

Opis delovnega mesta mladega raziskovalca/ke (*Description of the Young Researcher's position*)

1. Članica UL (*UL member*):

Biotehniška fakulteta (*Biotechnical Faculty*)

2. Ime, priimek in elektronski naslov mentorja/ice (*Mentor's name, surname and email*):

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3. Raziskovalno področje (*Research field*):

Genetika, biotehnologija (*Genetics, Biotechnology*)

4. Opis delovnega mesta mladega raziskovalca/ke (*Description of the Young Researcher's position*):

Vključuje morebitne dodatne pogoje, ki jih mora izpolnjevati kandidat/ka za mladega raziskovalca/ko, ki niso navedeni v razpisu za mlade raziskovalce.

slo:

Akutni respiratorni sindrom koronavirus 2 (SARS-CoV-2), ki povzroča boleznih dihal z različno bolezensko sliko se je v preteklih letih pridružil drugim zoonozam, ki jih povzročajo virusi in so v zadnjih desetletjih predstavljale v različnih delih sveta resno grožnjo zdravju človeške populacije. Globalne posledice SARS-CoV-2 pandemije zaradi njene obsežnosti in zaradi njenega vpliva na številna področja našega življenja bodo še nekaj časa prisotne. Ker natančne poti prenosa SARS-CoV-2 od živalskega gostitelja na človeka in potencialni prenos na druge živalske vrste, ki predstavljajo potencialno neidentificirano grožnjo za človeško populacijo niso v celoti znane, je pomembno, da za živalske vrste, ki živijo v tesnem kontaktu s človekom ocenimo tveganje, da bi te populacije domačih in divjih živali postale rezervoar za nove okužbe s SARS-CoV-2. Kandidat(-ka) bo v okviru delovanja v programske skupine P4-0220 Primerjalna genomika in genomska biodiverziteteta v skladu s konceptom One Health European Joint Program (OHEJP) izvedla (el) pregled genetske variabilnosti delov genoma, ki kodirajo najpomembnejše epitope za pritrjevanje virusnega Spike proteina na gostiteljske celice. Potencialni rezervoar gostitelja SARS-CoV-2 je lahko precej velik in okužbe širokega spektra potencialnih gostiteljskih vrst ni mogoče izključiti. Te ugotovitve bodo pomembno prispevale k pripravi eventualno potrebnih strategij za učinkovito preprečevanje nenadzorovanega širjenja okužb na lokalni ravni. Doktorsko delo bo temeljilo na pridobivanju lastnih laboratorijskih rezultatov, kompleksni bioinformatični analizi in uporabi programskih orodij za simuliranje interakcij med proteinskimi molekulami.

V analizo bodo vključene različne pasme domačih živali, kjer bomo analizirali mutacije, ki spremenijo aminokislinsko zaporedje v tarčnih genih gostitelja in proučevali vpliv sprememb v teh genih na afiniteto vezave različic SARS-Cov 2 virusa. Delo bo doprineslo k boljšemu razumevanju molekularnega ozadja občutljivosti na infekcije s SARS-CoV 2 in različnemu poteku bolezni. Z oceno ekspresijskega profila tarčnih proteinov gostitelja bo kandidat(ka) skušal(a) pojasniti tudi potencialni vpliv infekcij s SARS-CoV 2 na tkiva izven respiratornega trakta, ki imajo potencialni kontakt s povzročiteljem.

eng:

Acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which causes respiratory diseases with a different disease picture, has joined other zoonoses caused by viruses in recent years and has posed a serious threat to the health of the human population in various parts of the world in recent decades. The global consequences of the SARS-CoV-2 pandemic, due to its magnitude and its impact on many areas of our lives, will be present for some time. Since the exact routes of transmission of SARS-CoV-2 from the animal host to humans and the potential transmission to other animal species that represent a potential unidentified threat to the human population are not fully known, it is important that for animal species that live in close contact with humans we assess the risk of these domestic and wild animal populations becoming a reservoir for new SARS-CoV-2 infections. As part of the program group P4-0220 Comparative Genomics and Genomic Biodiversity, in accordance with the One Health European Joint Program (OHEJP) concept, the candidate will carry out (el) an examination of the genetic variability of parts of the genome that encode the most important epitopes for the attachment of the viral Spike protein to host cells. The potential host reservoir of SARS-CoV-2 may be quite large, and infection of a wide range of potential host species cannot be ruled out. These findings will significantly contribute to the preparation of possibly necessary strategies to effectively prevent the uncontrolled spread of infections at the local level. The doctoral work will be based on obtaining own laboratory results, complex bioinformation analysis and the use of software tools for simulating interactions between protein molecules.

Various domestic animal breeds will be included in the analysis, where we will analyze mutations that change the amino acid sequence in the target genes of the host and study the influence of changes in these genes on the binding affinity of the SARS-Cov 2 virus variants. The work will contribute to a better understanding of the molecular background of susceptibility to infection with SARS-CoV 2 and the different course of the disease. By evaluating the expression profile of the host's target proteins, the candidate will also try to explain the potential impact of SARS-CoV 2 infections on tissues outside the respiratory tract that have potential contact with the pathogen.