

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

*V. Brajkovic<sup>1</sup>, M. Ferenčaković<sup>1</sup>, M. Špehar<sup>2</sup>, D. Novosel<sup>1</sup>, V. Cubric-Curik<sup>1</sup>, I. Međugorac<sup>3</sup>, E. Kunz<sup>3</sup>, S. Krebs<sup>4</sup>, J. Sölkner<sup>5</sup> and I. Curik<sup>1</sup>*

*<sup>1</sup>University of Zagreb Faculty of Agriculture, Svetosimunska 25, 10000 Zagreb, Croatia, <sup>2</sup>Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia, <sup>3</sup>LMU München, Veterinärstraße 13, 80539 München, Germany, <sup>4</sup>LMU München, Gene Center, Feodor-Lynen-Straße 25, 81377 Munich, Germany, <sup>5</sup>University of Natural Resources and Life Sciences Vienna, Gregor Mendel Strasse 33, 1180 Vienna, Austria; [vbrajkovic@agr.hr](mailto:vbrajkovic@agr.hr)*

Mitochondrial genome is a part of the oxidative phosphorylation metabolic pathway and is responsible for the production of energy in an organism. Still, the impact of mitogenome inheritance on the production traits in livestock is rarely studied. We sequenced (NGS) complete mitogenomes of cows representing 109 maternal lineages. This enabled us to assign mitogenome sequence information to 3,040 cows with 7,576 milk production records (milk yield, fat yield; and protein yield). Thus, we were able to apply quantitative genetic model and estimate the proportion of total variance explained by mitochondrial inheritance ( $m^2$ ). We estimated  $m^2$  with three different models: (1) cytoplasmic model with maternal lineages ( $m^2_{\text{CYTO}}$ ), (2) haplotypic model with mitogenome haplotypes ( $m^2_{\text{MITO}}$ ) and (3) amino-acid model with unique amino-acid combinations ( $m^2_{\text{AMIN}}$ ). Effects of animal, parity, calving season, region, year, herd and age at first calving were also considered in each model. Estimated proportions of phenotypic variances explained by  $m^2_{\text{CYTO}}$  and  $m^2_{\text{MITO}}$  were almost identical ranging from 0.04 to 0.05 for all three milk traits. In amino-acid model, the explained proportion of total variance was higher for protein yield ( $m^2_{\text{AMIN}}=0.07$ ), equal for milk yield ( $m^2_{\text{AMIN}}=0.05$ ), and lower for fat yield ( $m^2_{\text{AMIN}}=0.03$ ). Obtained results show that considerable proportion of the phenotypic variance in milk traits is explained by mitogenome variation. While our further research is targeted towards identification of causal mutation, the utilisation of mitogenome inheritance in practical animal breeding remains challenging.