



IAEA

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国际原子能机构

International Atomic Energy Agency

Agence internationale de l'énergie atomique

Международное агентство по атомной энергии

Organismo Internacional de Energía Atómica

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In reply please refer to: FS-SAF5016-2207241

Dial directly to extension: (+43 1) 2600-24623

The Secretariat of the International Atomic Energy Agency (IAEA) presents its compliments to the Permanent Mission of the Czech Republic and has the honour to enclose herewith the application form of the following candidate who has been awarded a fellowship under the IAEA's technical cooperation programme and is recommended for placement in Czech Republic:

EVT2207241-0001-ZAF

Field of Activity: Crop production

Training programme awarded: Learn bioinformatics procedures and perform comparative genomic studies on mutants

Institute suggested: Academy of Sciences of the Czech Republic (ASCR)
Institute of Experimental Botany (ÚEB)
Rozvojová 135
165 02; 6 PRAHA
CZECH REPUBLIC

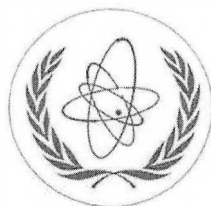
Recommended supervisor: Email: @ueb.cas.cz

Duration: 3 months

Availability: to 30 June 2023

It would be appreciated if the IAEA could be informed as soon as possible (e-mail response to: Ms Evelyn Anu Oluwapo Onyedikachi, E@iaea.org, if possible with completed Acceptance Form) whether a suitable programme of training can be arranged for this candidate in Czech Republic.

The Secretariat of the International Atomic Energy Agency avails itself of this opportunity to renew to the Permanent Mission of the Czech Republic the assurances of its highest consideration.



2022-11-25

Attachment: Application Form
Acceptance Form



Program for the training of Ms. Coetzee Beatrix under the IAEA's Technical Cooperation Program

IAEA reference number:	FS-SAF5016-2207241
Training programme awarded:	Learn bioinformatics procedures and perform comparative genomic studies on banana mutants
Institute suggested:	Institute of Experimental Botany of the Czech Academy of Sciences (IEB) Rozvojová 135 165 02 Praha 6 Czech Republic
Recommended supervisor:	Centre of Plant Structural and Functional Genomics of IEB Šlechtitelů 31 7790 0 Olomouc Czech Republic Email: @ueb.cas.cz
Duration:	3 months
Availability:	to 30 June 2023
Training fees:	A total of 5720 EUR for 13 weeks of training (440 EUR / week)
Additional costs:	295,143.2 CZK (including 21% VAT) for PacBio sequencing of two banana genotypes (approx.12,146 EUR)

1st month

Arrival of the trainee to the Centre

- Accommodation
- Overview of the work of the Laboratory
- Preparation of the program (bioinformatics and experimental part)

Discussion of bioinformatic tools used for the analysis of DNA sequencing data

- Bioinformatics pipelines used for the analysis of transcriptomes
- Bioinformatic pipelines used to create whole genome assemblies using third generation sequencing technologies (Oxford Nanopore and PacBio)

Discussion of Bionano optical mapping

- Preparation of high molecular weight DNA for optical mapping using Bionano technology
- Analysis of the Bionano data and construction of optical maps
- Validation of genome assemblies; identification of misassembled regions

Discussion and running jobs on Metacentrum computing facilities

- Overview on the use Metacentrum.cz computing facilities for DNA sequence data analysis
- Preparation of interactive jobs
- Initiation of data analysis: trimming of RNAseq and PacBio HiFi reads

2nd month

Analysis of RNAseq data

- De-novo transcriptome assembly of RNAseq data (Trinity program)
- Alignment of RNAseq data to the available reference and differential gene expression analysis using EDGER package

Analysis of PacBio HiFi data

- Creation of de-novo genome assemblies from PacBio HiFi sequence data using HiCanu and Flye assemblers

Validation of whole genome assemblies using Bionano optical mapping.

- Alignments of new de-novo genome assemblies (so-called hybrid scaffolding) to Bionano optical maps and creation of final chromosome-scale assemblies

Annotation of genome assemblies

- Use of banana-specific databases of repetitive DNA elements and other standard databases of DNA repeats and genes
- Use of new de-novo created transcriptome assemblies to support *in silico* identification of genic regions and to identify alternative splicing

3rd month

Analysis of RNAseq data

- Alignment of RNAseq data to the newly available reference and differential gene expression analysis using EDGER package – continuation in the analysis

Annotation of genome assemblies

- Use of banana-specific databases of repetitive DNA elements and other standard databases of DNA repeats and genes
- Use of new de-novo created transcriptome assemblies to support *in silico* identification of genic regions and to identify alternative splicing

Comparative analysis of the new whole genome assemblies

- Comparison of chromosome structures between and within the new genome assemblies and already existing genome assemblies of *M. acuminata* ssp. using 1) minimap2 program and visualized using D-genies; 2) comparison and alignments of protein coding regions using reciprocal BLAST/ program followed by MCScanX program
- If longer inversions, insertions-deletions, or translocation within new genome assemblies are identified, specific primers for the rearranged regions will be designed for future validation

Departure of the trainee

Prepared in Olomouc
RNDr. Jan Martinec, CSc.



1.6.2023