Abstract of the doctoral dissertation of Katarzyna Kowalska, entitled:

## Application of CGH microarray technique in detecting genomic microrearrangements in horses

Supervisor: Prof. dr hab. Monika Bugno-Poniewierska

Supporting supervisor: dr hab. Klaudia Pawlina-Tyszko

Date of abstract preparation: 11.07.2024

Doctoral dissertation conducted at National Research Institute of Animal Production in Balice.

Equine fertility plays a crucial role in advancing horse breeding practices. The presence of chromosomal abnormalities, whether numerical or structural, can significantly impact reproductive success, leading to issues like embryo loss, perinatal deaths, and decreased fertility in carriers. Given that mares reach their reproductive prime later in life and are often removed from breeding programs after two unsuccessful reproductive seasons, these abnormalities can have notable economic implications. Thus, precise cytogenetic diagnostics are essential for modern breeding strategies.

Reproductive processes in horses are complex, shaped by a combination of genetic and environmental factors. They result from a network of genes, intricately regulated during development. Selecting the proper research methods, paired with high-quality microscopic imaging, is crucial in cytogenetic diagnostics. Advanced techniques, like fluorescence in situ hybridization (FISH) and array-based comparative genomic hybridization (aCGH), offer better diagnostic precision for chromosomal abnormalities, allowing for early identification and potential removal of affected individuals from breeding programs.

The studies presented in this paper focus on the identification of microrearrangements and the detailed analysis of chromosomal abnormalities using advanced aCGH techniques in horses with reproductive and/or developmental disorders. The conducted analyses provide valuable information regarding copy number variations in the equine genome, as well as insights into potential correlations between diagnosed genomic microrearrangements and biological processes related to reproduction and sex determination.

The obtained results expand the knowledge of genetic factors determining and influencing fertility in the horse population. In the future, this knowledge may develop diagnostic tests that enable detailed and precise assessment of the reproductive potential of both mares and stallions.