Univerzita sv. Cyrila a Metoda v Trnave
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ENTRANCE EXAMINATIONS FOR DOCTORAL STUDIES IN ACADEMIC YEAR 2022/2023

The Faculty of Natural Sciences, University of Cyril and Methodius in Trnava, has launched the Entrance Examinations for the doctoral degree programme in

Molecular Biology

in the full-time and part-time forms of study. The graduates of Slovak or foreign higher education institutions may apply for admission to study providing that they have completed their master's or engineering studies.

APPLICATION FOR DOCTORAL STUDIES

The applicants should submit a filled-in application form with annexes at the Student Affairs Office at the Faculty of Natural Sciences of UCM no later than **15 June 2022.**

The applicants will register for the announced thesis topics.

Annexes to attach to the application form:

- A verified copy of the higher education diploma in the same or related field of study and programme;
- The state leaving examination certificate;
- A short curriculum vitae with the list of published and unpublished works;
- A medical certificate;
- A certificate of the accomplished practice (not obligatory);
- A dissertation thesis proposal.

Entrance examinations

The entrance examination has the character of a selection procedure in the form of a dialogue. The applicant presents his or her motives and study skills, the dissertation thesis proposal, and the foreign language knowledge. The admission commission will also take into consideration the applicant's participation in the student research conferences and the results of previous master's or engineering studies. The applicant applying for the part-time study will submit a certificate of employment in the specific field.

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doc. Ing. Jozef Sokol, PhD.

Dean of the the Faculty of Natural Sciences
UCM in Trnava

Proposal of topic of dissertations for Molecular Biology study program in academic year 2022/2023

1. Topic: Analysis of the grapevine (*Vitis vinifera* L.) virome and optimization of molecular detection of viral pathogens

Supervisor: Ing. Miroslav Glasa, DrSc.

Workplace: Department of Biology, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava

Annotation: The grapevine (*Vitis vinifera* L.) hosts the largest number of viruses among cultivated perennial crops. To date, more than 80 different viral and subviral pathogens have been identified in the grapevine. The recent introduction of next-generation sequencing (NGS) in plant virology has significantly changed the view of the complexity of plant viral infections, while opening up new possibilities for the study of plant virome. In addition, NGS data revealed that coinfection of plants with multiple viruses is clearly the rule rather than the exception, especially for vegetatively propagated crops. Continuous complete indexing of grapevine viruses is needed in view of the adoption of effective phytosanitary measures and the constant threat of emergence and re-emergence of viruses. The work focuses on the analysis of grapevine virome using massive parallel sequencing in order to identify the widest possible range of viral and subviral pathogens and their partial or whole genome molecular characterization. As the adoption of effective phytosanitary measures depends on the early and accurate detection of pathogens in plants, attention will also be paid to the optimization and validation of molecular detection tests (especially RT-PCR), taking into account the exceptional genetic variability of viruses. Evaluation of the molecular heterogeneity generated by different evolutionary mechanisms will allow a better understanding of the complexity of viral infections and their impact on the overall etiology of viruses.

Key words: virome; fruit trees; molecular diversity; next generation sequencing; detection.

2. Topic: Dynamics of digestive processes in carnivorous plants

Supervisor: doc. Mgr. Idikó Matušíková, PhD.

Workplace: Department of Ecochemistry and Radioecology, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava

Annotation: The plant origin of digestive enzymes in the traps of carnivorous plants has only recently been confirmed, and these studies have resulted in the isolation of the first nuclear genes from this group of plants at all. At present, the genome of several species of carnivorous plants has already been published, which confirms the huge increase in interest in studying their ecophysiology, evolution but also their application potential. The thesis will focus on the dynamics of digestive processes of sundews (Droseraceae) depending on the type of digestible substrate on the leaves and time. Changes in the activities of selected enzymes (hydrolases) in digestive secretions will be complemented by analyzes of the activities of members of the relevant gene families that have already been identified in silico. The results of the work will allow not only to describe and evaluate the involvement of selected types of hydrolases in the process of digestion of prey, but also to reveal their interplay or regulation. The results will also allow to evaluate the differences in the mechanisms of digestion of sundews with the mechanisms relatively well described for other types of traps (e.g. Nepenthes).

Key words: chitinases; nucleases; RT-PCR; enzyme substrate; digestive traps.

3. Topic: Bioinformatics approaches to study sequences, structures, specificities and evolution of amylolytic enzymes

Supervisor: prof. Ing. Štefan Janeček, DrSc.

Workplace: Department of Biology, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava

Annotation: PhD-study will be focused on amylolytic enzymes using bioinformatics, i.e. in silico approaches. The subject of study will be represented by amylolytic enzymes from alpha-amylase families classified in the sequence-based server CAZy (Carbohydrate-Active enZymes; http://www.cazy.org/) into several glycoside hydrolase (GH) families: (i) clan GH-H – families GH13, GH70 and GH77; (ii) families GH57 and GH119; and (iii) family GH126. For example, the main alpha-amylase family GH13 – part of the clan GH-H and simultaneously consisting of 44 subfamilies – contains more than 127 thousand protein sequences covering cca 30 different enzyme specificities (February 2022). Amylolytic enzymes from individual families differ from each other by their sequences and structures, domain arrangement of their protein molecules as well as their catalytic machineries. All this reflects their evolutionary history in relation to enzyme specificity and taxonomy. To contribute to the knowledge of unique sequence-structural features responsible for specific properties of amylolytic enzymes, especially with regard to their substrate preference and product profile, as well as to elucidating their evolution, will belong to the main goals of the PhD study. The results should also lead to establishing new enzyme subfamilies and assigning enzyme specificities for hypothetical proteins obtained from complete genomes sequencing. Protein design of amylolytic enzymes represents an additional possible use of achieved knowledge. The PhD-study program also includes participation in a wide international co-operation with the possibility to travel for both short- and long-term stays to renowned laboratories abroad – in Europe and overseas, where it is possible to undertake PhD-student's own experimental work in an effort to confirm the hypotheses from a bioinformatics approach to the study of amylolytic enzymes performed in the home Laboratory.

Key words: amylolytic enzymes; bioinformatics analysis; conserved sequence regions; structure-function relationships; evolutionary relatedness; protein design.

4. Topic: Gut microbiota and diabetic peripheral neuropathy: effect of cemtirestat in rat models of diabetes

Supervisor: Dr. Domenico Pangallo, DrSc.

Workplace: Department of Biology, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava

Annotation: A microbial imbalance inside the gastrointestinal tract (dysbiosis) can be associated with metabolic disorders such as obesity, insulin resistance, diabetes and immunity dysfunction. However, these relationships are still controversial and need further investigation. The aim of this project is focused on better understanding of mutual interactions of gut microbiota and the diabetic state and to reveal their consequences on development of chronic diabetic complications with the main attention to peripheral neuropathy. Effects of cemtirestat, a novel aldose reductase inhibitor, on the above mentioned processes will be studied. The experimental data will produce valuable knowledge on the role of microbiota alterations in the etiology of diabetic peripheral neuropathy and indicate potential therapeutic approaches.

Key words: diabetic complications; microbiome; cemtirestat; MinION platform.

5. Topic: Microbial starters and adjunct cultures for production of Slovakian bryndza cheese with traditional organoleptic properties

Supervisor: Mgr. lucia Kraková, PhD.

Workplace: Department of Biology, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava

Annotation: The aim of the present research project will be to synthesize the previously gained knowledge, make use of the collection of microbial isolates obtained in the previous research projects and to gain additional knowledge as well as obtain new strains of lactic acid bacteria, yeasts and filamentous fungi as candidate starter cultures. The presented research project will involve characterization of microbial communities and genetic characterization of microorganisms in natural whey cultures and in maturation chambers, which will be based on utilization of culture-based microbiological methods and modern molecular-biological methods including high-throughput sequencing. The outcomes of the project will be a collection of microbial strains and of knowledge on their metabolic potential, including characteristics obtained in small-scale application, which will directly facilitate technical development of starter cultures for production of bryndza cheese with traditional organoleptic properties.

Key words: cheese; lactic acid bacteria; yeasts; filamentous fungi; microbiome; MinION platform.

In Trnava 08.03.2022

approved by:

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in Biology

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