



Annex No. 1

Application form for the “Internal Support of Research Program” Directive  
of the Institute of Biophysics of the CAS, v. v. i.

**Project proposal for the Internal Support of Research Program  
of the Institute of Biophysics of the CAS, v. v. i.**

Project name:

**Dynamics of LTR retrotransposons in plant genomes with holocentric chromosomes**

Project type (delete if not applicable): **Pilot**

Name and surname of the applicant: Pavel Jedlička

Members of the team: Eduard Kejnovský (IBP), Matej Lexa (IBP), Petr Bureš (MUNI), František Zedek (MUNI)

Project abstract (max 1100 characters including spaces):

LTR retrotransposons (LTR-RTs) are mobile genetic elements constituting remarkable portions of plant genomes and significantly contribute to genome structure, size and regulations. Some LTR-RTs lineages are distributed uniformly while others are localized in centromeres of monocentric chromosomes. But little is known about characterization and distribution of retrotransposons within genomes with holocentric chromosomes. We will test our hypothesis that the LTR RTs in holocentrics will be evenly distributed along chromosomes. Therefore we designed the comparative study with three groups where each is composed from two holocentric plant species with different karyotypes and one phylogenetically closest monocentric relative. These species will be sequenced using: (1) Oxford Nanopore Technologies (long reads) and (2) Illumina sequencing (short reads). The primary assembly will be generated and subjected to the in-depth LTR-RTs detection analysis. Our investigation will provide information on LTR-RTs families abundance and distribution in relation to the phenomenon of holocentrism.

*I declare that the project does not overlap with any project that is ongoing or proposed to another agency.*

Signature of the Applicant

Signature of the Head of the Department

**Project description** (maximum range of 3 pages, minimum font size 11, max. 5 citations).

*Project name*

## **Dynamics of LTR retrotransposons in plant genomes with holocentric chromosomes**

### *Introduction*

Transposable elements (TEs) constitute a remarkable portions of eukaryotic genomes and significantly contribute to genome structure and regulation of gene at transcription, duplication and ectopic recombination levels. Besides, due to a replicative power of the 'copy-and-paste' type of TEs (retrotransposons), they can also strongly influence the genome size with classical examples of long terminal repeat (LTR) retransposons expanded in maize (~80% of 2.3 Gbp) and non-LTR retrotransposons in human (~50% of 3.2 Gbp) genomes, respectively. In **plant genomes** are **LTR retrotransposons** the major repetitive sequence class.

Distribution of LTR retrotransposons along chromosomes differs with their respective lineage and/or family affiliation. Some LTR retrotransposon lineages are distributed uniformly, but others are present in specific niches (e.g. Jedlicka et al., 2019). One of the most intriguing chromosomal niches is centromere which is colonized by distinctive LTR retrotransposon lineages and satellites (Neumann et al., 2011). Especially centromeric regions of plants are generally composed of large array of specific lineage of Gypsy LTR retrotransposons where interact with a specific H3 histone, playing a crucial function on kinetochore formation. These relationships are frequently reported from genomes with so called monocentric chromosomes where is only one centromere which forms a narrow constriction. Structural contrast to the monocentric chromosomal layout is represented by **holocentric chromosomes** in which the kinetochores and centromere-associated histones are distributed along entire chromosome length.

In plants, the holocentric chromosomes evolved at least four times and only in species belonging to flowering plants (Angiosperma) include both monocots and eudicots. Holocentric layout of chromosomes was numerously found in the rush grasses and sedges (family Juncaceae and Cyperaceae, respectively) whereas in eudicots is limited to two generas *Drosera* and *Cuscuta* (family Droseraceae and Convolvulaceae, respectively).

The holocentric plant genera revealed extraordinary broad karyotype variation given by wide range of chromosome number and higher ratio between largest and smallest average chromosome size than in monocentric plant genera (Bures et al., 2013).

Unlike plant genomes with monocentric chromosomes the distribution of LTR retrotransposons in holocentric plants is limited to two studies only. The former one dealing with the woodrush *Luzula elegans* (Heckmann et al., 2013) shows that more than sixty percent of *L. elegans* genome consists of repetitive DNA and half of this part is represented by Ty1/Copia LTR retrotransposon of Angela family. Further they found out that retroelements are uniformly dispersed along the chromosomes, while the satellite repeats occur in bands localized at the chromosome termini. The latter study, Souza et al. (2018), reports predominance of Ty1/Copia Sirevirus and Ty3/Gypsy Athila/Tat clade in *Eleocharis elegans* and *E. geniculata* genomes (Cyperaceae). They

found no typical chromosomal distribution pattern of retrotransposons in holocentric chromosomes with exception of CRM family with signals distributed along chromatids.

Therefore we are motivated to arrange more profound comparative study on basic characterization (annotation) and distribution of LTR retrotransposons in sets of close relative plant species with mono- and holocentric chromosomes, respectively.

## References

Bureš P., Zedek F., Marková M. 2012. Holocentric Chromosomes. In I. J. Leitch; J. Greilhuber, Jaroslav Doležel, J. F. Wendel. Plant Genome Diversity Volume 2 Physical Structure, Behaviour and Evolution of Plant Genomes. 1. vyd. Wien, Heidelberg, New York, London: Springer, 2012. p. 187-208, 22 pp. Life Sciences, Plant Sciences. ISBN 978-3-7091-1159-8. doi:10.1007/978-3-7091-1160-4\_12.

de Souza T.B., Chaluvadi S.R., Johnen L., Marques A., González-Elizondo M.S., Bennetzen J.L., Vanzela A.L.L. 2018. Analysis of retrotransposon abundance, diversity and distribution in holocentric *Eleocharis* (Cyperaceae) genomes. *Ann Bot.* 122(2):279-290. doi: 10.1093/aob/mcy066.

Heckmann S., Macas J., Kumke K., Fuchs J., Schubert V., Ma L., Novák P., Neumann P., Taudien S., Platzer M., Houben A. 2013. The holocentric species *Luzula elegans* shows interplay between centromere and large-scale genome organization. *Plant J.* 73(4):555-65. doi: 10.1111/tpj.12054.

Jedlicka P., Lexa M., Vanat I., Hobza R., Kejnovsky E. 2019. Nested plant LTR retrotransposons target specific regions of other elements, while all LTR retrotransposons often target palindromes and nucleosome-occupied regions: in silico study. *Mob DNA.* 10:50. doi: 10.1186/s13100-019-0186-z.

Neumann P., Navrátilová A., Koblížková A., Kejnovský E., Hříbová E., Hobza R., Widmer A., Doležel J., Macas J. 2011. Plant centromeric retrotransposons: a structural and cytogenetic perspective. *Mob DNA.* 2(1):4. doi: 10.1186/1759-8753-2-4.

### Aims and Project process flow:

The proposed project workflow is as follows:

1. Plant species selection:  
Holocentric plant species are chosen across phylogenetically distant taxons and concurrently within one taxon/genera pick up at least two species with remarkably different karyotype. Each higher holocentric taxon will be chosen its phylogenetically closest monocentric counterparts. Representatives of monocots and eudicots will be included (for plant species list see **Table 1**).
2. Genomic DNA sequencing:  
We will obtain a partial and/or full-length sequences of LTR retrotransposons from all plant species and a primary genome assembly of plant subset using combination of long (Oxford Nanopore Technologies) and short (Illumina sequencing) reads.
3. Subsequent analysis:
  - in-depth search and annotation of full-length LTR retrotransposons
  - their distribution in chromosomes (alternatively in assembled scaffolds)
  - identification of additional sequences carried within retroelements with possible function for the holocentric arrangement – satellites, tandem repeats, retrogenes, eORF, (micro) miRNA
4. Based on information about abundance of LTR retrotransposon families and their distribution in our model plant species, we will describe LTR retrotransposon landscape and its relation to holocentrism.

**Table 1.** Three groups of plant species are chosen for sequencing study. The first group cover monocots and the second and third group eudicots representatives, respectively.

| Holocentric |                                |                            |      | Monocentric  |                             |                                 |       |    |
|-------------|--------------------------------|----------------------------|------|--------------|-----------------------------|---------------------------------|-------|----|
| family      | species                        | 2C [Mbp]                   | 2n   | family       | species                     | 2C [Mbp]                        | 2n    |    |
| 1           | Cyperaceae                     | <i>Carex acutiformis</i>   | 800  | 78           | Poaceae                     | <i>Oryza sativa</i>             | 799   | 24 |
|             | Cyperaceae                     | <i>Cyperus papyrus</i>     | 542  | 100          | Poaceae                     | <i>Brachypodium distachyon</i>  | 355   | 10 |
|             | Juncaceae                      | <i>Luzula pilosa</i>       | 588  | 66           |                             |                                 |       |    |
|             | Juncaceae                      | <i>Luzula elegans</i>      | 8330 | 6            |                             |                                 |       |    |
| 2           | Droseraceae                    | <i>Drosera capensis</i>    | 789  | 40           | Drosophyllaceae             | <i>Drosophyllum lusitanicum</i> | 20833 | 12 |
|             | Droseraceae                    | <i>Drosera micrantha</i>   | 7489 | 10           | Nepenthaceae                | <i>Nepenthes ventricosa</i>     | 3315  | 80 |
| 3           |                                |                            |      | Polygonaceae | <i>Polygonum persicaria</i> | 882                             | 44    |    |
|             |                                |                            |      | Polygonaceae | <i>Rumex alpinus</i>        | 868                             | 20    |    |
|             | Melanthiaceae, Chionographidae | <i>Chionographis</i>       | 2989 | 24           | Melanthiaceae               | <i>Paris quadrifolia</i>        | 99019 | 10 |
|             | Melanthiaceae                  | <i>Chamaelirium luteum</i> | 1800 | 24           |                             |                                 |       |    |

***Applicant competencies:***

- *Relevant information for the assessment of the project proposal in accordance with the basic criteria set out in the "Internal Support of Research Program" Directive;*  
Applicant's qualification degree is "junior scientist" (V4) and he is in full-time employment at the IBP.
- *National or International Projects of the Applicant in the last 5 years and their evaluation, where the applicant was the principal investigator;*  
The applicant did not apply for any national or international projects of the applicant in the last 5 years as the principal investigator
- *Projects of the Internal Support of Research Program of the IBP in the last 5 years: granted - number, not granted - number;*  
The applicant did not apply for the Internal Support of Research Program of the IBP in the last 5 years
- *Justification of the requested costs;*  
The requested foundation is necessary to cover costs of:
  - high quality DNA isolation kits
  - DNA sequencing services



**Brief scientific curriculum vitae of the applicant** (maximum range of one page, list your own publications with citations on the relevant topic, max. 3 pcs);

Applicant's CV is attached as separate file in pdf format.

**Project budget** to the project proposal on the prescribed form - see Annex 2 of the Directive;

Project budget file is attached.

# Pavel Jedlička

---

Postdoctoral fellow at Department of Plant Developmental Genetics  
Institute of Biophysics of the CAS, v. v. i., Královopolská 135, 612 65 Brno, Czech Republic  
E-mail: [jedlicka@ibp.cz](mailto:jedlicka@ibp.cz) Phone: +420 728 215 151 | Updated: Jan. 3, 2020

---

## EDUCATION AND QUALIFICATION

Ph.D. studies, Department of Ecology, Faculty of Science, Charles University in Prague 2004–2008  
M.Sc. studies, Faculty of Agriculture, University of South Bohemia, České Budějovice 1996–2002

## POSTDOCTORAL FELLOWSHIPS

Institute of Biophysics of the CAS, v. v. i. since 2018  
Institute of Organic Chemistry and Biochemistry ASCR 2015–2018  
National Taiwan University, Department of Entomology, Taipei, Taiwan 2012–2013

## RESEARCH INTERESTS

I am highly interested in bioinformatic analyses in general. At present, I am engaged in development and testing of tool for identification of LTR retrontransposons in plant genomes.

## PROJECTS PARTICIPATION (selected)

The role of transposable element in the dynamics of plant genomes. GACR, No. 18-00258S. 2018–2020  
Stress response of the pea aphid, *Acyrtosiphon pisum*. Founded within „Top 100“ project by National Taiwan University, Taipei, Taiwan. Principal Investigator. 2012–2013  
Physiological role of aphid adipokinetic hormone: its interaction with juvenile hormone and influence on vitellogenin synthesis and reproduction. GACR, No. 522/09/P382. Principal Investigator. 2009–2011

## COMPUTER PROGRAM SKILLS

Scripting in Python and Bash. Windows and Unix (Linux) operating systems. NGS data analysis. Statistical analyses and output visualization in R software environment.

## PUBLICATIONS

Author or co-author of 17 impacted original scientific articles, 1 book chapter, 12 conference presentations. 86 citations, H-index: 7.

### Selected Journal Articles:

**Jedlicka, P.**, Lexa, M., Vanat, I., Hobza, R., Kejnovsky, E., 2019. Nested plant LTR retrotransposons target specific regions of other elements, while all LTR retrotransposons often target palindromes and nucleosome-occupied regions: in silico study. *Mobile DNA* 10, 50, [doi:10.1186/s13100-019-0186-z](https://doi.org/10.1186/s13100-019-0186-z).

**Jedlicka, P.**, Lexa, M., Kejnovsky, E. What cat long terminal repeats say about the age of LTR retrotransposons, gene conversion and ectopic recombination? *Frontiers in Plant Science*, under review.

Lexa, M., **Jedlicka, P.**, Vanat, I., Cervenansky, M., Kejnovsky, E. TE-nester: software for structure-based detection of LTR retrotransposons and their nesting relationships. *Bioinformatics*, revisions.

**Annex No. 2****Project budget for the "Internal Research Support Program" of the Institute of Biophysics of the CAS, v. v. i.**

|                                     |                           |                   |
|-------------------------------------|---------------------------|-------------------|
| Applicant:                          |                           | Pavel Jedlička    |
| <b>Total funds required in CZK:</b> |                           | <b>300,000.00</b> |
| of which                            | <b>Material expenses</b>  |                   |
|                                     | Material                  | 60,000.00         |
|                                     | Services                  | 210,000.00        |
|                                     | Subtotal                  | <b>270,000.00</b> |
|                                     | <b>*Personal expenses</b> |                   |
|                                     | Rewards (team)            | 19,260.00         |
|                                     | Statutory levies (35.8 %) | 10,740.00         |
|                                     | Subtotal                  | <b>30,000.00</b>  |

\* Personal costs cannot exceed 10% of the total budget.