



## PHD STUDENT IN THE DOCTORAL SCHOOL – CALL FOR APPLICATIONS

**Position:** PhD student in biology

**Unit of the project realization:** Faculty Natural Sciences – University of Silesia in Katowice

**Unit realizing the PhD student education:** Doctoral School at the University of Silesia in Katowice

The project included a global analysis of the repetitive fraction of the *Brachypodium* genomes followed by bioinformatic analyses. The results will then be verified using the cytogenetic and molecular approaches in order to estimate the genomic organisation, chromosome localisation and the copy number of various repeats.

Research will be carried out in the frame of the project „**Repetitive DNA sequences and the evolution of the *Brachypodium* genus**” (type of a program and number of the project **PRELUDIUM BIS-2 nr 2020/39/O/NZ8/00184** , financed from **NCN** under management of dr. hab. Bożena Kolano

**Duration of the scholarship: 48 month**

**Scholarship amount: 4 266,58 PLN/month – during the first and second year**

**5 119,89 PLN/month - during the third and fourth year**

### **Project description:**

#### **Repetitive DNA sequences and the evolution of the *Brachypodium* genus**

Model organisms are simplified tractable systems that are used to study larger scientific questions and to address complex research problems. The data that is obtained from studying such organisms are thought to be applicable to other, more complex organisms. *Brachypodium distachyon* was developed as a model system for grasses (a taxon that includes the key cereals like maize, rice and wheat) approximately 20 years ago. It is now well established in this role and offers substantial experimental and genomic resources, e.g. high-quality whole-genome assemblies and the libraries of large chunks of DNA that has been cloned into high-capacity vectors such as Bacterial Artificial Chromosomes. Some of these resources have also been exploited in evolutionary and phylogenetic analyses of the genus. *Brachypodium* consists of approximately 20 diploid and polyploid species that have small genomes and diverse basic chromosome numbers. Earlier studies showed that chromosome rearrangements, mostly nested chromosome fusions, accompanied the evolution of the genus. These chromosomal changes are very often accompanied by the reorganisation of the repetitive sequences. Repetitive DNA is a major driving force of genome evolution. This fraction of nuclear genomes is often abundant and may contribute to more than 90% of the whole genome, especially in higher plants. Thus, knowledge about this relatively rapidly evolving part of plant genomes is essential for making hypotheses and drawing conclusions on the mechanisms that are involved in genome evolution. NGS (Next Generation Sequencing) technologies have been successfully used to investigate the repetitive sequences in many plant genomes. In this current project, a global analysis of the repetitive fraction of the *Brachypodium* genomes will be performed followed by bioinformatic analyses. The results will then be verified using the cytogenetic (fluorescence *in situ* hybridisation; FISH) and molecular (Southern blotting) approaches in order to estimate the genomic organisation, chromosome localisation and the copy number of the repeats. **We plan to test the following hypotheses: (i) The repetitive DNA composition and organisation in selected**





***Brachypodium* representatives is correlated with their phylogeny; (ii) After hybridisation and polyploidisation, the repetitive DNA sequences underwent reorganisation in the allotetraploid *B. hybridum* and (iii) Different repeat lineages had different rates and/or patterns of evolution.** The evolutionary trends of the different repetitive sequences that accompany the speciation of a genus can be inferred by comparing the pattern of the distribution of each individual repetitive sequence in different *Brachypodium* species. We expect that such a combined molecular phylogenetic, cytogenetic, molecular and bioinformatic approach will permit a comprehensive picture of repetitive sequence organisation in both diploid and polyploid *Brachypodium* representatives to be drawn. A comparative evolutionary analysis of the repetitive sequences will enable the mechanisms that underlie the diversification and speciation of diploid species and the evolution of parental subgenomes in polyploids to be determined and will possibly also provide additional evidence that would help to elucidate the exact phylogenetic relationships in this model grass genus.

#### Requirements:

- A MSc or equivalent experience in biological sciences, plant genetics, plant molecular biology or related discipline (essential criterion)
- Motivation and enthusiasm to undertake challenging research work, and a willingness to further scientific development (essential criterion)
- Ability to work independently, plan and conduct experiments, analyse results (essential criterion)
- Effective operational proficiency in English (will be verified by the recruiting panel during the interview; essential criterion)
- Mobility – this is an international research collaboration project with University of Zaragoza, Huesca, Spain. The PhD student is obligated to apply to NAWA (National Agency for Academic Exchange) for scholarship which will support his/her foreign fellowships carried out over the period of 3 to 6 months (essential criterion)

#### Required documents:

1. Motivation list with a description of the scientific interests
2. Scientific CV
3. List of scientific publications
4. Copy of the MSc diploma
5. Reference letter prepared by person with PhD degree in biological sciences (or contact information of such person)
6. Declaration of consent to processing of personal data

Candidates should register in IRK system and select „Doctoral School – admission to a grant”.

Documents should be delivered till **27 of July** to an e-mail: [bozena.kolano@us.edu.pl](mailto:bozena.kolano@us.edu.pl).

In case of any questions, before the formal application please contact to the grant leader for the e-mail address given above.



Documents will be rated by the commission, led by the project leader. Admission will be carried out according to the NCN regulations. Admission can be carried out both in Polish and in English. Meeting will be organized on 21-23 July in the Doctoral School office / on-line. Final decision will be sent to candidates via e-mail till 02.08.2021