Genome contains a set of genetic instructions coded in the form of just four letters (A, C, G, T) which defines the basic behavior of every plant species. Since the discovery of DNA, researchers have continuously been trying to understand the instructions encoded in the genome and finding out ways to manipulate these instructions for achieving desirable phenotype in a crop species. The pace of such understanding for desirable traits in peanut has been extensively slow because of the genetic complexity and large-sized genome. The availability of reference genome sequences for both the diploid progenitor species has provided acceleration to this process of understanding and deploying modern approaches for candidate gene discovery and marker development for key traits in peanut. Genomics research has revolutionized the pace of genetics and breeding research due to low-cost sequencing and high throughput genotyping technologies. These resources not only helped in developing better understanding the basic biology of the crop plants but also used together with other genetic resources for developing genomics tools to deploy them in breeding for developing improved varieties.

The peanut, also known as groundnut (*Arachis hypogaea*), is an important legume crop mainly utilized for cooking oil and confectionary and table purpose. This crop is widely cultivated in >100 countries with a total production of million tons during 2014. The cultivated peanut came into existence from hybridization between two diploid species (*A. duranensis* and *A. ipaensis*) possessing different genomes. The current understanding is that the hybridization event gave rise initially to a wild form of tetraploid peanut species, *A. monticola*, which after the long domestication process gave rise to the cultivated tetraploid species, dramatically different from its wild relatives. This crop has unique feature of geotropism and skotomorphogenesis, i.e., flowering happens above ground and seed development happens below the ground. The year 2016 has been a very significant year for peanut research community as reference genome sequence for both the diploid progenitors as well as a high throughput genotyping array with 56K single nucleotide polymorphisms (SNPs) have become available for genomics studies, candidate gene discovery, high resolution trait-mapping, and marker development and breeding.

This book is very timely in peanut as part of the genome compendium series for different crops. It contains 11 different chapters providing detailed overview on different aspects of botanical classification, genetics, genomics,
and breeding. This book not only provides information on recent advances on genome sequencing, genome architecture, genetic mapping for few traits and marker identification, but also presents case studies of developing molecular breeding products for foliar diseases, nematode resistance, and oil quality.

A total of 30 authors from Argentina, Brazil, China, India, and USA have contributed 11 chapters for this volume (see “Contributors”). The editors of this volume are grateful to all the authors for their contribution in writing chapters of high quality of their area of expertise and reviewers (see “Reviewers”) for their constructive suggestions and corrections helping in improving the quality of the chapters further. The editors are also thankful to Dr. David Bergvinson, Director General, ICRISAT and Dr. Peter Carberry, Deputy Director General—Research, ICRISAT for their support. The editors thank Prof. C. Kole, Series Editor for his invitation and help in editing this volume. The cooperation received from Abirami Purushothaman, Jegadeeswari Diravidamani and Nareshkumar Mani from Springer has been a great help in completion of this book and is gratefully acknowledged. The cooperation and encouragement from publisher have been of great help in completion of this book and are gratefully acknowledged.

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We hope that our efforts in compiling the information on different aspects of peanut will help the peanut genomics and breeding researchers in developing better understanding and research strategies. This book will also benefit students, academicians, and policy makers in updating their knowledge on recent advances in peanut research.

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