1. Raziskovalna organizacija (*Research organisation)*:

Univerza v Ljubljani, *Biotehniška fakulteta*

2. Ime in priimek mentorja (*Name and surname of a mentor*):

Prof. dr. Peter DOVČ

3. Področje znanosti iz šifranta ARRS (*Primary research field*):

4.02.01 Genetika in selekcija
4.06.01 Tehnologija rekombinantne DNA

4. Kontaktni e-naslov mentorja (*Contact of a mentor)*:

Peter.dovc@bf.uni-lj.si

5. Kratek opis programa usposabljanja (*Short description of the program)*:

SLO

Mladi raziskovalec bo delal na področju genomskih študij s pomočjo tehnologije sekveniranja eksoma humanega genoma s pomočjo aparata MiSeq Illumina ter ožje usmerjenih panelov izbora genov za specifična patološka stanja. Eksomske regije vsebujeno mutacije, ki so razlog za bolezenska stanja. Bolezni, ki ne sledijo Mendelejevemu vzorcu dedovanja in so produkt delovanja več genov in okolja, lahko analiziramo samo s pomočjo analiz celotnega genoma. V to skupino spadajo nevrološke, psihiatrične in autoimune bolezni. Mladi raziskovalec se bo osredotočil na preiskovance, kjer smo v okviru naše raziskovalne skupne že določili strukturne genomske variabilnosti s tehnologijo mikromrež, to so otroci s prirojenimi malformacijami, motnjami v duševnem in telesem razvoju ter nevropsihiatričnimi stanji (avtizem, shizofrenija). Poleg dela na eksomu človeka bo kandidat uvedel metodo sekvenciranja eksoma tudi pri nekaterih vrstah domačih živali in miši in na ta način odprl možnost za komparativni študij eksoma sesalskih vrst.

Nadalje bo madi raziskovalec analiziral primere nenadne srčne smrti, ki je v 25% genetsko in dedno pogojena in genetske vzroke drugih dednih kardioloških stanj. Razumevanje in določanje genetske komponente je ključno za prognozo bolezni, terapijo in verjetni izzid zdravljenja. Za analizo bo uporabil TruSight Cardio Kit (Illumina) ki zagotavlja celovito pokritost dobro poznanih 174 vzročnih genov in novih genov z jasno povezavo z 17 oblikami dednih kardioloških stanj, ki vključujejo kardiomiopatije, aritmije in aortopatije. Vzročni geni so tisti s poznanimi povezavami z boleznimi srca; geni, kjer pa te povezave še niso jasno postavljene, so opredeljeni kot geni z dokazanimi povezavami s srčnimi boleznimi, vendar patofiziologije še ne razumemo popolnoma.

V vseh primerih gre za kompleksne bolezni, ki so produkt delovanja mutacij več genov in genskih polimorfizmov. Velik izziv bo v postavitvi korelacije DNA polimorfizmov s fenotipom bolnikov ter ugotoviti njihov dejanski pomen v etiologiji bolezni, za kar bo

potrebno osvojiti tudi veliko znanja iz bioinformatike in uporabe bioinformatskih orodij.

ANG

The young researcher will work in the field of genomic studies using exome sequencing technology, this sequencing panel provides comprehensive coverage of > 4,800 clinically relevant genes using MiSeq sequencer developed by Illumina and narrowly targeted selection of panels of genes for specific pathological conditions. Exome region contains mutations that cause the disease. Diseases that do not follow Mendelian patterns of inheritance and are the product of multiple genes and the environment can be analyzed only through analysis of the entire genome. This group includes neurological, psychiatric and autoimmune diseases. Young researcher will focus on subjects where we in the context of our research group have analyzed structural genomic variations (CNV) using microarray technology in children with congenital malformations, mental and developmental delay and neuropsychiatric conditions (autism, schizophrenia). In about 15% of cases causative CNV was detected. Using the whole genome sequencing methods we expect additional clarification of at least 40% of cases. In addition to human exome will the candidate establish sxome sequencing also in other mammalian species (farm animals and mouse) and so enable comparative exome studies within the research program.

Furthermore, young researcher will analyze the cases of sudden cardiac death, which have at least 25% genetic component and other inherited cardiac conditions (ICC). Understanding and determining those genetic component is crucial for the prognosis of the disease, treatment, therapy choice, and, possibly, outcome. For analysis he will use TruSight Cardio Kit (Illumina) to provide comprehensive coverage well-characterized 174 core genes and emerging genes with known associations to 17 ICCs, including cardiomyopathies, arrhythmias, and aortopathies. Core genes are those with well-established links to cardiac conditions; emerging genes are defined as those genes with demonstrated, but not necessarily understood, connections to cardiac conditions.

In all cases, young researcher will work on complex diseases, which result from the cooperation of several mutations and gene polymorphisms. The big challenge will be to establishe the correlation of DNA polymorphisms with the phenotype of the patients and to determine their actual importance in the etiology of the disease. This will required also a lot of knowledge from bioinformatics and the use of bioinformatics tools.