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## Preface

No other animal group has gained importance for society and environment to the extent ruminants (cattle and relatives) have. Accordingly, the attention they receive in science, public and politics is vast and conveys the picture of an excessively explored faunal element known in any conceivable aspect. However, this only applies to a very restricted taxonomical and thematic scope and cannot be generalized for Ruminantia in its entirety. In fact, the range of adaptations displayed by this predominant group of large-sized land animals, and their modern diversity encompassing the >1000 kg giraffe and the <1 kg mouse deer, the speciose antelopes and monotypic pronghorn, and the circumpolar reindeer to the desert-inhabiting Addax, render the ruminants, ironically, an understudied taxon with regard to many aspects of their biology. On the other hand, extinctions of several taxa in recent historical times and many highly endangered species let us fear that we will never be able to exhaustively research extant ruminant diversity and biology.

From an evolutionary point of view, ruminants represent the thriving part of terrestrial artiodactyls; with over 3 billion individuals and a possible total species number of more than 300 they are the most abundant and diverse group of large land animals. Yet, the phylogenesis of ruminants - their lines of descent or the superordinate macroevolutionary process linking all specific characteristics of their organismic, organic, and molecular levels through deep time - remains incompletely understood. Its reconstruction is a challenging task because of the number of species, data, and homoplasies, as the many competing hypotheses show. The fossil record documents 45 million years of diversification including several key radiations, each marking important steps in ruminant cladogenesis. Almost 25 million years of this history occurred before the origin of the crown clades. This long history of radiation and extinction makes ruminants an ideal group for the study of many aspects of evolutionary theory, including selection and speciation processes. The accomplishments of molecular sciences led to a revival of phylogenetic analyses of living ruminants and augmented a new line of evidence to the classical morphological one. Advances in genome sequencing and computational phylogenetics have yielded new forms of data and methodologies. In some instances, this has helped to support and resolve previous results. In others, it has enlarged the variety of phylogenetic reconstructions and created conflicts with palaeontological data. The time has come for a closer interaction between disciplines, substantial increase in species and data sampling, and the inclusion of areas that have been neglected in previous studies (e.g. soft tissue biology, behaviour) to establish a coherent and logical synthesis of this enormous quantity of data.

In this context, the International Conference on Ruminant Phylogenetics, held on 3-6 September 2014 in Munich at the GeoBio-Center<sup>LMU</sup>, was intended to function as the initial event towards a concerted transdisciplinary effort to overcome deficits in ruminant phylogenetics. More than 60 ruminant experts from all over the world represented anatomy, palaeontology, neontology, genetics, physiology, behavioural biology, evolutionary biology, population biology, and conservation biology. As anticipated, the meeting promoted vigorous debate on crucial issues at an interdisciplinary level. Through these discussions, insight was gained that allowed for a few controversies in ruminant phylogenetics to be resolved. More importantly, critical deficiencies were recognized and collaborative efforts initiated to address them. We, the scientific organizing committee, hope that this meeting serves as a start-up for more in the future.

The present volume includes original contributions to the conference, with benefit from subsequent discussions and review. These articles include reviews on the state of certain fields, new results, and critical inspections on nomenclatorial, taxonomical, and analytical issues.

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