Expression of interest in collaborating on Horizon Europe calls

On behalf of Prof. Joanna Szyda from Wroclaw University of Environmental and Life Sciences (UPWr), we would like to express interest to cooperate as a partner in the following area of Horizon Europe. Please find below more information on expertise of research group and contribution to the project.

In case of any questions or remarks, please email international.research@upwr.edu.pl

HORIZON EUROPE calls

HORIZON-CL6-2022-BIODIV-01-07: Protection and sustainable management of forest genetic resources of high interest for biodiversity, climate change adaptation, and forest reproductive materials
Deadline: 15 February 2022 17:00

Brief description of contribution as a partner:

Performing the task related to the bioinformatic and statistical analysis of in silico data comprising whole genome DNAseq, and targeted sequencing. The bioinformatic part comprises implementation of full pipelines leading to the identification of point variants (Single Nucleotide Polymorphisms and InDels) and structural variants (Copy Number Variants) as well as, for metagenomic data, pipelines leading to the identification of microbes on the level of species or some higher taxonomic levels. The statistical analysis comprises standard, but also custom written programs and analyses of tree genomic data including among others the genome-wide association study of complex and binary phenotypes, the estimation of population parameters, the estimation of runs of homozygosity, comparison and significance testing of genomic diversity between populations and particular trees.

Potential results to be delivered comprise: the identification of polymorphisms on the genome-wide scope which can be used to assess individual tree or population genetic variability, the identification of trees/populations with outstanding contributions to the genetic variability, identification of genomic regions under high selection intensity, estimation and statistical testing of genomic differences between populations (e.g. Fst, Jacckard index, alpha and beta diversity indices).

Contribution to expected outcomes in the call text are related to evaluation of the impact of forestry activities on forest genetic diversity as well as on breeding forest reproductive material with a higher genetic diversity.

Added value comprises the fact that the group is a unique mixture of researchers with various backgrounds involving mathematics, biology, animal genetics and bioinformatics, which combined, allows for a broad expertise and results in wide range of tools for data analysis. The group has experience in the analysis of various data structures from whole throughput technologies (e.g. whole genome DNA seq, whole genome RNAseq, metagenomic analysis, population genetic data, human clinical data) and with various species (farm animals, wild animals, laboratory species, humans).

Relevance of expertise/previous research:

The group is composed of the PI (Prof. Joanna Szyda) and Bartosz Czech (PhD Student with major expertise in bioinformatic analysis of various structures of biological data), Krzysztof Kotlarz (PhD Student with major expertise in efficient computing and statistical modelling of biological data), Dr. Magdalena Frąszczak (major expertise in statistical modelling of biological data), Dr. Magda Mielczarek (major expertise in bionformatic analysis of DNA and RNAseq data), and Prof. Tomasz Suchocki (major expertise in statistical modelling of population and clinical data).

List of publications:

1. Sierpinski, R., Josiak, K., Suchocki, T., Wojtas-Polc, K., Mazur, G., Butrym, A., Rozentryt, P., Meer, P., Comin-Colet, J., Haehling, S., Kosmala, W., Przewlocka-Kosmala, M., Banasiak, W., Nowak, J., Voors, A.A., Anker, S.D., Cleland, J., Ponikowski, P., and Jankowska, E.A. (2020) High Soluble Transferrin Receptor in Patients With Heart Failure: a Measure of Iron Deficiency And a Strong Predictor of Mortality. European Journal of Heart Failure Online ahead of print.
2. Kosińska-Selbi, B., Suchocki, T., Egger-Danner, Ch., Schwarzenbacher, H., Frąszczak, M. and Szyda, J. (2020) Exploring the potential genetic heterogeneity in the incidence of hoof disorders in Austrian Fleckvieh and Braunvieh cattle. Frontiers in Genetics 11: 1423
3. Kotlarz, K., Mielczarek, M., Suchocki, T., Czech, B., Guldbrandtsen, B., and Szyda, J. (2020) The application of deep learning for the classification of correct and incorrect SNP genotypes from whole-genome DNA sequencing pipelines. Journal of Applied Genetics 61, 607–616
4. Czech, B., Guldbrandtsen, B., and Szyda, J. (2020) Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in Bos taurus genome. Scientific Reports 10, 13641
5. Suchocki, T, Egger-Danner, Ch., Schwarzenbacher, H., and Szyda, J. (2020) Two-stage GWAS for the identification of causal variants underlying hoof disorders in cattle. Journal of Dairy Science 103, 4483–4494
6. Szyda, J., Mielczarek, M., Frąszczak, M. Minozzi, G., Williams, J.L. and Wojdak-Maksymiec, K. (2019) The genetic background of clinical mastitis in Holstein-Friesian cattle. Animal 13, 2156-2163
7. Mielczarek, M, Frąszczak, M, Williams, J., Nicolazzi, E.L. and Szyda, J. (2018) Landscape of Copy Number Variations in Bos taurus: individual – and inter-breed variability. BMC Genomics 19, 410
8. Szyda, J., Suchocki, T., Qanbari, S., Liu, Z., and Simianer, H. (2017) Assessing the degree of stratification between closely related Holstein-Friesian populations. Journal of Applied Genetics 58, 521–526
9. Mielczarek, M., Frąszczak, M., Giannico, R., Minozzi, G., Williams, J.L., Wojdak-Maksymiec, K., and Szyda, J. (2017) Analysis of Copy Number Variations in Holstein-

Friesian Cow Genomes Based on Whole Genome Sequence Data. Journal of Dairy Science 100, 5515-5525

10. Suchocki, T., Wojdak-Maksymiec, K. and Szyda, J. (2016) Using gene networks to identify genes and pathways involved in milk production traits in Polish Holstein dairy cattle. Czech Journal of Animal Science 61(11), 526–538

Projects:

- Biodiversity within and between European Red dairy breeds – conservation through utilization, ERA-NET SUSAN
- The application of deep learning methods in the analysis of livestock genomes, Polish Science Foundation

Main collaboration partners:

- University of Kopenhagen, Denmark.
- Aarhus University, Denmark
- University of Göttingen, Germany,
- West Pomeranian University of Technology, Poland
- MNM Diagnostics, Poland
- University of Science and Technology in Bydgoszcz, Poland
- Centre for Heart Diseases, University Hospital, Wroclaw, Poland