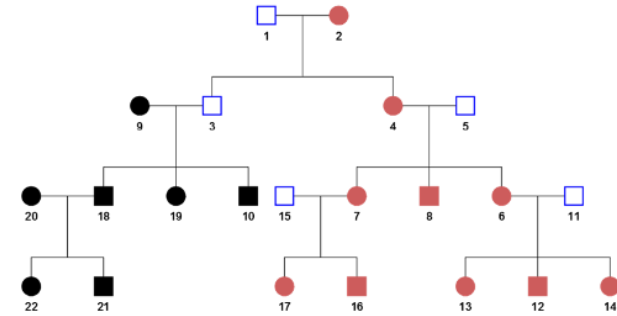
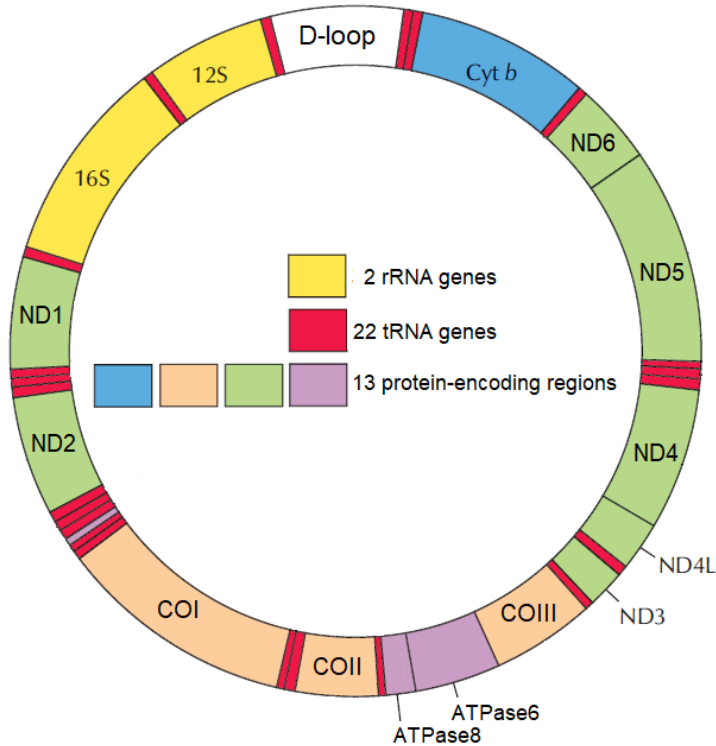
Vladimir Brajkovic, Maja Ferenčaković, Marija Špehar, Dinko Novosel, Vlatka Cubric-Curik, Ivica Međugorac, Elisabeth Kunz, Stefan Krebs, Johann Sölkner, Ino Curik



HPA
HRVATSKA POLJOPRIVREDNA AGENCIJA



Background



T	G	G
C	G	G
C	A	G



Mitogenome

- maternal transmission ♀
- small circular molecule (mtDNA \approx 16,472 bp : nDNA \approx 3*10⁹ bp)
- coding of 37 genes (13 of \sim 85 OXPHOS components \rightarrow cell energy)

Mitogenome impact on the phenotypic variability

Analyses with maternal lineage and D-loop mtDNA :

→ 0 to 4-5% phenotypic variability

Bell et al., 1985; maternal lineage

Kennedy 1986; maternal lineage

Schutz et al., 1994; mtDNA D-loop

Boettcher et al., 1996; mtDNA D-loop, rRNA

Boettcher and Gibson 1997; maternal lineage

Roughsedge et al., 1999; maternal lineage

Špehar et al., 2017; maternal lineage

milk production traits in cattle

Aim of this research

→ estimation of **mitogenome polymorphism** contribution to the **total variance for milk traits in first three lactations**:

- **milk yield - MY**
- **fat yield - MY**



Material - sampling

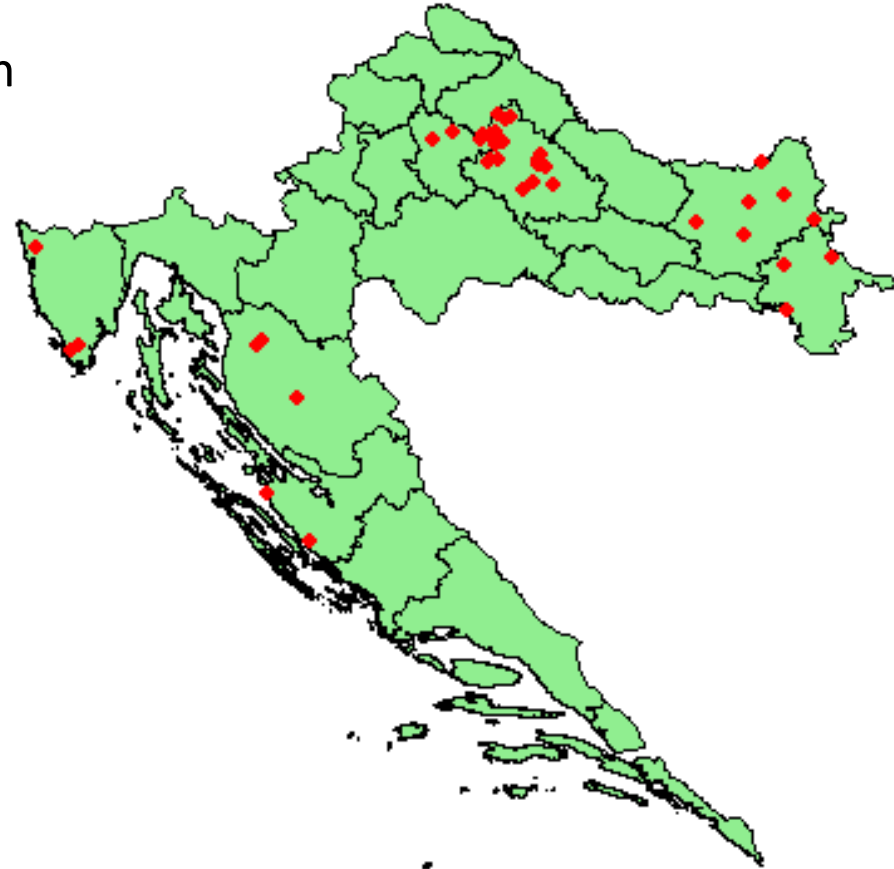
pedigree of Holstein cows ← HPA



295 349 individuals – phenotypic information



20 973 lactating individuals in 2016.



Stat	N
Samples	109
- milk	86
- tissue	1
- hair	22
Regions	7
Places	39
Farms	40

Pedigree analysis and imputation

Ristov et al. *Genet Sel Evol* (2016) 48:65
DOI 10.1186/s12711-016-0242-9

SOFTWARE

Open Access



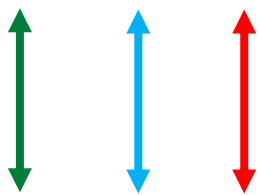
MaGelLAn 1.0: a software to facilitate quantitative and population genetic analysis of maternal inheritance by combination of molecular and pedigree information

Strahil Ristov^{1*}, Vladimir Brajkovic², Vlatka Cubric-Curik², Ivan Michieli¹ and Ino Curik²

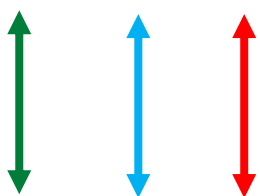
Maternal lineages



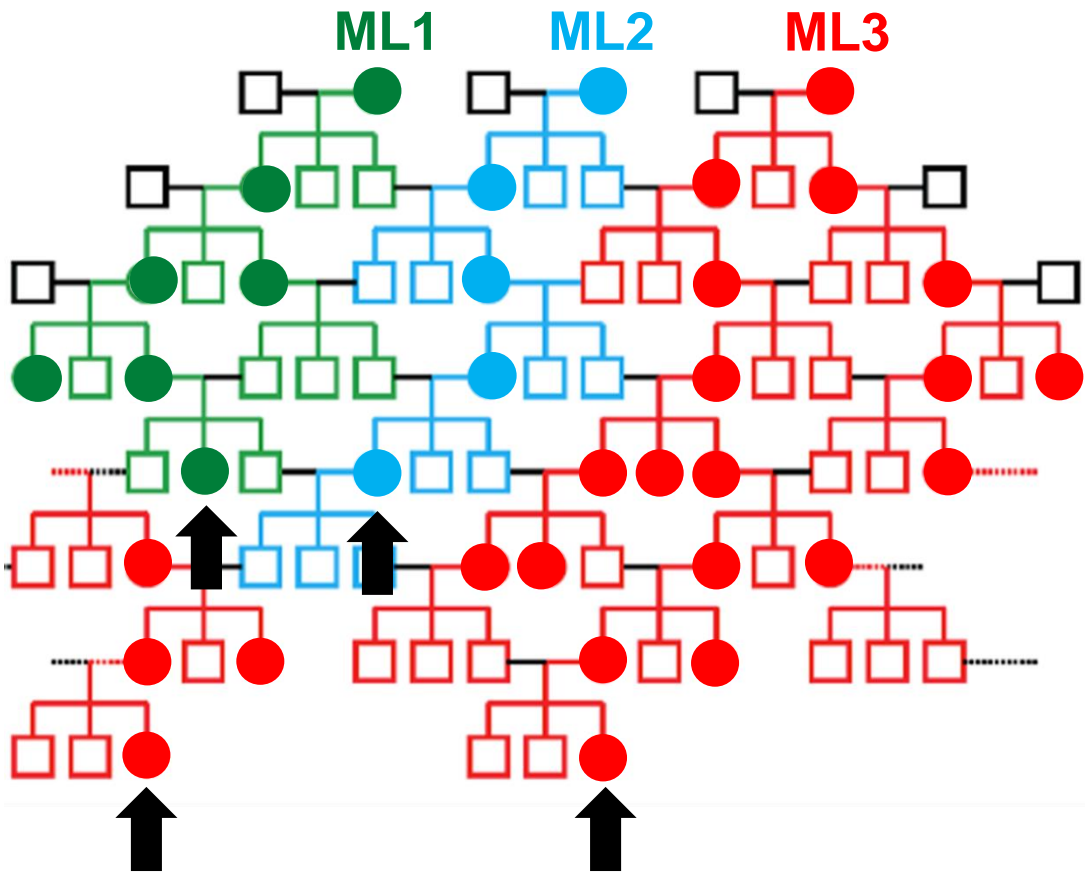
founders = 109



individuals = 2373



individuals = 109



”Maternal inheritance without recombination”

MaGelLAn (Maternal Genealogy Lineage Analyser)

Methods – sequence analysis workflow

NGS analysis
(3 step PCR)
↓
sequences –
fastqsanger format

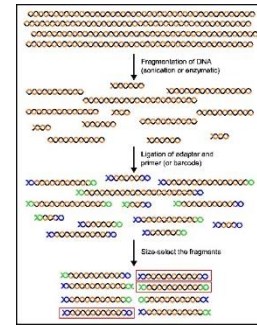


↓
.fasta



aminoacid haplotypes

sequence haplotypes



aminoacid haplotypes

Part of mitogenome	Number of variable sites	Length bp	Position bp
ND1	7	957	3104-4060
ND2	5	1044	4269-5312
COX1	2	1545	5691-7235
COX2	1	684	7380-8063
ATP8	2	201	8135-8335
ATP6	4	681	8296-8976
COX3	7	804	8976-9779
ND3	2	357	9829-10185
ND4L	1	297	10245-10541
ND4	6	1425	10535-11959
ND5	11	1821	12115-13935
ND6	1	528	13919-14446
CYTb	10	1140	14520-15659
	59	11484	

A T G T T C A T T A A C C G C T G A C T A T T C T C A A C C A A

AIDIYVVATVVSIAMLIAIYTIIMMMPMLALTVVVIYMFTYDSVIVVVIIVSAVFSVLDMV

48 aminoacid haplotypes

sequence haplotypes

Mitogenome

16345 bp



363 variable sites



96 sequence haplotypes

Methods – statistical model

- mitogenome impact on the phenotypic variability
- linear mixed model – animal model:

MTDFREML



$$\underline{Y_{klmop}} = \mu + b1(\underline{x_{klmop}} - \mu_{\bar{x}}) + \underline{s_{kl}} + \underline{h_{mo}} + a_o + e_{klmop}$$

Milk yield; (y_{klmop})
Fat yield; (y_{klmop})

} dependent variable → first three lactation

Age at first calving (x_{klmop})

} covariate

Herd_Year_Season - HYS (s_{kl});

Cytoplasmatic effect (h_{mo})::

- maternal lineage (Lineage)
- sequence haplotype (Sequence)
- aminoacid haplotype (Aminoacid)

Direct additive genetic effect (a_o)

} random effects

Lactation	N	Lineage	Sequence	Aminoacid	Regions	Herd	HYS
1 st	2373	109	96	48	7→16	40→202	1285
2 nd	1975	109	96	48	7→16	40→191	1195
3 rd	1332	109	96	48	7→16	40→171	904



Results

Lactation	Variable (kg)	N	Mean	SD	Min	Max
1 st	MY	2373	6761.90	1549.01	3022.20	11980.20
	FY	2372	258.31	63.22	109.00	500.20
2 nd	MY	1975	7462.48	1841.52	3067.70	11960.10
	FY	1975	288.74	78.42	102.10	597.50
3 rd	MY	1332	7497.19	1899.16	3103.10	11982.30
	FY	1332	290.77	80.65	94.10	585.90

Results - variance components ratios (\pm SE) for milk yield (kg)

Lactation	Model	Heritability	“Mito-effect”	HYS	Δ AICc
1 st	Lineage	0.39 \pm 0.04	0.07 \pm 0.02	0.15 \pm 0.02	26.9
	Sequence	0.40 \pm 0.04	0.07 \pm 0.02	0.15 \pm 0.02	0.0
	Aminoacid	0.42 \pm 0.04	0.09 \pm 0.03	0.15 \pm 0.02	35.1
2 nd	Lineage	0.28 \pm 0.04	0.07 \pm 0.02	0.19 \pm 0.03	0.2
	Sequence	0.29 \pm 0.04	0.07 \pm 0.02	0.19 \pm 0.03	0.0
	Aminoacid	0.31 \pm 0.04	0.09 \pm 0.03	0.18 \pm 0.03	1.4
3 rd	Lineage	0.31 \pm 0.06	0.07 \pm 0.02	0.26 \pm 0.04	0.2
	Sequence	0.31 \pm 0.05	0.07 \pm 0.02	0.26 \pm 0.04	0.0
	Aminoacid	0.32 \pm 0.05	0.10 \pm 0.04	0.25 \pm 0.04	0.2

Herd_Year_Season - HYS

Results - variance components ratios (\pm SE) for fat yield (kg)

Lactation	Model	Heritability	“Mito-effect”	HYS	Δ AICc
1 st	Maternal lineage	0.38 \pm 0.05	0.10 \pm 0.04	0.12 \pm 0.02	39.2
	Sequence hap	0.38 \pm 0.05	0.10 \pm 0.04	0.15 \pm 0.03	0.0
	Aminoacid hap	0.38 \pm 0.04	0.07 \pm 0.03	0.16 \pm 0.03	37.8
2 nd	Maternal lineage	0.30 \pm 0.04	0.08 \pm 0.02	0.15 \pm 0.03	0.0
	Sequence hap	0.30 \pm 0.04	0.08 \pm 0.02	0.15 \pm 0.03	0.0
	Aminoacid hap	0.32 \pm 0.04	0.07 \pm 0.03	0.16 \pm 0.03	5.0
3 rd	Maternal lineage	0.28 \pm 0.06	0.08 \pm 0.02	0.23 \pm 0.04	2.2
	Sequence hap	0.29 \pm 0.06	0.06 \pm 0.02	0.24 \pm 0.04	0.0
	Aminoacid hap	0.32 \pm 0.06	0.11 \pm 0.05	0.20 \pm 0.04	13.8

Herd_Year_Season - HYS

Conclusion

- Significant contribution of mitogenome on milk production traits in Holstein cows in Croatia:

milk yield → 7 – 11%
fat yield → 6 – 10 % } of phenotypic variability

IN PROGRESS:

- nucleotide polymorphism
- coding regions (or mini haplotypes)



contribution to the total variance on milk traits



Acknowledgement

MitoTAUROmics: "Utilisation of the **whole mitogenome** in cattle **breeding** and **conservation** genetics - "

Miroslav Kaps



Strahil Ristov



Nikola Raguž and Boris Lukić



Thank you for your attention!