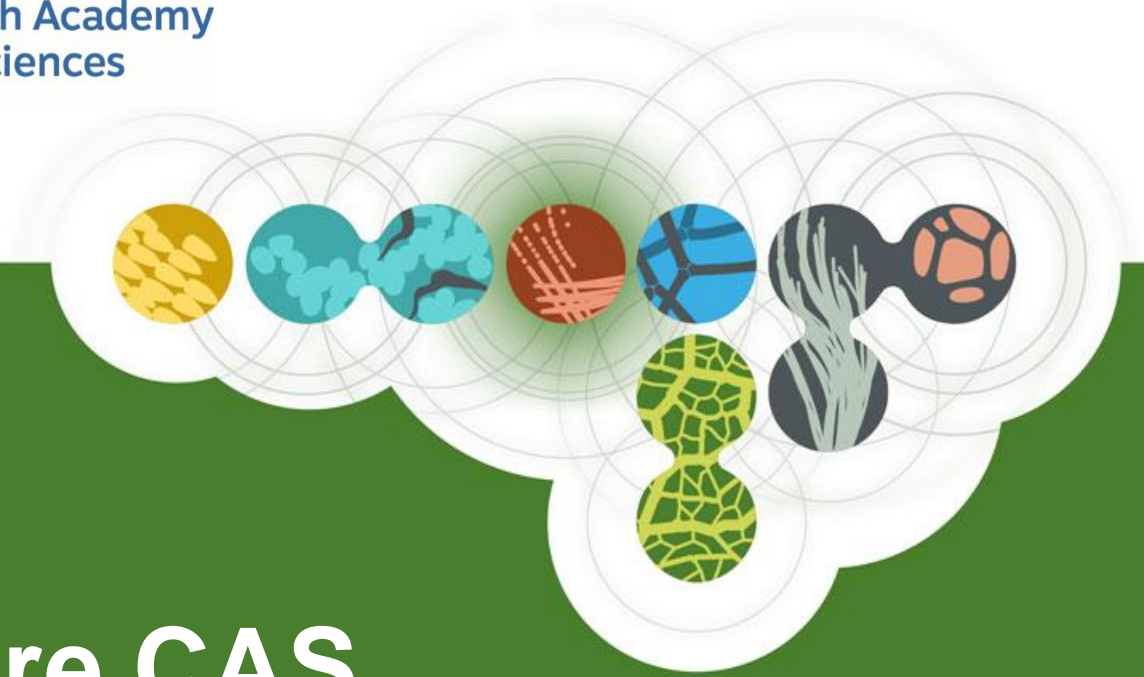




BIOLOGY  
CENTRE  
CAS



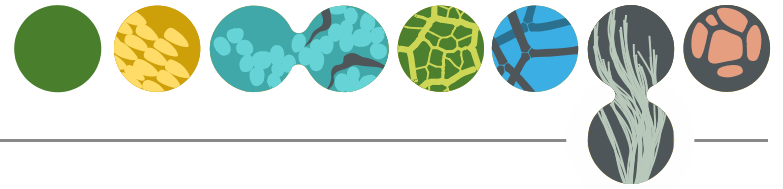
Czech Academy  
of Sciences



# Biology centre CAS

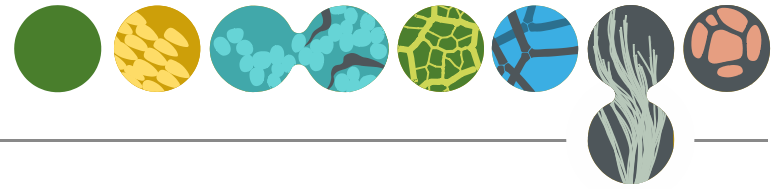
**National information day about the  
European Research Council**

**Martina Teringlová, November 6, 2019**



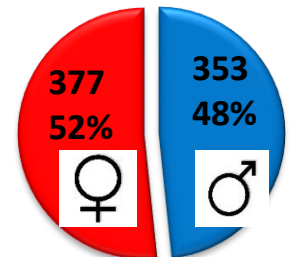
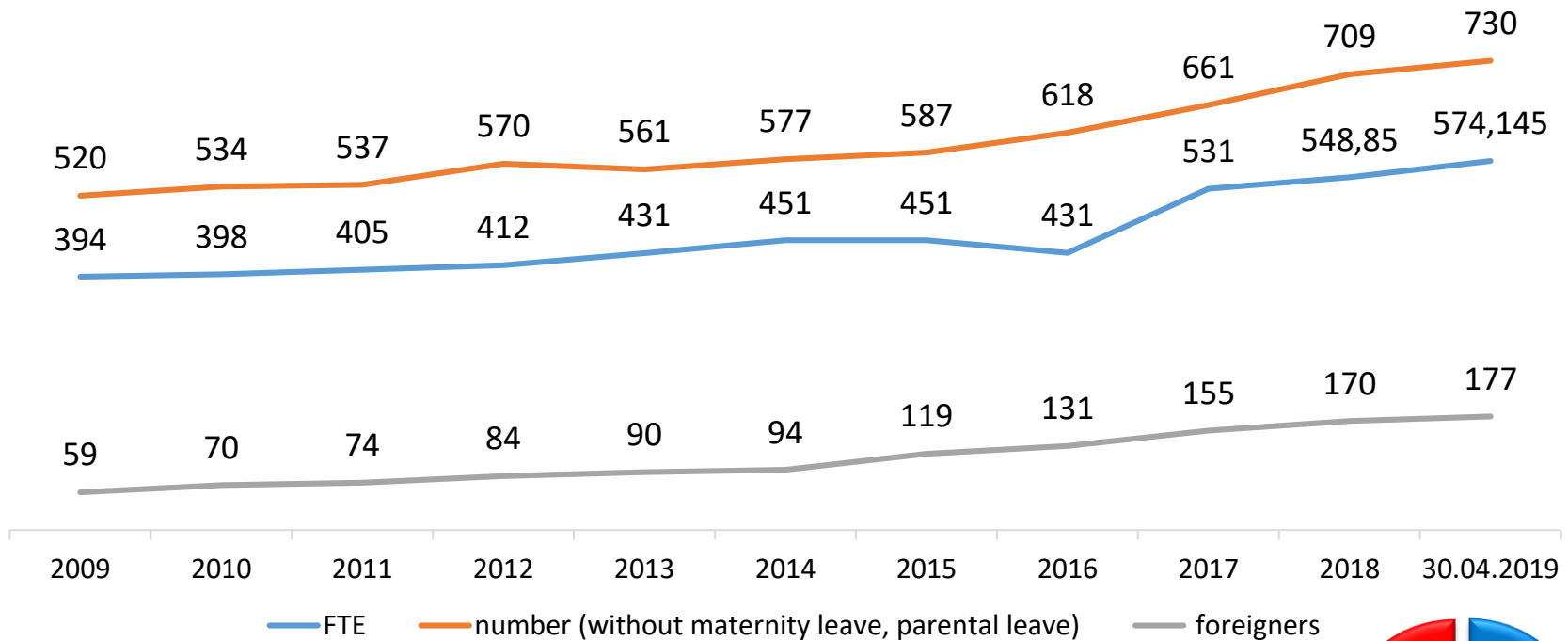
# Biology centre CAS consists of five scientific institutes and a single research infrastructure:

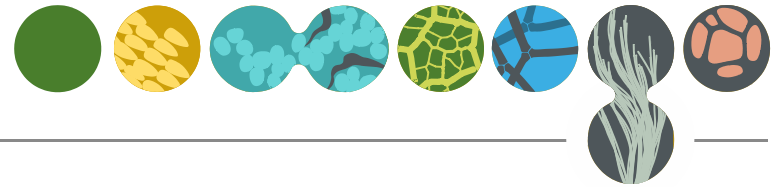
- Entomology Institute
- Hydrobiology Institute
- Parasitology Institute
- Institute of the Molecular Biology of Plants
- Institute of Soil Biology
- Soil and Water Research Infrastructure



# Biology Centre CAS

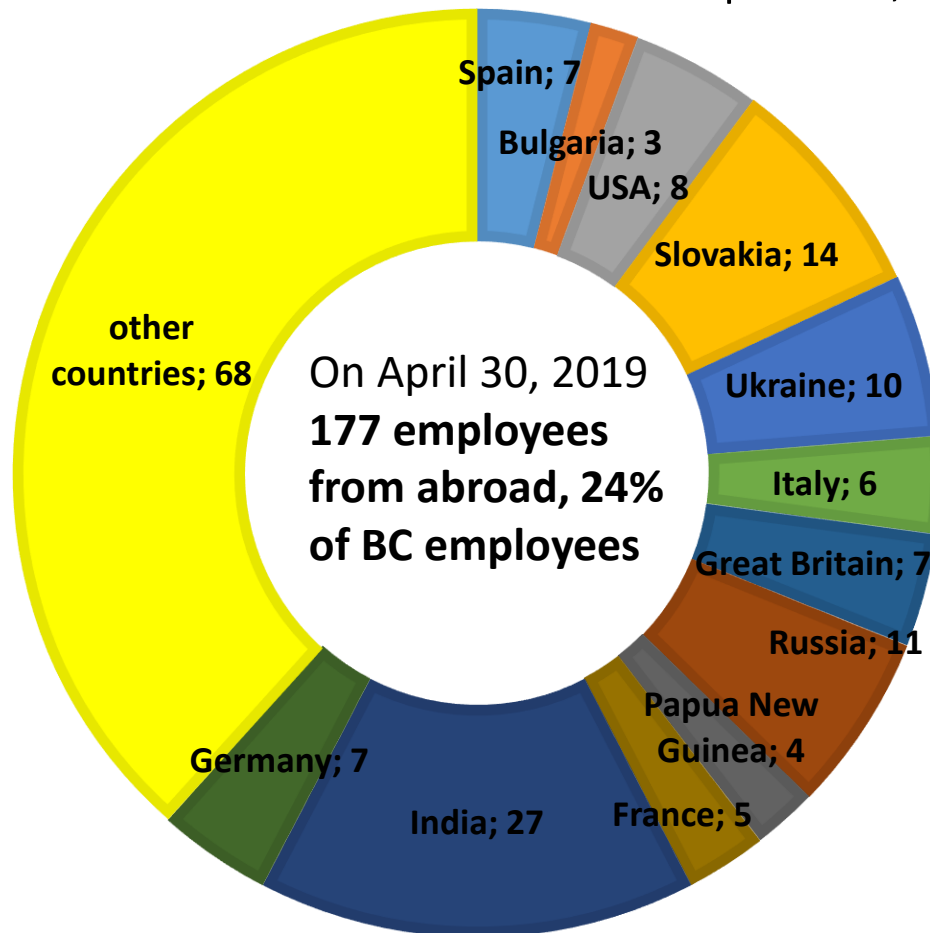
On April 30, 2019: **730 employees** (574 FTE)





# Biology Centre CAS

On April 30, 2019: **730 employees** (574 FTE)



**Other countries:** Egypt, Bangladesh, Brazil, Romania, Pakistan, Switzerland, Chile, Hungary, Serbia, Portugal, France, Canada, Colombia, Latvia, Croatia, Australia, Austria, Taiwan, Poland, Greece, Netherlands, China, Sweden, Finland, Peru, Argentina, Iran, Ghana, Ireland, Venezuela, Republic of South Africa, Tajikistan, Japan



# Institutional Project Support

## Project Department

- Project Manager for Funding & Tender Portal (Participant Portal)
- Financial Manager for H2020 Program - experience with EU audits

## Support for researches

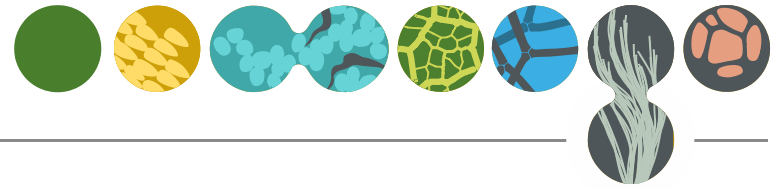
Monitoring actual calls

Consultations

Administration of successful projects



HR EXCELLENCE IN RESEARCH

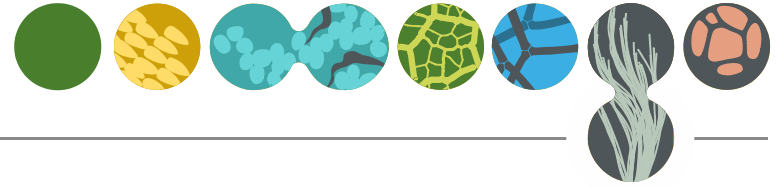


## Part A – administrative forms

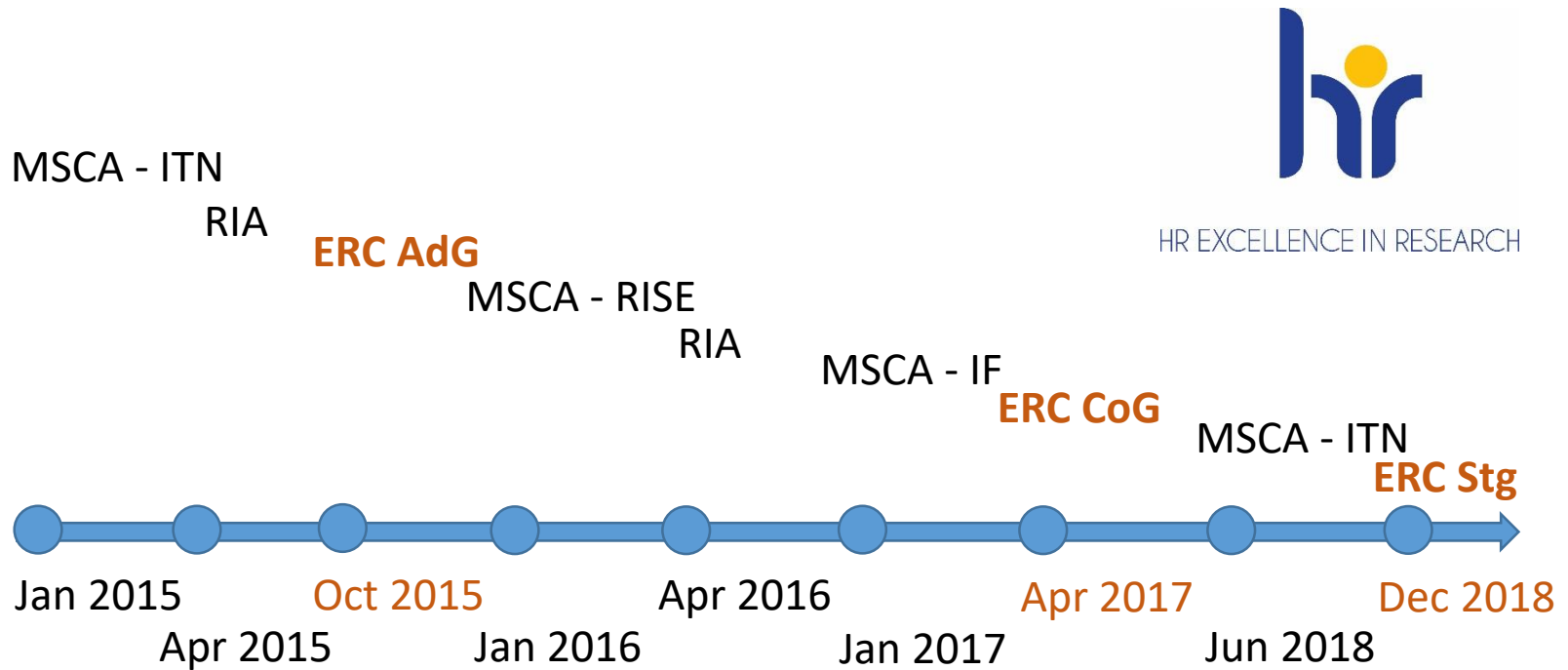
- Basic info about project (title, duration, key words, abstract), host institution (PIC)
- Budget
- Ethics
- Call-specific questions

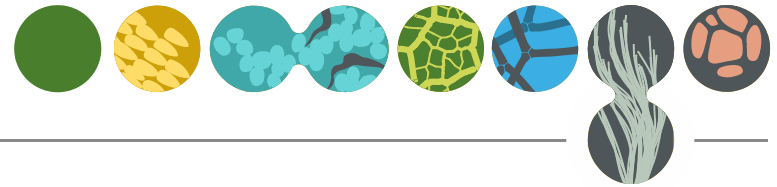
## Part B – project proposal

- Scientific part B1 and B2 – Resources (including project costs)



# Successful H2020 Projects





# ECR Advanced Grant - Diversity6continents

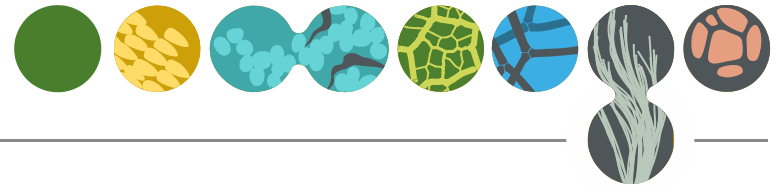
Coordinator: prof. Vojtěch Novotný

Duration: 60 Month from 01 October 2015 till 30 September 2020

Budget: 3 349 618 EUR

The study will examine one of the most fundamental, yet poorly understood patterns of global biodiversity distribution: How can so many species coexist in a tropical forest? This key question of current ecology will be studied using quantitative surveys of plant-herbivore-parasitoid food webs within paired sets of tropical and temperate forests from six continents, in Papua New Guinea (PNG), Gabon, Panama, the Czech Republic, Japan, and USA, sampled using canopy cranes, truck-mounted elevated platforms and forest felling. This novel type of data will be analysed using a new rarefaction method, developed to test mechanistic explanations for biodiversity patterns along ecological gradients. It will evaluate competing hypotheses explaining latitudinal trends in insect herbivore diversity by the variation in either phylogenetic or functional diversity of plants, the host specificity of herbivores, or the diversity and specificity of their parasitoids and predators. The study will thus examine the importance of bottom-up (plants) and top-down (enemies) drivers of latitudinal trends in herbivore food webs, central to ecological theory that postulates the role of specialized herbivores as density-dependent agents of mortality involved in maintaining high tropical plant diversity. The project builds upon prior research that produced one of the largest tropical food web data sets to expand it conceptually, methodologically and geographically. It will build a globally important research facility (a canopy crane in PNG) and link researchers and infrastructure from several countries in a major effort to draw together separate lines of tropical and temperate research. Study sites in the ILTER, NEON, CTFS/SIGEO, and Canopy Crane Network will participate. The internationally recognized paraecologist program will be expanded, PhD students from both European and developing countries will be trained, and conservation of rainforests by indigenous rainforest dwellers will be leveraged.





# ECR Consolidator Grant - InPhoTime

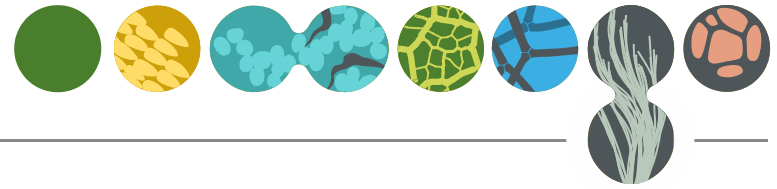
Coordinator: Dr. David Doležal

Duration: 60 Month from 01 April 2017 till 31 March 2022

Budget: 2 000 000 EUR

Daylength measuring devices such as the photoperiodic timer enable animals to anticipate and thus survive adverse seasons. This ability has contributed to the great success of insects living in temperate regions. Yet the basis of photoperiodic sensing remains elusive, because of the lack of suitable genetic models expressing photoperiod-dependent seasonal phenotypes. We have developed the linden bug, *Pyrrhocoris apterus*, into a genetically tractable model with a robust, photoperiod-dependent reproductive arrest (diapause). With the available tools, this insect has become ideal for deciphering the regulation of seasonality. The project has 3 clear and ambitious objectives:

- 1) Our goal is to define the molecular and anatomical bases of the photoperiodic timer. To achieve this, we propose to identify photoperiodic timer genes, genes regulating input to the timer, and early output markers, through an RNA interference screen(s). To define the molecular mechanism of the timer, we will employ genome editing to precisely alter properties of the key players.
- 2) Next, we will combine techniques of neuronal backfilling, in-vivo fluorescent reporters, and microsurgery to define the photoperiodic timer anatomically and to examine its spatial relationship to the circadian clock in the insect brain.
- 3) We will exploit the great natural geographic variability of photoperiodic timing in *P. apterus* to explore its genetic basis. Genetic variants correlating with phenotypic differences will be causally tested by genome editing within the original genetic backgrounds. Both the established and the innovative strategies provide a complementary approach to the first molecular characterization of the seasonal photoperiodic timer in insects. The proposed research aspires to explain mechanisms underlying the critical physiological adaptation to changing seasons. Deciphering mechanisms underpinning widespread adaptation might bring general implications for environment-friendly pest control.



# ECR Starting Grant - BABE

Coordinator: Dr. Kateřina Sam

Duration: 60 Month from 01 December 2018 till 30 November 2023

Budget: 1 455 031 EUR

Why is the world green? Because predators control herbivores, allowing plants to flourish. This >50 years old answer to the deceptively simple question remains controversial. After all, plants are also protected from herbivores physically and by secondary chemistry. My goal is to test novel aspects of the “green world hypothesis”:

- How the importance of top-down effects varies with forest diversity and productivity along a latitudinal gradient?
- How the key predators, birds, bats and ants, contribute to top-down effects individually and in synergy? I strive to understand this because:
  - While there is evidence that predators reduce herbivore abundance and enhance plant growth, the importance of top-down control is poorly understood across a range of forests.
  - The importance of key predatory groups, and their antagonistic and synergic interactions, have been rarely studied, despite their potential impact on ecosystem dynamics in changing world. I wish to achieve my goals by:
    - Factorial manipulations of key insectivorous predators (birds, bats, ants) to measure their effects on lower trophic levels in forest understories and canopies, accessed by canopy cranes, along latitudinal gradient spanning 75° from Australia to Japan.
    - Studying compensatory effects among predatory taxa on herbivore and plant performance.



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# Thank you for your attention