
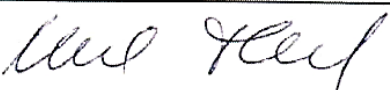
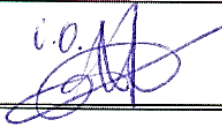
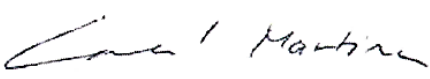
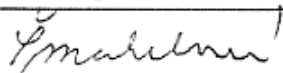
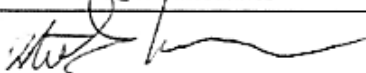




## CELSA - Collaborative research project - Application form - COVER PAGE

<b>1. Identification of the principal investigator (co-ordinator at KU Leuven)</b>
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<b>2. Identification of the second investigator (co-ordinator at Charles University)</b>
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<b>3. Identification of other co-investigator(s)</b>	
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Signature: 	Signature: 

### 3. Non confidential and public friendly summary (max. 2000 characters)

#### Metagenomic analysis of the virome of the honeybee (*Apis mellifera*) in the Czech Republic

The microbiomes of humans, animals, and ecological niches are currently being intensively studied. However, most of these studies only focus on bacteria, thereby neglecting the largest group of microbiome members: the viruses.

The European honeybee (*Apis mellifera*) plays a crucial role in agriculture through pollination. Sudden losses of honeybee colonies sporadically occurred in the past but in last ten years the frequency of losses is increasing. The sudden decline of colonies is named Colony Collapse Disorder (in the US) or Winter Loss (WL) in Europe and the Middle-East. Different factors, including parasitic and viral pathogens, play a role in these sudden declines. Even though methods of next generation sequencing recently allowed for a discovery of many new viruses of honeybees, the study of the virome in WL is unexplored.

The Laboratory of Viral Metagenomics at KU Leuven recently optimized a method (NetoVIR) to accurately study the virome in biological samples. This method uses optimized purification techniques, followed by random amplification of the viral genomes, deep sequencing using Illumina NGS technology, and bioinformatic interpretation of the virome data.

In this CELSA project we propose to accomplish a technology transfer of the virome analysis methods and the associated bioinformatics pipeline from KU Leuven to Charles University (CU) by applying these virome methods on ecologically and parasitologically well characterized collections of Czech bees. The transfer of technology will allow the CU team to gain the „know how“ in microbiome analysis and interpretation, and will enhance existing collaborations and foster novel collaborations between our laboratories in Belgium and the Czech Republic. The CU team provides expertise in proteomic analysis of viral proteins in bee parasites. This CELSA grant will broaden our capacities, both in Leuven and in Prague, to successfully explore future European funding opportunities.

#### 4. List 5 key words

microbiome, virome, parasitome, next generation sequencing, metagenomics