Preface

There are several reasons why recent research in the field of the genome and chromosomes in reptiles is in the focus of interest. Reptiles occupy a key position in the evolution of terrestrial vertebrates, not to forget that both mammals and birds have reptile-like ancestors in common. Their evolutionary history is well-known thanks to the existing meticulous fossil records. Reptilia show wide morphological and ecological differences, with forms adapted to broadly diverse environments. A large amount of data has been collected defining their biogeography, ecology, reproductive biology, and physiology. Their sex differentiation system is particularly complex, ranging from strict genetic determination with or without differentiated sex chromosomes to strict thermal determination.

The pioneer studies of reptilian cytogenetics date back to the 1920s, when Dalq and Painter published the karyotype of *Anguis* and *Anolis*, respectively. For the first time, these studies demonstrated the presence of macrochromosomes and microchromosomes. Subsequent research until the 1970s, especially on chromosomes morphology, provided relevant data on the phylogenesis of this class.

Paying special attention to the genome composition, which began in the early 1980s, researchers suggested their nature as a transitional group between anamniotes and amniotes.

Molecular studies, mainly phylogenetic analyses with mitochondrial and nuclear genes, have recently been gathering pace, yielding important data and disclosing novel scenarios on phyletic relationships and the taxonomy of the different reptilian taxa. Albeit still quite limited (only the genome of *Anolis* has been completely se-

quenced), genome sequencing is also providing important insights. New methods, allowing the isolation specific DNA sequences and detecting gene localization on chromosomes using FISH techniques, are further advancing our understanding of reptiles.

This themed issue collects contributions on diverse facets of reptilian cytogenetics and genomics, reporting on the current state of our knowledge of the genome and chromosomes of living reptiles.

The introducing aspect concentrates on the study of the genome's structure by a phylogenomic approach based on the analysis of two proto-oncogenes and the study of the presence and evolution of transposable elements. Another interesting topic is the role of molecular and chromosomal variations in phylogenetic processes. Among these studies, the description of the wide inter- and intraspecific chromosomal variability of the iguanid *Sceloporus*, and their possible role in speciation, is of great interest.

While concentrating on the structure of reptile chromosomes, stimulating progress in research, such as the isolation of specific sequences and chromosome painting studies, led to the first cytogenetic maps of taxa, such as crocodiles, lizards and *Sphenodon*.

One of the most extensively investigated issues in this class is the sex determination mechanism and the possible involvement of chromosomes in this process. The papers addressing this aspect highlight the coevolutionary interaction between sex chromosomes and genome organization. As in lizards, sex determination may result from an interplay between sex chromosomes and temperature.

Squamate reptiles are the only vertebrates exhibiting true, naturally occurring parthenogenesis. The chromosome studies reported in this section confirm the hybrid origin of parthenogenetic lizards and offer opportunities to study functional genomics and the disruption of co-evolved gene complexes in a potentially perpetual hybrid background.

Finally, the last contributions address some particular aspects such as a rare case of mosaicism in a turtle and the cytogenetic characterization of established primary cell cultures in snakes and crocodiles.

I am grateful to the authors who have participated in this themed issue. Their excellent scientific contributions illustrate the high level achieved by reptilian cytogenetics and genomics and the encouraging prospects for research in these exciting fields of endeavour. I also thank the reviewers for their competent examination of the papers invited to this special issue. Finally, I am indebted to the Chief Editors of *Cytogenetic and Genome Research* for the opportunity to edit this themed issue.

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