

PREFACE

The present volume is part of a comprehensive series of books of the «*Advances in Botanical Research*» that will describe the genome organization of photosynthetic bacteria up to land plants. This volume focuses on mitochondrial genome evolution in photosynthetic organisms. It includes 12 chapters written by internationally recognized authors.

The opening chapter by B. Franz Lang is logically dedicated to "Mitochondrial and eukaryotic origins". The symbiotic introduction of mitochondria that occurred some one billion years ago represents a key event in eukaryotic evolution. The origin of the eukaryotic cell and of mitochondria has intrigued life scientists for many decades. However, remaining traces are difficult to find and speculative evolutionary theories for the origin of eukaryotes and mitochondria have been developed. Several lines of evidence support that mitochondria originate from an α -proteobacterial symbiont. In this chapter, B. Franz Lang is going to discuss how the close α -proteobacterial outgroup not only improves the phylogenetic resolution of the mitochondrial heritage but also allows addressing question on eukaryotic origins. Exciting questions on the first emergence of mitochondria in eukaryotes will be presented and the two major hypotheses on the origin of eukaryotes, the "serial endosymbionts" and the symbiogenesis" hypotheses will be deeply discussed.

Present-day mitochondrial genomes have mostly nothing in common in term of form organization, expression and gene content with the ancestral bacterial genome from which they derive. Among the different forces responsible for the evolution of plant mitochondrial genomes, the loss and transfer of genes to the nucleus or the acquisition of foreign DNA play a crucial role. This is the topic of the two following chapters. In their contribution entitled "Gene content and gene transfer from mitochondria to the nucleus during evolution", Minoru Ueda and Koh-ichi Kadowaki discuss insights into gene transfer and substitution revealed by comparative genomic analysis. During the process of gene transfer from the mitochondria to the nucleus, transferred mitochondrial genes must undergo several changes to be expressed in the nuclear DNA. They present interesting data showing that studying the mitochondrial genome of angiosperms is a powerful way to understand the steps leading to a complete gene transfer. In the contrary, plant mitochondrial DNA can acquire foreign DNA either

from the plastidial or the nuclear genomes *via* intracellular transfer or from other species *via* horizontal transfer. In the third chapter, Kanika Jain, Nancy J.G. Hepburn and Jeffrey P. Mower explain the "Role of horizontal transfer in shaping plant mitochondrial genomes". The role played by parasitic plants, the importance of recombination events and the fixation of the transferred gene by drift in the mechanisms of transfer will be tackled. Beyond the evolutionary significance of such process, it is obvious that understanding mechanisms of transfer into mitochondria could offer clues for a still missing plant mitochondrial transformation system.

As emphasized above, mitochondrial function depends on the coordinate action of nuclear and mitochondrial genomes. One of the best examples to illustrate the importance of mitochondrial-nuclear interaction is the trait cytoplasmic male sterility (CMS). CMS is determined by plant mitochondrial genomes and many mitochondrial genes that determine CMS can be suppressed or counteracted by the products of one or more nuclear genes known as restorer-of-fertility genes. This CMS trait has been found and is used in numerous crop species for hybrid production. In the fourth chapter entitled "Mitochondrial genome evolution and gynodioecy", Pascal Touzet explains how the coexistence of female and hermaphrodite plants, a process called gynodioecy, is under the nuclear-cytoplasmic control implicating CMS genes and nuclear restorers. From an evolutionary point of view, the effect of the dynamics of gynodioecy on mitochondrial diversity and the question whether gynodioecy contributes to the fast evolution of CMS mitochondrial genomes is tackled. Our knowledge on the importance of mitochondrial-nuclear interactions in evolutionary issues is now expanded rapidly. Françoise Budar and Sota Fujii in their contribution "Cyto-nuclear adaptation in plants" also provide several lines of evidence demonstrating how the co-evolution of organellar (mitochondrial and also plastidial) and nuclear genomes led to the co-adaptation of the different genetic compartments at the species level. In a first part, they present the mechanisms underlying this co-adaptation and illustrate them by experimental data. In a second part, the question of the contribution of organelle genomes to the adaptation of plants to their environment in frame of the cyto-nuclear co-adaptation process is tackled. Improving our knowledge in this domain of research will undoubtedly be of crucial importance for crop improvement and breeding strategies in a near future.

In chapter 6, intriguing features of the "Mitochondrial genomes of photosynthetic euglenids and alveolates" are presented by Pavel Flegontov

and Julius Lukes. The world of protists illustrates well the huge eukaryotic diversity. Euglenida belong to the eukaryotic supergroup Excavata, the members of which possess the most varied mitochondrial genomes in terms of their structure and gene content. Another interesting feature of the Euglenida is the presence of a green plastid acquired by secondary endosymbiosis. The major peculiarities of the mitochondrial genome of the most studied member of Euglenida, *Euglena gracilis*, will be detailed here. On the other hand, photosynthetic dinoflagellates and parasitic apicomplexans with a relic plastid constitute a large and diverse group within alveolates. All species of this group share the most reduced mitochondrial genome found. Very “bizarre” non-canonical features in structure and expression will be presented. From the contribution of P. Flegontov and J. Lukes, an evolutionary picture that emerges is that of convergent evolution of radically reduced mitochondrial genomes.

Another very exciting example of the evolutionary history of plant mitochondrial genomes is linked to the existence of introns. In the following chapter, Linda Bonen summarizes the “Evolution of mitochondrial introns in plants and photosynthetic microbes”. Two types of introns, categorized as group I or group II according to their distinctive structural properties, play a crucial role in mitochondrial gene expression. Thanks to the huge amount of mitochondrial genome sequences obtained over recent years, the importance of introns in mitochondrial gene expression has been strengthened. The behavior of introns, the machineries required for their splicing, the relationships between splicing and other expression events in mitochondria and their potential roles are highlighted here.

Among eukaryotes, the group Archaeplastidia contains the photosynthetic organisms. They can be classified into three lineages, namely Glaucophyta, Rhodophyta and Chloroplastidia. Among the latter lineage belong higher plants and green algae. Chapter 8 written by Elizabeth Rodriguez-Salinas, Claire Remacle and Diego Gonzales-Halphen and entitled “Green algae genomics: a mitochondrial perspective” is entirely devoted to green algae mitochondrial genomes. Quite surprisingly, the increasing number of fully sequenced mitochondrial genomes of green algae revealed an extraordinary diversity in their genome organization, structure and gene content. This information, in synergy with the sequences of the plastidial and nuclear genomes of green algae, helps us to understand the phylogenetic relationships among green algae, the interconnection between their mitochondria and chloroplasts, their mitochondrial metabolic plasticity and their adaptative advantages. Green algae represent a biomass that appears to be

more and more important for energy and food production. Deciphering the fundamental processes of the evolution and function of their mitochondria as well as their interaction with the other compartments of the cells represent major challenges for the next following years.

Dysfunction of mitochondrial DNA inheritance often results in detrimental phenotypes such as CMS. During evolution, plant mitochondria (and chloroplasts) have developed several strategies to maintain the integrity of the organellar genomes. In chapter 9 entitled «Recombination in the stability, repair and evolution of the mitochondrial genome», Kristina Kühn and José Gualberto describe our present knowledge on these processes. In particular, recombination processes seem to play central roles in mitochondrial DNA repair and replication. Deregulation of recombination in organelles results in genomic instability. The different recombination pathways (e.g. frequent recombination via large repeated sequences, ectopic recombination involving medium size repeats or illegitimate recombination involving sequence microhomologies), the occurrence of alternative mitochondrial DNA configurations and its dynamic nature will be discussed here as well as the multiple factors that act in these pathways to maintain plant mitochondrial DNA.

The following chapter "Mitochondrial genome evolution and the emergence of PPR proteins" deals with the evolutionary history and diversity of the pentatricopeptide repeat (PPR) proteins. In this contribution Bernard Gutmann, Anthony Gobert and Philippe Giegé highlight the most exciting recent developments related to the huge PPR family. Three main features of higher plant mitochondria are the occurrence of very large genomes, the existence of specific gene expression processes such as splicing and RNA editing and the very high numbers of PPR proteins as compared to other eukaryotes (80 times more PPR genes in higher plants than in animal genomes). As emphasized by the authors, the incidence of these features should not be considered as independent but should rather be regarded as evolutionary connected phenomena. The huge PPR protein family was discovered only ten years ago in plants, but is clearly one of the most fascinating families of proteins working in plant organelles and this timely review relates their evolution in relation with the occurrence of the specific gene expression processes existing in plant mitochondria.

Present-day mitochondrial genomes only contain a very limited set of genes (e.g. about 35 protein-coding and 20 structural RNA-coding genes in *Arabidopsis* mitochondrial DNA). As plant mitochondria contain more than 1000 proteins, the biogenesis and the function of mitochondria mainly rely

on the expression of nuclear-encoded genes. Thus, the majority of mitochondrial proteins and a small number of transfer RNAs (tRNAs) are imported from the cytosol to the organelle. Therefore a crucial evolutionary step was the establishment of specific intracellular macromolecule trafficking, processing and assembly machinery to allow the come back of proteins and RNAs into the organelle. Furthermore, in plants, the presence of another organelle of cynaobacterial origin, the chloroplast that also imports most of its proteins, leads to an even more complex situation. The two last chapters of this volume are devoted to protein and RNA mitochondrial import in plants. Monika Murcha, Elzbieta Glaser and James Whelan in their section "Evolution of protein import pathways" present a very detailed analysis on the targeting peptides, the signal recognition and the processing steps of mitochondrial proteins. They also offer a wide overview on the different components and multiple machineries that emerged during evolution to translocate mitochondrial proteins across the double mitochondrial membrane. The second contribution in this research field written by Morgane Michaud and Anne-Marie Duchêne and entitled "Macromolecules trafficking to plant mitochondria" gave more emphasis on three other important aspects of macromolecule trafficking. First, they focus on the phenomenon of dual targeting of proteins to mitochondria and chloroplasts, which raises interesting questions for inter-organelle communication. Second, they present the latest developments in an emerging area of research that is the subcellular localization of cytosolic mRNAs to the vicinity of mitochondria. This offers new perspectives in the biogenesis of mitochondria in the plant cells, but the implicated processes are still largely unknown. Finally, the importance of tRNA mitochondrial import for the plant mitochondrial translation machinery, and our present knowledge on the mechanisms implicated are described.

As a whole, this up-to-date book covers a wide range of topics, and must therefore form an authoritative reference in the field for years to come. It will be useful for a wide range of students and for scientists wishing to follow progress not only inside but also outside their own specialized field.