
Plant Genome Diversity Volume 2

Ilia J. Leitch
Editor-in-chief

Johann Greilhuber · Jaroslav Doležal ·
Jonathan F. Wendel
Editors

Plant Genome Diversity Volume 2

Physical Structure, Behaviour
and Evolution of Plant Genomes

Editor-in-chief

Ilia J. Leitch
Jodrell Laboratory
Royal Botanic Gardens,
Kew Richmond, Surrey
United Kingdom

Editors

Johann Greilhuber
Department of Systematic and Evolutionary Botany
Faculty of Life Sciences
University of Vienna
Vienna
Austria

Jaroslav Doležal
Institute of Experimental Botany ASCR
Centre of the Region Hana for
Biotechnological and Agricultural
Research
Olomouc
Czech Republic

Jonathan F. Wendel
Department of Botany
Iowa State University
Ames, Iowa
USA

ISBN 978-3-7091-1159-8 ISBN 978-3-7091-1160-4 (eBook)

DOI 10.1007/978-3-7091-1160-4

Springer Wien Heidelberg New York Dordrecht London

Library of Congress Control Number: 2012935228

© Springer-Verlag Wien 2013

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed. Exempted from this legal reservation are brief excerpts in connection with reviews or scholarly analysis or material supplied specifically for the purpose of being entered and executed on a computer system, for exclusive use by the purchaser of the work. Duplication of this publication or parts thereof is permitted only under the provisions of the Copyright Law of the Publisher's location, in its current version, and permission for use must always be obtained from Springer. Permissions for use may be obtained through RightsLink at the Copyright Clearance Center. Violations are liable to prosecution under the respective Copyright Law.

The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

While the advice and information in this book are believed to be true and accurate at the date of publication, neither the authors nor the editors nor the publisher can accept any legal responsibility for any errors or omissions that may be made. The publisher makes no warranty, express or implied, with respect to the material contained herein.

Printed on acid-free paper

Springer is part of Springer Science+Business Media (www.springer.com)

Preface

Ever since the origin of life, the evolution of living organisms and their hereditary information has been accompanied by the development of genetic machinery capable of storing, utilizing, and transmitting this information between generations. Importantly, this machinery has had to be flexible, able to respond to the environment and evolve. A characteristic feature of the genetic machinery in eukaryotes is the partitioning of the hereditary information into smaller portions—chromosomes. Indeed, the appearance of linear chromosomes was one of the great evolutionary inventions and paved the way for the formation of large and complex genomes, in plants as well as in animals. Any consideration of plant genome structure, evolution, and function is thus incomplete if it does not take into account its higher-order structure and the behaviour of its principal units—the chromosomes.

The chromosome theory of heredity, which linked the behaviour of Mendel's "factors" (units of inheritance) with that of chromosomes, was coined by Walter S. Sutton more than a century ago. This was followed, only a few decades later by Cyril D. Darlington's demonstration that the behaviour of chromosomes and meiotic crossing over in particular, was the main force behind evolution as opposed to single gene mutations and deletions. This set in motion the quest to understand the nature of inheritance, leading to the discovery of the structure of DNA and the advent of molecular biology and genomics. At this point the goal seemed clear—all that was needed was to establish the sequence of bases in the DNA. However, as increasing amounts of DNA sequences were generated, it became obvious that there was still a lot to discover about how DNA was organized within chromosomes and how the DNA sequence information was interpreted, processed, and utilized in the nuclear and cellular environments. The days when the DNA sequence itself was considered a holy grail are over and we now know that things are considerably more complicated.

Luckily, progress in genomics has been complemented by advances in understanding the dynamic structure of chromatin, the organization of interphase nuclei, and the behaviour of chromosomes during mitosis and meiosis. The latter includes novel insights into modified cell cycles, which may lead to chromosomes with more than two chromatids. Impressive progress has also been made in understanding the origin and function of specialized chromosomes (e.g., B chromosomes and sex chromosomes) and in appreciating the extent and significance of polyploidy in plant evolution. Although the frequent occurrence of polyploidy has been known for a long time based on chromosome counts and behaviour, the advent of DNA sequencing and comparative genomics has been instrumental in uncovering evidence of further rounds of polyploidy buried within the genome and now no longer visible at the chromosome level. Such studies have reinforced and extended our understanding of the significance of this mechanism as one of the main forces underlying the evolution and large diversity of many plant genomes. The effect has been multiplied by the extensive structural chromosome changes, which, together with alterations in chromosome number and genome size, can accompany plant speciation.

To fully understand and appreciate the diversity, functioning, and evolution of plant genomes, a holistic knowledge of the current status in each of these individual areas is vital, yet there is no single accessible source of information currently available. Thus, we felt it timely to fill this gap.

This book is the second volume of a two-volume set on Plant Genome Diversity. Our aim is to assist students and researchers by providing as complete an overview as possible of each respective area of research. We have succeeded in engaging leading experts in each field who describe the current state-of-the-art knowledge without overwhelming the reader with details that can be found elsewhere. What we offer in the present volume are 20 chapters whose topics have been chosen carefully to provide a complete picture. Each chapter can stand on its own and thus the reader does not need to read all chapters if he/she is only interested in a specific area. We sincerely hope that this model serves our readers well. It is up to them to decide if we have succeeded.

The 20 chapters deal with individual aspects of plant genome structure, function, and evolution and they are divided into five informal sections.

Evolutionary Framework for Studying the Diversity of Plant Genomes

Although we do not necessarily expect our readers to read all chapters, we do recommend that those interested in the evolution of plant genomes read the first chapter by Soltis and Soltis (Chap. 1) who provide an overview of plant phylogeny, with an emphasis on angiosperms. Among other things, they highlight research projects that have deposited phylogenetic trees in public databases and can be downloaded for analysis.

Architecture and Dynamics of the Plant Cell Nucleus

In nondividing cells, the chromosomes are organized within the nucleus, although the structural and functional complexity of this organization is still poorly understood. One can hardly imagine the intricacy of interactions of DNA with various molecules necessary to control tens of thousands of genes and process transcripts of genic and non-genic DNA. In addition, this is all taking place in a tightly packed nuclear environment, which also harbors structures needed for DNA synthesis and repair, chromosome reduplication, posttranscriptional modifications, and synthesis of ribosomal subunits, to name but a few. Jones and Langdon (Chap. 2) review nuclear organization and discuss the consequences of interspecific hybridization, which results in two different genomes being accommodated within a single nucleus. This cohabitation may not be peaceful and can result in dramatic structural and epigenetic reorganizations in subsequent generations.

The way DNA is organized and packaged into chromatin, particularly at the higher-order level has never been entirely clear although numerous models have been proposed. However, recent discoveries question even the existence of the 30-nm fibre, which traditionally has been considered to originate by folding the 11 nm nucleosome fibre. In Chap. 3, Takata et al. address this topic by describing the composition of chromatin in relation to chromosome condensation and DNA packing. Moreover, they present a novel model for chromosome structure, which suggests that the nucleosome fibres exist in a highly disordered state and do not form 30-nm chromatin fibres at all.

In addition to separating the nuclear environment from the cytoplasm, the nuclear envelope performs many important functions; one of which is the control of molecular traffic between both cellular compartments. Kiseleva et al. (Chap. 4) describe the composition of the nuclear envelope, the nuclear pore complexes, and their assembly and function and discuss possible interactions of the envelope with the cytoplasmic and nucleoplasmic components.

Nuclei are known to contain a variety of nuclear bodies, but only the nucleolus can be easily identified by optical light microscopy. It is where the cell produces ribosomes, which are required by the cell in large numbers. Shaw (Chap. 5) summarizes the current state of knowledge of the nucleolus, which is formed on nucleolar organizing regions of chromosomes.

For plants to grow and reproduce, the cells must divide either through mitosis or meiosis. The aim is that the hereditary material is faithfully transmitted to the daughter cells. Not only must the chromosomes be fully reduplicated but their chromatids must separate at the right moment and move in the right direction to form daughter nuclei. In addition, the nuclear envelope breaks down during cell division and this represents an additional major challenge for the genetic apparatus. Magyar et al. (Chap. 6) provide an insightful review on molecular events underlying the mitotic cell cycle and mitosis itself.

Following cell division, cell and tissue differentiation is often accompanied by modified cell cycles in which the mitosis step is omitted and the nuclear envelope does not break down. Maluszynska et al. (Chap. 7) outline these different types of endopolyploidy and describe the molecular pathways involved in switching from the mitotic to the endopolyploidization cycle and how the number of endocycles are regulated. They also review the occurrence of endopolyploidy, its biological significance, and the structure of endopolyploid nuclei.

The production of gametes provides an important means to generate genetic variation via recombination of parental chromatids and their random segregation. Given the complexity of the process, it is not surprising that it is unclear exactly how the mitotic machinery is modified for the purpose of meiosis. Nevertheless, Jenczewski et al. (Chap. 8) describe the current knowledge in this area, covering chromosome dynamics during meiosis, initiation of meiotic recombination, regulation of double strand break repair, crossover formation and interference, genetic control of crossing-over formation, and its distribution in polyploids.

Karyotype Diversity Across Plants and Trends in Evolution

One of the ways in which the diversity of plant genomes is manifested is through a wide range of chromosome numbers. Lysák and Schubert (Chap. 9) explain that in many cases this originates via chromosome rearrangements. The authors outline in detail the mechanisms of chromosome rearrangements detectable by microscopic techniques and highlight those that have had an impact on the alteration of chromosome number and structure during evolution and thus may have played a role in speciation.

The compartmentalization of genomes into chromosomes has provided opportunities for the development of specialized chromosomes. One such example is the B chromosome (often called supernumerary chromosome), and Houben et al. (Chap. 10) describe its structure, DNA composition, and evolution. The authors explain peculiarities in the behaviour of Bs during mitosis and meiosis and list various drive mechanisms responsible for retaining Bs in the population.

Sex chromosomes are another classic example of specialized chromosomes, and Janoušek et al. (Chap. 11) review sex determination systems in various plant groups and, based on taxonomic distribution, argue that dioecy has originated independently many times during evolution. The authors introduce the genus *Silene* as an excellent system to study the evolution of sex chromosomes and present the first ever evidence of sex dimorphism in dioecious plants.

Bureš et al. (Chap. 12) describe holocentric chromosomes which differ from the more common monocentric chromosomes by the way in which spindle microtubules attach along the whole chromosome length through kinetochores that cover a substantial part of their poleward surfaces during mitosis. They review the occurrence of holocentric chromosomes in plants and describe their chromatin structure and behaviour during mitosis and meiosis and the evolutionary processes that have contributed to the diversity of holocentric karyotypes.

The remaining three chapters in this section analyse karyotype diversity in three different groups of plants. Weiss-Schneeweiss and Schneeweiss (Chap. 13) provide a comprehensive account of karyotype diversity and evolutionary trends in angiosperms. They discuss in detail how changes in chromosome number, including dysploidy and aneuploidy, as well as changes in chromosome morphology contribute to the karyotype diversity observed. They also outline various cytogenetic methods which can be used to characterize chromosomes in a karyotype and study their changes during evolution and speciation. Murray (Chap. 14) presents a survey of chromosome numbers and size variation in gymnosperms, the sister group to angiosperms, and describes the methods used to analyse karyotype diversity in this group of seed plants. After reviewing available data, the author concludes that in contrast to angiosperms, gymnosperms are characterized by much greater uniformity in chromosome number and karyotype. The third chapter in this block is by Barker (Chap. 15) who focuses on karyotype and genome evolution in pteridophytes (monilophytes and lycophytes). He draws attention to the high chromosome numbers typical of many ferns, particularly the homosporous species, which on average contain over three-fold more chromosomes than the average flowering plant. Interestingly, there is currently no conclusive answer as to why this should be so although it is expected that the availability of complete genome sequences will contribute to solving this long-standing mystery.

Generative Polyploidy

The three chapters in this section evaluate various features of generative polyploidy, which is widespread in land plants. Husband et al. (Chap. 16) examine patterns of polyploid occurrence, such as the variation among taxonomic groups at or above the species level, intraspecific variation, variation in mechanisms of formation, geographic and ecological patterns of polyploid incidence, and associations between ploidy and reproduction.

Thanks to the advances in DNA sequencing and genomics there is now evidence to suggest that most seed plants have undergone at least one episode of polyploidization. Thus, one cannot consider the evolution of land plants without understanding polyploidy. Fawcett et al. (Chap. 17) explain how the episodes of ancient polyploidization can be identified and dated and describe the immediate consequences of polyploidization to genes and genomes. They also discuss changes within polyploid genomes during evolution and the contribution of polyploidization to the evolutionary success of descendant lineages.

While the majority of studies on polyploidy have focused on angiosperms, Rensing et al. (Chap. 18) consider the importance of polyploidy in haploid-dominant land plants, the bryophytes. Here, polyploidy may play an even more essential evolutionary role than in other evolutionary lineages, rendering a bryophyte more robust against somatic mutations, while changes in chromosome number through polyploidy can lead to changes in the sexual system. The need for more genomic data and model species is paramount and the sequencing of the genome of the moss *Physcomitrella patens* together with the eagerly anticipated genome sequences from other moss species and the liverwort *Marchantia polymorpha* in the near future should shed further light on genome evolution and the role of polyploidy in these haploid-dominant land plants.

Genome Size Diversity and Consequences

The book closes with chapters that consider the whole genome in bulk. Leitch and Leitch (Chap. 19) take advantage of the recent increase in the number of species with genome size data and provide a comprehensive review on diversity of genome sizes across all groups of land plants. Evaluation of individual groups suggests that most plant genomes are rather small, probably due to strong selection pressure to limit genome size. Importantly, the chapter also considers how the diversity in genome size might have evolved. The last chapter of this volume by Greilhuber and Leitch (Chap. 20) examines the phenotypic correlates of variation in genome size, which include cell size and cell division rate. It also discusses the theories to explain the causality behind this variation observed, considers alternative views, and puts important studies into focus.

There is no doubt that it was an ambitious goal to cover the broad range of biological phenomena related to the structure, function, and evolution of plant genomes. However, we were motivated by the lack of a single resource, which is so needed in this era of rapid DNA sequence data generation. The chapters included in this volume deliver exciting facts from the history and life of plant genomes and present unanswered questions and hypotheses. We hope that the readers will find that the time spent with the book is both enjoyable and stimulating.

This volume would not exist without the contribution of the authors of individual chapters. Busy leaders in their areas of research, they spared precious time to share with us their knowledge and visions. We cannot be grateful enough for this and we appreciate their efforts and patience when responding to our requests for revisions. The only reward for them may be a response from the readers. So why not contact them? Sincere thanks go to the publisher, Springer-Verlag, Vienna and New York, who initiated and accompanied this project and made the publication of this volume possible. We appreciate the careful and professional management of the project.

RBG Kew, United Kingdom
Vienna, Austria
Olomouc, Czech Republic
Ames, Iowa, USA
March, 2012

Ilija J. Leitch
Johann Greilhuber
Jaroslav Doležal
Jonathan F. Wendel

Contents

1	Angiosperm Phylogeny: A Framework for Studies of Genome Evolution	1
	Pamela S. Soltis and Douglas E. Soltis	
2	The Plant Nucleus at War and Peace: Genome Organization in the Interphase Nucleus	13
	R. Neil Jones and Tim Langdon	
3	The Organization of Genomic DNA in Mitotic Chromosomes: A Novel View	33
	Hideaki Takata, Sachihito Matsunaga, and Kazuhiro Maeshima	
4	Structural Organization of the Plant Nucleus: Nuclear Envelope, Pore Complexes and Nucleoskeleton	45
	Elena Kiseleva, Jindriska Fiserova, and Martin W. Goldberg	
5	The Plant Nucleolus	65
	Peter Shaw	
6	Cell Cycle Modules in Plants for Entry into Proliferation and for Mitosis	77
	Zoltán Magyar, Masaki Ito, Pavla Binarová, Binish Mohamed, and Laszlo Bogre	
7	Endopolyploidy in Plants	99
	Jolanta Maluszynska, Bozena Kolano, and Hanna Sas-Nowosielska	
8	Meiosis: Recombination and the Control of Cell Division	121
	Eric Jenczewski, Raphael Mercier, Nicolas Macaisne, and Christine Mézard	
9	Mechanisms of Chromosome Rearrangements	137
	Martin A. Lysák and Ingo Schubert	
10	Biology and Evolution of B Chromosomes	149
	Andreas Houben, Ali Mohammad Banaei-Moghaddam, and Sonja Klemme	
11	Chromosomes and Sex Differentiation	167
	Bohuslav Janoušek, Roman Hobza, and Boris Vyskot	
12	Holocentric Chromosomes	187
	Petr Bureš, František Zedek, and Michaela Marková	
13	Karyotype Diversity and Evolutionary Trends in Angiosperms	209
	Hanna Weiss-Schneeweiss and Gerald M. Schneeweiss	

14 Karyotype Variation and Evolution in Gymnosperms	231
Brian G. Murray	
15 Karyotype and Genome Evolution in Pteridophytes	245
Michael S. Barker	
16 The Incidence of Polyploidy in Natural Plant Populations: Major Patterns and Evolutionary Processes	255
Brian C. Husband, Sarah J. Baldwin, and Jan Suda	
17 Significance and Biological Consequences of Polyploidization in Land Plant Evolution	277
Jeffrey A. Fawcett, Yves Van de Peer, and Steven Maere	
18 Evolutionary Importance of Generative Polyploidy for Genome Evolution of Haploid-Dominant Land Plants	295
Stefan A. Rensing, Anna K. Beike, and Daniel Lang	
19 Genome Size Diversity and Evolution in Land Plants	307
Ilia J. Leitch and Andrew R. Leitch	
20 Genome Size and the Phenotype	323
Johann Greilhuber and Ilia J. Leitch	
Index	345

Contributors

Dr. Sarah J. Baldwin Department of Integrative Biology, University of Guelph, Guelph, ON, Canada

Michael S. Barker Department of Ecology & Evolutionary Biology, University of Arizona, Tucson, USA, msbarker@email.arizona.edu

Dr. Anna K. Beike Plant Biotechnology, Faculty of Biology, University of Freiburg, Freiburg, Germany

Dr. Pavla Binarová Institute of Microbiology, ASCR, Prague 4, Czech Republic

Prof. Laszlo Bogre Royal Holloway, University of London, Centre for Systems and Synthetic Biology, Egham, UK, l.bogre@rhul.ac.uk

Prof. RNDr. Petr Bureš Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic, bures@sci.muni.cz

Dr. Jeffrey A. Fawcett Graduate University for Advanced Studies, Hayama, Kanagawa, Japan

Dr. Jindriska Fiserova Department of Biological and Biomedical Sciences, Durham University, Durham, UK

Dr. Martin W. Goldberg Department of Biological and Biomedical Sciences, Durham University, Durham, UK

Prof. Johann Greilhuber Department of Systematic and Evolutionary Botany, Faculty of Life Sciences, University of Vienna, Vienna, Austria

Dr. Roman Hobza Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic

Dr. Andreas Houben Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, houben@ipk-gatersleben.de

Prof. Dr. Brian C. Husband Department of Integrative Biology, Science Complex, University of Guelph, Guelph, ON, Canada, bhusband@uoguelph.ca

Dr. Masaki Ito Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan

Dr. Bohuslav Janoušek Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic

Dr. Eric Jenczewski Institut Jean-Pierre Bourgin, Institut National de Recherche Agronomique, cedex, France

Prof. R. Neil Jones Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Wales, UK, rnj@aber.ac.uk

Dr. Elena Kiseleva Laboratory of Morphology and Function of Cell Structure, Institute of Cytology and Genetics, Novosibirsk, Russia, elka@bionet.nsc.ru

Dr. Sonja Klemme Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Chromosome Structure and Function Laboratory, Gatersleben, Germany

Dr. Bozena Kolano Department of Plant Anatomy and Cytology, University of Silesia, Katowice, Poland

Dr. Daniel Lang Plant Biotechnology, Faculty of Biology, University of Freiburg, Freiburg, Germany

Dr. Tim Langdon Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Wales, UK

Prof. Andrew R. Leitch School of Biological and Chemical Sciences, Queen Mary, University of London, London, UK

Dr. Iia J. Leitch Jodrell Laboratory Royal Botanic Gardens, Kew, Richmond, Surrey, UK, I.Leitch@kew.org

Dr. Martin Lysák Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czech Republic, lysak@sci.muni.cz

Dr. Nicolas Macaisne Institut Jean-Pierre Bourgin, Institut National de Recherche Agronomique, Versailles, cedex, France

Prof. Steven Maere Department of Plant Systems Biology, VIB, Ghent, Belgium, stmae@psb.vib-ugent.be

Dr. Kazuhiro Maeshima Laboratory for Biological Macromolecules, Structural Biology Center, National Institute of Genetics, Mishima, Shizuoka, Japan, kmaeshim@lab.nig.ac.jp

Dr. Zoltán Magyar Institute of Plant Biology, Biological Research Centre, Szeged, Hungary

Prof. Jolanta Maluszynska Department of Plant Anatomy and Cytology, University of Silesia, Katowice, Poland, jolanta.maluszynska@us.edu.pl

Dr. Michaela Marková Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic

Dr. Sachihiko Matsunaga Department of Biotechnology, Graduate School of Engineering, Osaka University, Suita, Osaka, Japan

Dr. Raphael Mercier Institut Jean-Pierre Bourgin, Institut National de Recherche Agronomique, Versailles, cedex, France

Prof. Christine Mézard Station de Génétique et d'Amélioration des Plantes, Versailles, France, Christine.Mezard@versailles.inra.fr

Dr. Binish Mohamed Royal Holloway, University of London, Centre for Systems and Synthetic Biology, Egham, UK

Dr. Ali Mohammad Banaei Moghaddam Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

Prof. Brian G. Murray School of Biological Sciences, University of Auckland, Auckland, New Zealand, b.murray@auckland.ac.nz

Dr. Stefan A. Rensing FRISYS, Faculty of Biology, University of Freiburg, Freiburg, Germany, stefan.rensing@biologie.uni-freiburg.de

Prof. Ingo Schubert Leibniz Institute of Plant Genetics and Crop Plant Research (IPK),
Gatersleben, Germany

Dr. Hanna Sas-Nowosielska Department of Plant Anatomy and Cytology, University of
Silesia, Katowice, Poland

Prof. Gerald M. Schneeweiss Department of Systematic and Evolutionary Botany, Faculty
Center Botany, University of Vienna, Vienna, Austria

Dr. Peter Shaw Cell and Developmental Biology Department, John Innes Centre, Norwich,
UK, peter.shaw@bbsrc.ac.uk

Prof. Douglas E. Soltis Department of Biology and the Genetics Institute, University
of Florida, Gainesville, FL, USA, dsoltis@botany.ufl.edu

Prof. Pamela S. Soltis Laboratory of Molecular Systematics and Evolutionary Genetics,
Florida Museum of Natural History, University of Florida, Gainesville, FL, USA,
psoltis@flmnh.ufl.edu

Prof. Jan Suda Department of Botany, Faculty of Science, Charles University in Prague,
Prague, Czech Republic

Dr. Hideaki Takata Biological Macromolecules Laboratory, Structural Biology Center,
National Institute of Genetics, Mishima, Shizuoka, Japan

Prof. Yves Van de Peer Department of Plant Systems Biology, VIB, Ghent, Belgium, yves.
vandepeer@psb.vib-ugent.be

Prof. Boris Vyskot Institute of Biophysics, Czech Academy of Sciences, Laboratory of
Plant Developmental Genetics, Brno, Czech Republic, vyskot@ibp.cz

Prof. Hanna Weiss-Schneeweiss Department of Systematic and Evolutionary Botany,
Faculty Center Botany, University of Vienna, Vienna, Austria, Hanna.Weiss@univie.ac.at

Dr. František Zedek Department of Botany and Zoology, Faculty of Science, Masaryk
University, Brno, Czech Republic

