



Katedry genetiky a biochémie PriF UK  
a občianske združenie *NATURA*



Vás pozývajú na 99. prednášku v rámci Kuželových seminárov:

**Jan Šafář**

**Centre of Plant Structural and Functional Genomics of the  
Institute of Experimental Botany ASCR, Olomouc**

# **PLANT CHROMOSOME GENOMICS**

ktorá sa uskutoční **26. februára 2015** (štvrtok) o **13:00**

v miestnosti **CH1-222** Prírodovedeckej fakulty UK

<http://www.natura.oz.org/seminare.html>  
<http://www.natura.oz.org/KuzeloveSeminare.html>

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## Jan Šafář

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### Education:

- 1994-1997 Masaryk University, Brno, B.Sc., General Biology
- 1997-1999 Masaryk University, Brno (1999), M.Sc., Microbiology
- 1999-2003 Palacký University, Olomouc (2004), Ph.D., Construction of BAC libraries in plants, Department of Botany

### Professional experience:

- 2002–2004 short term visits at CIRAD, Montpellier, France, Unité de Recherches en Génomique Végétale (URGV-INRA), Paris-Evry, France and Department of Plant Sciences, University of Arizona, Tucson, USA
- 2003–2004 Postdoctoral Fellow, University of Arizona, Plant Sciences, Tucson, USA
- 2004–2010 Postdoctoral Fellow, Laboratory of Molecular Cytogenetics and Cytometry, Institute of Experimental Botany, Olomouc, Czech Republic
- 2010– Senior Researcher, Centre of Plant Structural and Functional Genomics, Institute of Experimental Botany ASCR, Czech Republic

### Abstract of the lecture:

Nuclear genomes of many plant species, including important crops, are large and characterized by extensive DNA sequence redundancy. The production of reference genome sequence may be hampered by those facts. We have been developing chromosome-centric approaches to overcome these difficulties. Single chromosomes can be isolated in large quantities by flow cytometric sorting and their DNA has been shown suitable for all methods of plant genomics. These include physical mapping using PCR, FISH and DNA arrays, targeted development of DNA markers, construction of BAC libraries to support development of sequence-ready physical maps, long-range optical maps, and positional cloning. The application of chromosome-centric approaches stimulated a rapid advance in genomics of species, which were considered intractable using whole-genome strategies. In one of them, hexaploid wheat, large-insert BAC libraries were constructed from all chromosomes and their availability facilitates construction of ready to sequence physical maps and production of reference genome sequence. Coupling chromosome sorting with next generation sequencing provides a powerful approach to study genome organization at chromosomal level, perform comparative analyses with related species and validate whole genome assemblies. The number of plant species from which chromosomes can be sorted keeps increasing and chromosome genomics is bound to contribute significantly to the analysis of plant hereditary information.

### Selected publications:

- Šafář, J., Bartoš, J., Janda, J., Bellec, A., Kubaláková, M., Valárik, M., Pateyron, S., Weiserová, J., Tušková, R., Číhalíková, J., Vrána, J., Šimková, H., Faivre-Rampant, P., Sourdille, P., Caboche, M., Bernard, M., Doležel, J., Chalhou, B.: Dissecting large and complex genomes: flow sorting and BAC cloning of individual chromosomes from bread wheat. – *Plant Journal* 39: 960-968, 2004.
- Šafář, J., Noa-Carranza, J.C., Vrána, J., Bartoš, J., Alkhimova, O., Lheureux, F., Šimková, H., Caruana, M.L., Doležel, J., Piffanelli, P.: Creation of a BAC resource to study the structure and evolution of the banana (*Musa balbisiana*) genome. – *Genome* 47: 1182–1191, 2004.
- Paux, E., Sourdille, P., Salse, J., Saintenac, C., Choulet, F., Leroy, P., Korol, A., Michalak, M., Kianian, S., Spielmeier, W., Lagudah, E., Somers, D., Kilian, A., Alaux, M., Vautrin, S., Bergès, H., Eversole, K., Appels, R., Safar, J., Šimková, H., Doležel, J., Bernard, M., Feuillet, C.: A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. – *Science* 322, 101-104, 2008.
- Šafář, J., Šimková, H., Kubaláková, M., Číhalíková, J., Suchánková, P., Bartoš, J., Doležel, J.: Development of chromosome-specific BAC resources for genomics of bread wheat. – *Cytogenet. Genome Res.* 129: 211-223, 2010.
- Milec, Z., Valárik, M., Bartoš, J., Šafář, J.: Can a late bloomer become an early bird? Tools for flowering time adjustment. – *Biotechnol. Adv.* 32: 200-214, 2014 (review).
- Choulet, F., Alberti, A., Theil, S., Glover, N., Barbe, V., Daron, J., Pingault, L., Sourdille, P., Couloux, A., Paux, E., Leroy, P., Mangenot, S., Guilhot, N., Le Gouis, J., Balfourier, F., Alaux, M., Jamilloux, V., Poulain, J., Durand, C., Bellec, A., Gaspin, C., Šafář, J., Doležel, J., Rogers, J., Vandepoele, K., Aury, J.M., Mayer, K., Berges, H., Quesneville, H., Wincker, P., Feuillet, C.: Structural and functional partitioning of bread wheat chromosome 3B. – *Science* 345: 1249721, 2014.