



INTEG-RNA

# INTEGRATION OF RNA BIOLOGY FOR NEXT- GENERATION SCIENTISTS

*H2020-WIDESPREAD-2020-5*

*Project Number: 952541*



## **D1.3 Short report by research staff**

Work Package: WP1  
Deliverable due date: 31/12/2023  
Responsible partner: MU  
Editors: Michaela Musilová  
Deliverable number: D3  
Deliverable type: Report  
Dissemination level: Confidential  
Created: 1/12/2023  
Version: 1.0

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## 1 INTRODUCTION

Work Package 1, "Pathway to Excellence in RNA Cluster", focuses on establishing, enhancing and nurturing the collaboration between partners in the consortium and equipping CEITEC MU researchers with the necessary knowledge and expertise in techniques and methods to perform excellent research in RNA cluster and beyond. Among the main objectives is enhancing the excellence capacity of CEITEC MU ESRs and researchers in RNA biology.

The Deliverable D1.3 relates to Task 1.3 Secondments of research staff. It includes reports from stays in laboratories of partner institutes in the period January 2022 – November 2023.

Unfortunately, the outgoing problems with COVID during the 1st reporting period affected the start of secondments and internships. No one was allowed to join another lab last year due to measures applied by national governments and by the director of CEITEC MU. We resumed the secondments and internships in February 2022. The list of the travels is presented in Table 1 below.

Despite the numerous advantages associated with secondments, such as skill enhancement, networking, and collaborative research opportunities, a notably low number of postdocs have taken advantage of this professional development avenue. The key reasons are:

- **Low Total Number of Postdocs at CEITEC MU** - Our overall population of postdoctoral researchers is considerably lower than anticipated. This scarcity inherently contributes to a limited pool of potential candidates for secondment opportunities. For CEITEC MU, this is currently one of the most important priorities of our institution's strategy - increase efforts to attract and recruit more postdoctoral researchers to the university, addressing factors such as funding availability, supportive research environment, and competitive benefits.
- **Family Obligations and Responsibilities** - A significant proportion of postdoctoral researchers at our institution already have families, making it challenging for them to commit to longer periods of travel associated with secondments.

## 2 REPORTS BY RESEARCH STAFF

In this section of the Deliverable, the reports of postdocs and research staff are included in the sequence of their travels throughout the years 2022 to 2023 (as per Table 1).

**Table 1. Secondments in WP1**

<b>Secondee</b>	<b>Hosting institution</b>	<b>Term</b>
Lucie Bozděchová	Laboratory of Mark Helm, JGU	20.2.2022-18.3.2022
Vojtěch Bystrý	Laboratory of Vladimír Beneš, EMBL	06.11.2022-12.11.2022
Vojtěch Bystrý	Core facility of Shaun Webb, UEDIN	31.07.2023-06.08.2023
Karla Plevová	Laboratory of Vladimír Beneš, EMBL	13.11.2023-24.11.2023

## 2.1 LUCIE BOZDĚCHOVÁ, MAINZ – GERMANY

**Name, Surname, Title:** Mgr. Lucie Bozděchová, Ph.D.

**Date of business trip, No. of Travel Order:** 20.2.2022 – 18.3.2022

**Name of Institution/Conference:** Johannes Gutenberg-University Mainz

**Address of the Institution/Conference venue:** Staudingerweg 5  
55128 Mainz – Germany

**Aim of the business trip:** Secondment within the INTEG-RNA project - Telomerase RNA sample preparation for epitranscriptomic analysis

### **Description of activities:**

The aim of my secondment was to prepare plant telomerase RNA samples for analysis of RNA modifications by sequencing or LC-MS. The method for determining modifications depends on the amount of material we are able to prepare. Because telomerase RNA is low abundant transcript, it is difficult to isolate it from the cells. During my stay, we wanted to prepare RNA samples that correspond in size to the telomerase RNA and get rid of the other RNA (like tRNA, rRNA etc.)

We used ion exchange chromatography to separate RNA of different sizes. It was necessary to optimize the salt gradient, which would separate the fraction corresponding to the size of the telomerase RNA. Collected fractions were precipitated and samples with correct size were further used for hybridization with a specific oligonucleotide. We were able to enrich telomerase RNA fraction after hybridization and subsequent isolation of samples from the gel. Samples prepared during my secondment will be sent for sequencing and epitranscriptomic analysis.

The time I spend in Mark Helm's group was very nice and inspiring. I gained new knowledges and improve my skills in work with RNA samples. I have tried different methods of isolating specific RNAs and the possibility of future cooperation seems to be very promising.

**Business trip /secondment /conference outcomes:** Samples for further sequencing analysis

**Useful contacts:** Prof. Mark Helm

### **Future Cooperation with the Institution:**

Cooperation in analysis of RNA modifications

## 2.2 VOJTĚCH BYSTRÝ, HEIDELBERG – GERMANY

**Name, Surname, Title:** Vojtěch Bystrý Ph.D.

**Date of business trip, No. of Travel Order:** 6.11.2022 - 12.11.2022, CES/7101/0427/22

**Name of Institution/Conference:** European Molecular Biology Laboratory

**Address of the Institution/Conference venue:** Meyerhofstrasse 1, 69117 Heidelberg, Germany

**Aim of the business trip:** To explore the integration of spatial transcriptomics RNA sequencing with PET-MRI imaging in prostate cancer samples, as part of the CF Bioinformatics proposal. The primary objective was to gain insights and collaborate on cutting-edge techniques in spatially resolved transcriptomics, particularly in the context of prostate cancer research.

### **Description of activities:**

- Attended presentations and workshops focused on the latest advancements in spatial transcriptomics.
- Engaged in discussions about the integration of spatial transcriptomics with imaging techniques.
- Explored potential tools and methods for data cleaning and analysis in the context of prostate cancer samples.

### **Business trip /secondment /conference outcomes:**

- Established a collaborative relationship with key researchers in the field.
- Gained insights into advanced tools such as SpotClean for data cleaning and techniques for achieving high-definition resolution from histology images.
- Learned about the challenges and potential solutions for dealing with heterogeneous samples, including the use of deconvolution tools.
- Discussed the importance of recognizing patterns in the spatial distribution of cellular states within tissues.

### **Useful contacts:**

- Jan-Philipp Mallm
- Denis Schapiro
- Kristy Ou
- Wouter-Michiel Adrien Maria Vierdag
- Vladimir Benes
- Tobias Rausch

### **Future Cooperation with the Institution (not valid for Conferences):**

- Continuous collaboration for the technological transfer of spatial transcriptomics expertise to CEITEC.
- Joint efforts in the development and application of advanced tools and methods in the study of prostate cancer.
- Possible co-authorship in future publications and sharing of data analysis experiences.

### 2.3 VOJTĚCH BYSTRÝ, EDINBURGH – UK

**Name, Surname, Title:** Vojtěch Bystrý Ph.D.

**Date of business trip, No. of Travel Order:** 31.7. - 6.8.2023, CES/7101/0251/23

**Name of Institution/Conference:** University of Edinburgh

**Address of the Institution/Conference venue:** Michael Swann Building, Max Born Crescent, Edinburgh, EH9 3BF

**Aim of the business trip:** The main objective was to discuss and advance bioinformatics analysis of RNA and spatial RNA, specifically in the context of the CEITEC's spatial transcriptomics pilot project focusing on RNA bioinformatics analysis. This involved collaborative discussions on automating and standardizing bioinformatics workflows and exploring potential collaborations in providing software solutions like SeqUIa.

**Description of activities:**

- Met with Shaun Webb, head of the bioinformatics core facility, to discuss the standardization and automation of bioinformatics workflows.
- Engaged in detailed discussions with David Tollervey and Aleksandra Helwak about the intricacies of RNA analysis and the novel approaches in spatial transcriptomics.
- Explored the potential of integrating SeqUIa software into existing workflows to enhance the analysis and interpretation of complex RNA data.

**Business trip /secondment /conference outcomes:**

- Established a framework for collaboration on automating and standardizing bioinformatics workflows.
- Discussed the potential integration of SeqUIa in the University of Edinburgh's bioinformatics projects.
- Gained valuable insights into advanced methods of spatial transcriptomics, enhancing the understanding of RNA biology and bioinformatics analysis of RNA interactions.

**Useful contacts:**

- Shaun Webb
- David Tollervey
- Aleksandra Helwak

**Future Cooperation with the Institution (not valid for Conferences):**

- Ongoing collaboration in the field of bioinformatics, particularly in spatial transcriptomics.
- Potential integration and application of SeqUIa software in various research projects at the University of Edinburgh.
- Joint efforts in advancing the field of RNA research, with a focus on cancer studies and molecular biology.

## 2.4 KARLA PLEVOVÁ, HEIDELBERG – GERMANY

**Name, Surname, Title:** Karla Plevová, MSc., Ph.D.

**Date of business trip, No. of Travel Order:** 13. - 25.11.2023, CES/7101/0435/23

**Name of Institution/Conference:** EMBL Heidelberg

**Address of the Institution/Conference venue:** Meyerhofstraße 1, 69117 Heidelberg, Germany

**Aim of the business trip:** Workshop on advanced NGS analysis, Cancer Genomic 2023 conference and research secondment at the Genomic Core Facility, EMBL, Heidelberg

**Description of activities:** The workshop consisted of several parts. We visited three sites: the Genomic Core Facility, the IT Department, and the Imaging Centre of EMBL Heidelberg. Apart from the tour, we had an opportunity to discuss data analyses individually and in focused groups with local experts. We elaborated mainly on the Oxford Nanopore Technology sequencing and data analysis, Hi-C analysis, and single-cell RNA data analysis. The stay at EMBL went on with the Cancer Genomics conference, which is one of the most renewed conferences in the field and showcased recent findings in genomics of various cancer types. I had the opportunity to talk to multiple experts focusing on novel approaches for exploring cancer genomes. Furthermore, my students presented the results of their projects during the conference poster sessions and we had an excellent possibility to network and discuss our findings with conference attendees on how to advance our observations. The conference content was highly relevant to the preceding workshop and the following secondment. During the secondment, I worked on data analyses together with EMBL bioinformatician Tobias Rausch, who helped me design the proper way of data analysis focusing on understanding the consequences of structural genomic variants on chromatin conformation and gene expression.

**Business trip /secondment /conference outcomes:** A deeper understanding of the modern sequencing methods and their bioinformatic analyses. Learning novel findings on cancer genome structure and function. Networking opportunity. Obtaining new data that will advance my current project.

**Useful contacts:** Laura Villacorta ([laura.villacorta@embl.de](mailto:laura.villacorta@embl.de)), Tobias Rausch ([tobias.rausch@embl.de](mailto:tobias.rausch@embl.de)), Jan Korbelt ([jan.korbelt@embl.de](mailto:jan.korbelt@embl.de)), Kevin Nzumbi Mutemi ([kevin.mutemi@embl.de](mailto:kevin.mutemi@embl.de))

**Future Cooperation with the Institution:** We agreed on further collaboration toward finishing our current project.